

**TABLE 1: GENES IN THE APPLICATION**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXN03097	VW0062	3	557	AMMONIUM TRANSPORT SYSTEM
3	4	RXA02099	GR00630	6198	6470	AMMONIUM TRANSPORT SYSTEM
5	6	RXA00104	GR00014	15895	16650	CYSQ PROTEIN, ammonium transport protein

### Polyketide Synthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
7	8	RXA01420	GR00416	775	17	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.-.-.-)
9	10	RXN02581	VW0098	30482	28623	POLYKETIDE SYNTHASE
11	12	F RXA02581	GR00741	1	1527	POLYKETIDE SYNTHASE
13	14	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
15	16	RXA01138	GR00318	1656	2072	ACTINORHODIN POLYKETIDE DIMERASE (EC -.-.-.-)
17	18	RXA01980	GR00573	1470	838	POLYKETIDE CYCLASE
19	20	RXN01007	VW0021	2572	866	FRNA
21	22	RXN00784	VW0103	27531	28265	FRNE

### Fatty acid and lipid synthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXA02335	GR00672	550	2322	BIOTIN CARBOXYLASE (EC 6.3.4.14)
25	26	RXA02173	GR00641	7473	8924	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (EC 6.4.1.2)
27	28	RXA01764	GR00500	2178	3110	3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
29	30	RXN02487	VW0007	6367	4664	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
31	32	F RXA02487	GR00718	4937	4650	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
33	34	F RXA02490	GR00720	817	5	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
35	36	RXA01467	GR00422	920	1210	ACYL CARRIER PROTEIN
37	38	RXA00796	GR00212	202	5	Acyl carrier protein phosphodiesterase
39	40	RXA01897	GR00544	617	1159	Acyl carrier protein phosphodiesterase
41	42	RXN02809	VW0342	380	6	Acyl carrier protein phosphodiesterase
43	44	F RXA02809	GR00790	277	5	Acyl carrier protein phosphodiesterase
45	46	RXN00113	VW0129	103	5724	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41;
47	48	F RXA00113	GR00017	2	3295	FATTY-ACID SYNTHASE (EC 2.3.1.85)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
49	50	RXN03111	VW0084	6040	5	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
51	52	F RXA00158	GR00024	2088	4	FATTY ACID SYNTHASE (EC 2.3.1.85)
53	54	F RXA00572	GR00155	2	3832	FATTY ACID SYNTHASE (EC 2.3.1.85)
55	56	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
57	58	RXA02691	GR00754	15347	14541	FATTY ACYL RESPONSIVE REGULATOR
59	60	RXA00880	GR00242	6213	8057	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
61	62	RXA01060	GR00296	9566	10489	OMEGA-3 FATTY ACID DESATURASE (EC 1.14.99.-)
63	64	RXN01722	VW0036	2938	1214	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
65	66	F RXA01722	GR00488	5746	4022	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
67	68	RXA01644	GR00456	9854	8577	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
69	70	RXA02029	GR00618	356	1669	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
71	72	RXA01801	GR00509	3396	2380	ENOYL-COA HYDRATASE (EC 4.2.1.17)
73	74	RXN02512	VW0171	16147	15185	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
75	76	F RXA02512	GR00721	3303	4259	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
77	78	RXA00899	GR00245	1599	2864	CARDIOLIPIN SYNTHETASE (EC 2.7.8.-)
79	80	RXN00819	VW0054	18127	19455	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
81	82	F RXA00819	GR00221	18	1007	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
83	84	F RXA01766	GR00500	4081	4371	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
85	86	RXN01762	VW0054	15318	13783	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
87	88	F RXA01762	GR00500	1272	10	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
89	90	RXA00681	GR00179	3405	2662	3-OXOACYL-JACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
91	92	RXA00802	GR00214	3803	4516	3-OXOACYL-JACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
93	94	RXA02133	GR00639	3	308	3-OXOACYL-JACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
95	96	RXN01114	VW0182	9118	10341	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
97	98	F RXA01114	GR00308	2	793	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
99	100	RXA01894	GR00542	1622	2476	PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41)
101	102	RXA02599	GR00742	3179	3655	PHOSPHATIDYLGLYCEROPHOSPHATE B (EC 3.1.3.27)
103	104	RXN02638	VW0098	54531	53656	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
105	106	F RXA02638	GR00749	8	511	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
107	108	RXA00856	GR00232	720	1256	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
109	110	RXA02511	GR00721	2621	3277	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
111	112	RXN02836	VW0102	32818	33372	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
113	114	F RXA02836	GR00827	106	411	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
115	116	RXA02578	GR00740	2438	3541	PUTATIVE ACYLTRANSFERASE
117	118	RXA02150	GR00639	18858	19658	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
119	120	RXA00607	GR00160	1869	2249	POLY(3-HYDROXYALKANOATE) POLYMERASE (EC 2.3.1.-)
121	122	RXA02397	GR00698	1688	2683	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
123	124	RXN03110	VW0083	16568	17929	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
125	126	F RXA00660	GR00171	1027	5	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
127	128	RXA00801	GR00214	3138	3770	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
129	130	RXA00821	GR00221	1469	2311	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
131	132	RXN02966	VW0143	12056	13462	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
133	134	F RXA01833	GR00517	1666	260	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
135	136	RXA01853	GR00525	5561	5010	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)

137	138	RXN02424	VW0116	10570	11169	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
139	140	F RXA02424	GR00706	808	428	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
141	142	RXN00419	VW0112	1024	266	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
143	144	F RXA00419	GR00095	3	464	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
145	146	F RXA00421	GR00096	565	723	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
147	148	RXN02923	VW0088	3301	2564	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
149	150	RXN02922	VW0321	11407	10328	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
151	152	RXN03065	VW0038	6237	6629	Holo- $\beta$ -ACYL-CARRIER PROTEIN[IN] SYNTHASE (EC 2.7.8.7)
153	154	RXN03132	VW0127	39053	39472	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
155	156	RXN03157	VW0188	1607	1170	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB (AE000805) LPS biosynthesis RfbU related protein [Methanobacterium thermoautotrophicum]
157	158	RXN00934	VW0171	15181	14099	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
159	160	RXN00792	VW0321	10328	9132	ACYL-COA THIOESTERASE II (EC 3.1.2.-)
161	162	RXN00931	VW0171	13011	12166	thioesterase II
163	164	F RXA00931	GR00253	4959	4114	ACYLTRANSFERASE (EC 2.3.1.-)
165	166	RXN01421	VW0122	16024	15638	BIOTIN-- $\beta$ -ACETYL-COA-CARBOXYLASE] SYNTHETASE (EC 6.3.4.15)
167	168	RXN02342	VW0078	3460	4266	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
169	170	RXN00563	VW0038	1	2739	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
171	172	RXN02168	VW0100	2894	81	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
173	174	RXN01090	VW0155	6483	5686	Lipopolysaccharide N-acetylglucosaminyltransferase
175	176	RXN02062	VW0222	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
177	178	RXN02148	VW0300	16561	17703	Lipopolysaccharide N-acetylglucosaminyltransferase
179	180	RXN02595	VW0098	11098	9935	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
181	182	RXS00148	VW0167	9849	12059	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)
183	184	RXS00149	VW0167	7995	9842	LIPOATE-PROTEIN LIGASE A (EC 6.-.-.-)
185	186	RXS02106	VW0123	22649	21594	LIPOATE-PROTEIN LIGASE B (EC 6.-.-.-)
187	188	RXS01746	VW0185	934	1686	LIPOIC ACID SYNTHETASE
189	190	RXS01747	VW0185	1826	2869	protein involved in lipid metabolism
191	192	RXC01748	VW0185	3001	3780	Cytosolic Protein involved in lipid metabolism
193	194	RXC00354	VW0135	33604	32792	Membrane Spanning Protein involved in lipid metabolism
195	196	RXC01749	VW0185	3953	5569	

## Fatty acid degradation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXA02268	GR00655	2182	3081	LIPASE (EC 3.1.1.3)
199	200	RXA02269	GR00655	3094	4065	LIPASE (EC 3.1.1.3)
201	202	RXA01614	GR00449	8219	7197	LYSOPHOSPHOLIPASE L2 (EC 3.1.1.5)
203	204	RXA01983	GR00573	3559	3053	LIPASE (EC 3.1.1.3)
205	206	RXN02947	VW0078	1319	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
207	208	F RXA02320	GR00667	593	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
209	210	F RXA02851	GR00851	524	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
211	212	RXN02321	VW0078	3291	1663	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
213	214	F RXA02321	GR00667	1380	937	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
215	216	F RXA02343	GR00675	1403	1816	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
217	218	F RXA02850	GR00850	2	493	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
219	220	RXA02583	GR00741	6743	8290	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
221	222	RXA00870	GR00239	809	2320	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27) 2-Methyl-3-oxopropanoate:NAD <sup>+</sup> oxidoreductase (CoA-propanoylating)
223	224	RXA01260	GR00367	2381	1200	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
225	226	RXA01261	GR00367	2607	2437	LIPAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
227	228	RXA01136	GR00318	685	1116	ISOVALERYL-COA DEHYDROGENASE (EC 1.3.99.10)
229	230	RXN00559	VW0103	7568	6552	PROTEIN VDLD
231	232	F RXA00559	GR00149	218	6	PROTEIN VDLD
233	234	RXA01580	GR00440	707	6	Glycerophosphoryl diester phosphodiesterase
235	236	RXA02677	GR00754	3119	3877	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
237	238	RXS01166	VW0117	18142	16838	EXTRACELLULAR LIPASE PRECURSOR (EC 3.1.1.3)

## Terpenoid biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
239	240	RXA00875	GR00241	2423	1857	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2)
241	242	RXA01292	GR00373	1204	2388	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
243	244	RXA01293	GR00373	2370	2696	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
245	246	RXA02310	GR00665	1132	2394	GERANYLGERANYL HYDROGENASE
247	248	RXA02718	GR00758	18539	19585	GERANYLGERANYL PYROPHOSPHATE SYNTHASE (EC 2.5.1.1)
249	250	RXA01067	GR00298	1453	2181	undecaprenyl-diphosphate synthase (EC 2.5.1.31)
251	252	RXA01269	GR00367	20334	19894	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
253	254	RXA01205	GR00346	3	533	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXA01576	GR00438	8053	8811	DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE (EC 2.4.1.117)
257	258	RXN02309	VW0025	28493	29542	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
259	260	F RXA02309	GR00665	978	4	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
261	262	RXN00477	VW0086	38905	37262	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
263	264	F RXA00477	GR00119	13187	11544	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
265	266	RXA00478	GR00119	14020	13190	PHYTOENE SYNTHASE (EC 2.5.1.-)
267	268	RXA01291	GR00373	345	1277	PHYTOENE SYNTHASE (EC 2.5.1.-)
269	270	RXA00480	GR00119	17444	16329	FARNESYL DIPHOSPHATE SYNTHASE (EC 2.5.1.1) (EC 2.5.1.10)
271	272	RXS01879	VW0105	1505	573	isopentenyl-phosphate kinase (EC 2.7.4.-)
273	274	RXS02023	VW0160	3234	4001	P450 cytochrome, isopentenyltransf. ferridox
275	276	RXS00948	VW0107	4266	5384	12-oxophytodienoate reductase (EC 1.3.1.42)
277	278	RXS02228	VW0068	1876	2778	TRNA DELTA(2)-ISOPENTENYLPYROPHOSPHATE TRANSFERASE (EC 2.5.1.8)
279	280	RXC01971	VW0105	4545	3715	Metal-Dependent Hydrolase involved in metabolism of terpenoids
281	282	RXC02697	VW0017	31257	32783	membrane protein involved in metabolism of terpenoids



# ABC-Transporter

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
283	284	RXN01946	VV0228	2	1276	Hypothetical ABC Transporter ATP-Binding Protein
285	286	F RXA01946	GR00559	1849	575	(AL021184) ABC transporter ATP binding protein [Mycobacterium tuberculosis]
287	288	RXN00164	VV0232	1782	94	Hypothetical ABC Transporter ATP-Binding Protein
289	290	F RXA00164	GR00025	1782	94	P, G, R ATPase subunits of ABC transporters
291	292	RXN00243	VV0057	28915	27899	P, G, R ATPase subunits of ABC transporters
293	294	F RXA00243	GR00037	930	4	P, G, R ATPase subunits of ABC transporters
295	296	RXN00259	GR00039	8469	6268	P, G, R ATPase subunits of ABC transporters
297	298	RXN00410	VV0086	51988	51323	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
299	300	F RXA00410	GR00092	829	164	P, G, R ATPase subunits of ABC transporters
301	302	RXN00456	VV0076	6780	8156	P, G, R ATPase subunits of ABC transporters
303	304	F RXA00456	GR00114	316	5	P, G, R ATPase subunits of ABC transporters
305	306	F RXA00459	GR00115	1231	245	P, G, R ATPase subunits of ABC transporters
307	308	RXN01604	VV0137	8117	7470	P, G, R ATPase subunits of ABC transporters
309	310	F RXA01604	GR00448	2	607	P, G, R ATPase subunits of ABC transporters
311	312	RXN02547	VV0057	27726	25588	P, G, R ATPase subunits of ABC transporters
313	314	F RXA02547	GR00726	22055	19932	P, G, R ATPase subunits of ABC transporters
315	316	RXN02571	VV0101	12331	13359	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
317	318	F RXA02571	GR00736	1469	2497	P, G, R ATPase subunits of ABC transporters
319	320	RXN02074	VV0318	12775	11153	TRANSPORT ATP-BINDING PROTEIN CYDD
321	322	F RXA02074	GR00628	5798	4176	P, G, R ATPase subunits of ABC transporters
323	324	RXA02095	GR00629	14071	15474	P, G, R ATPase subunits of ABC transporters
325	326	RXA02225	GR00652	3156	2275	P, G, R ATPase subunits of ABC transporters
327	328	RXA02253	GR00654	20480	21406	P, G, R ATPase subunits of ABC transporters
329	330	RXN01881	VV0105	529	95	Hypothetical ABC Transporter ATP-Binding Protein
331	332	F RXA01881	GR00537	3092	3532	ATPase components of ABC transporters with duplicated ATPase domains
333	334	RXA00526	GR00136	1353	664	Hypothetical ABC Transporter ATP-Binding Protein
335	336	RXN00733	VV0132	1647	2531	Hypothetical ABC Transporter ATP-Binding Protein
337	338	F RXA00733	GR00197	411	4	Hypothetical ABC Transporter ATP-Binding Protein
339	340	RXA00735	GR00198	849	181	Hypothetical ABC Transporter ATP-Binding Protein
341	342	RXA00878	GR00242	3733	1871	Hypothetical ABC Transporter ATP-Binding Protein
343	344	RXN01191	VV0169	10478	12067	Hypothetical ABC Transporter ATP-Binding Protein
345	346	F RXA01191	GR00341	1571	165	Hypothetical ABC Transporter ATP-Binding Protein
347	348	RXN01212	VV0169	3284	4207	Hypothetical ABC Transporter ATP-Binding Protein
349	350	F RXA01212	GR00350	1	813	Hypothetical ABC Transporter ATP-Binding Protein
351	352	RXA02749	GR00764	4153	5028	Hypothetical ABC Transporter ATP-Binding Protein
353	354	RXA02224	GR00652	2271	475	Hypothetical ABC Transporter ATP-Binding Protein
355	356	RXN01602	VV0229	1109	2638	Hypothetical ABC Transporter ATP-Binding Protein
357	358	RXN02515	VV0087	962	1717	Hypothetical ABC Transporter ATP-Binding Protein
359	360	RXN00525	VV0079	26304	27566	Hypothetical ABC Transporter Permease Protein
361	362	RXN02096	VV0126	20444	22135	Hypothetical ABC Transporter Permease Protein
363	364	RXN00412	VV0086	53923	52844	Hypothetical Amino Acid ABC Transporter ATP-Binding Protein
365	366	RXN00411	VV0086	52844	52170	Hypothetical Amino Acid ABC Transporter Permease Protein
367	368	RXN02614	VV0313	5964	5236	TAURINE TRANSPORT ATP-BINDING PROTEIN TAUB
369	370	RXN02613	VV0313	5223	4267	TAURINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
371	372	RXN00368	VW0226	2300	726	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
373	374	F RXA00368	GR00076	1	579	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
375	376	F RXA00370	GR00077	6	803	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
377	378	RXN01285	VW0215	1780	1055	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
379	380	RXN00523	VW0194	1363	338	FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEPC
381	382	RXN01142	VW0077	5805	6302	NITRATE TRANSPORT ATP-BINDING PROTEIN NRTD
383	384	RXN01141	VW0077	4644	5468	NITRATE TRANSPORT PROTEIN NRTA
385	386	RXN01002	VW0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
387	388	RXN01000	VW0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
389	390	RXN01732	VW0106	9944	8895	PHOSPHONATES-BINDING PERIPLASMIC PROTEIN PRECURSOR
391	392	RXN03080	VW0045	1670	2449	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
393	394	RXN03081	VW0045	2476	2934	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
395	396	RXN03082	VW0045	3131	3451	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR

## Other transporters

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
397	398	RXA02261	GR00654	30936	32291	AMMONIUM TRANSPORT SYSTEM
399	400	RXA02020	GR00613	1015	5	AROMATIC AMINO ACID TRANSPORT PROTEIN AROP
401	402	RXA00281	GR00043	4721	5404	BACITRACIN TRANSPORT ATP-BINDING PROTEIN BCRA
403	404	RXN00570	VW0147	855	4	BENZOATE MEMBRANE TRANSPORT PROTEIN
405	406	F RXA00570	GR00153	1	498	BENZOATE MEMBRANE TRANSPORT PROTEIN
407	408	RXN00571	VW0173	1298	42	BENZOATE MEMBRANE TRANSPORT PROTEIN
409	410	F RXA00571	GR00154	2	1186	BENZOATE MEMBRANE TRANSPORT PROTEIN
411	412	RXA00962	GR00268	2	667	BENZOATE MEMBRANE TRANSPORT PROTEIN
413	414	RXA02811	GR00792	177	560	BENZOATE MEMBRANE TRANSPORT PROTEIN
415	416	RXA02115	GR00635	2	1198	BENZOATE MEMBRANE TRANSPORT PROTEIN
417	418	RXN00590	VW0178	5043	6230	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
419	420	F RXA00590	GR00157	178	564	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
421	422	F RXA01538	GR00427	5040	5429	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
423	424	RXA01727	GR00489	1471	194	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN
425	426	RXA00623	GR00163	6525	7862	C4-DICARBOXYLATE TRANSPORT PROTEIN
427	428	RXA01584	GR00441	55	597	CHROMATE TRANSPORT PROTEIN
429	430	RXA00852	GR00231	3137	2448	COBALT TRANSPORT ATP-BINDING PROTEIN CBIO
431	432	RXA00690	GR00181	1213	68	COBALT TRANSPORT PROTEIN CBIQ
433	434	RXA00827	GR00223	1319	567	COBALT TRANSPORT PROTEIN CBIQ
435	436	RXA00851	GR00231	2448	1840	COBALT TRANSPORT PROTEIN CBIQ
437	438	RXS03220				D-XYLOSE-PROTON SYMPORT
439	440	F RXA02762	GR00768	346	630	D-XYLOSE PROTON-SYMPORTER
441	442	RXN00092	VW0129	27509	26844	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
443	444	F RXA00092	GR00014	1	204	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
445	446	RXN03060	VW0030	6227	5376	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
447	448	F RXA02618	GR00745	1914	2351	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
449	450	F RXA02900	GR10040	2979	2128	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
451	452	RXS03212				GLYCINE BETAINES TRANSPORTER BETP
453	454	F RXA01591	GR00446	3	947	GLYCINE BETAINES TRANSPORTER BETP
455	456	RXN00201	VV0096	197	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
457	458	F RXA00201	GR00032	191	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
459	460	RXA01221	GR00354	2108	2833	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN BRAG
461	462	RXA01222	GR00354	2844	3542	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVF
463	464	RXA01219	GR00354	151	1032	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
465	466	RXA01220	GR00354	1032	2108	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVM
467	468	RXA00091	GR00013	7762	8514	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
469	470	RXA00228	GR00032	29232	28642	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
471	472	RXA00346	GR00064	1054	1743	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
473	474	RXA00524	GR00135	779	1111	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
475	476	RXA01823	GR00516	591	1367	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
477	478	RXA02767	GR00770	1032	1814	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
479	480	RXA02792	GR00777	8581	7829	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
481	482	RXN02929	VV0090	36837	37874	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
483	484	F RXA01235	GR00358	1165	194	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
485	486	RXN02794	VV0134	10625	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
487	488	F RXA01419	GR00415	888	1151	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
489	490	F RXA02794	GR00777	10172	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
491	492	RXN03079	VV0045	644	1660	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
493	494	F RXA02865	GR10007	3832	2816	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
495	496	RXA00181	GR00028	3954	2383	PROLINE TRANSPORT SYSTEM
497	498	RXA00591	GR00158	229	1581	PROLINE/BETAINE TRANSPORTER
499	500	RXA01629	GR00453	3476	1965	PROLINE/BETAINE TRANSPORTER
501	502	RXA02030	GR00618	3072	1687	PROLINE/BETAINE TRANSPORTER
503	504	RXA00186	GR00028	12242	12988	SHORT-CHAIN FATTY ACIDS TRANSPORTER
505	506	RXA00187	GR00028	13097	13447	SHORT-CHAIN FATTY ACIDS TRANSPORTER
507	508	RXA01667	GR00464	703	1908	SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN
509	510	RXA02171	GR00641	6571	4919	SODIUM/PROLINE SYMPORTER
511	512	RXA00902	GR00245	4643	5875	SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN
513	514	RXA00941	GR00257	1999	683	sodium-dependent phosphate transport protein
515	516	RXN00449	VV0112	30992	32572	Sodium-Dicarboxylate Symport Protein
517	518	F RXA00449	VV0109	2040	1036	Sodium-Dicarboxylate Symport Protein
519	520	F RXA01755	GR00498	352	5	Sodium-Dicarboxylate Symport Protein
521	522	RXA00269	GR00041	1826	1038	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
523	524	RXA00369	GR00076	583	1299	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
525	526	RXA02073	GR00628	4176	2647	TRANSPORT ATP-BINDING PROTEIN CYDD
527	528	RXA01399	GR00409	1	1119	TRANSPORT ATP-BINDING PROTEIN CYDD
529	530	RXA01339	GR00389	8408	7164	TYROSINE-SPECIFIC TRANSPORT PROTEIN
531	532	RXA02527	GR00725	5519	6847	2-OXOGLUTARATE/MALATE TRANSPORT PRECURSOR
533	534	RXN00298	VV0176	40228	42072	HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN
535	536	F RXA00298	GR00048	4459	6303	Ectoine/Proline/Glycine betaine carrier ectP

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
537	538	RXA00596	GR00159	335	787	potassium efflux system protein phaE C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN PRECURSOR, transport protein
539	540	RXA02364	GR00686	841	215	
541	542	RXN01411	VW0050	26015	26779	SHIKIMATE TRANSPORTER PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
543	544	RXN00960	VW0075	1139	105	
545	546	RXN02447	VW0107	14297	13203	
547	548	RXN02395	VW0176	16747	14858	GLYCINE BETAIN TRANSPORTER BETP KUP SYSTEM POTASSIUM UPTAKE PROTEIN
549	550	RXN02348	VW0078	6027	7910	
551	552	RXN00297	VW0176	38630	39541	
553	554	RXN03103	VW0070	845	1087	Hypothetical Malonate Transporter GLUTAMATE-BINDING PROTEIN PRECURSOR
555	556	RXN02993	VW0071	736	65	
557	558	RXN00349	VW0135	35187	36653	
559	560	RXN03095	VW0057	4056	4424	Hypothetical Trehalose Transport Protein CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
561	562	RXN03160	VW0189	5150	5617	
563	564	RXN02955	VW0176	8666	9187	
565	566	RXN03109	VW0082	659	6	DICARBOXYLATE TRANSPORTER HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMUO
567	568	RXN02979	VW0149	2150	2383	
569	570	RXN02987	VW0234	527	294	
571	572	RXN03084	VW0048	900	1817	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
573	574	RXN03183	VW0372	1	417	
575	576	RXN01139	VW0077	2776	1823	
577	578	RXN00378	VW0223	8027	5418	TREHALOSE/MALTOSE BINDING PROTEIN CATION EFFLUX SYSTEM PROTEIN CZCD
579	580	RXN01338	VW0032	2	1903	
581	582	RXN00980	VW0149	2635	4428	
583	584	RXN00099	VW0129	18876	17704	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-) CATION-TRANSPORTING P-TYPE ATPASE B (EC 3.6.1.-)
585	586	RXN02662	VW0315	1461	1724	
587	588	RXN02442	VW0217	5970	6818	
589	590	RXN02443	VW0217	6818	7771	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC zinc transport system membrane protein
591	592	RXN00842	VW0138	8686	7487	
593	594	F RXA00842	GR00228	3208	2009	
595	596	RXN00832	VW0180	3133	4182	zinc-binding periplasmic protein precursor BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
597	598	RXN00466	VW0086	63271	64266	
599	600	RXN01936	VW0127	40116	41387	
601	602	RXN01995	VW0182	2139	3476	Permeases CALCIUM/PROTON ANTIPORTER Ferrichrome transport proteins
603	604	RXN00661	VW0142	9718	9029	
						PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
						PNUC PROTEIN

## Permeases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
605	606	RXN02566	VW0154	11823	13031	NUCLEOSIDE PERMEASE NUPG NUCLEOSIDE PERMEASE NUPG
607	608	F RXA02561	GR00732	664	5	
609	610	F RXA02566	GR00733	782	345	
611	612	RXA00051	GR00008	5770	7173	NUCLEOSIDE PERMEASE NUPG PROLINE-SPECIFIC PERMEASE PROY SULFATE PERMEASE
613	614	RXA01172	GR00334	2687	4141	
615	616	RXA02128	GR00637	2906	4600	

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
617	618	RXA02634	GR00748	6045	7655	SULFATE PERMEASE
619	620	RXN02233	VW0068	6856	8142	URACIL PERMEASE
621	622	F RXA02233	GR00653	6856	8067	URACIL PERMEASE
623	624	RXN02372	VW0213	9311	11197	XANTHINE PERMEASE
625	626	F RXA02372	GR00688	6	560	XANTHINE PERMEASE
627	628	F RXA02377	GR00689	3336	4526	XANTHINE PERMEASE
629	630	RXA02676	GR00754	2897	1309	GLUCONATE PERMEASE
631	632	RXN00432	VW0112	14751	13267	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
633	634	F RXA00432	GR00100	1	891	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
635	636	F RXA00436	GR00101	45	569	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
637	638	RXA00847	GR00230	1829	381	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
639	640	RXN01382	VW0119	8670	9761	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR
641	642	F RXA01382	GR00405	1067	6	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
644	644	RXA02659	GR00753	2	313	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
646	646	RXN02933	VW0176	30042	29233	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
647	648	RXN02991	VW0072	618	4	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
649	650	RXN02992	VW0072	842	621	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
651	652	RXN02996	VW0069	1980	2648	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE
653	654	RXN03126	VW0112	9894	9001	PROTEIN LIVH
655	656	RXN00443	VW0112	21572	20769	TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG
657	658	RXN00444	VW0112	20785	19949	MOLYBDATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
659	660	RXN00193	VW0371	1	594	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
661	662	RXN01298	VW0116	2071	1142	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD

## Channel Proteins

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
663	664	RXA01737	GR00493	2913	3971	POTASSIUM CHANNEL PROTEIN
665	666	RXN02348	VW0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
667	668	RXA02426	GR00707	2165	633	PROBABLE NA(+)/H(+) ANTIPORTER
669	670	RXN03164	VW0277	1586	2455	POTASSIUM CHANNEL BETA SUBUNIT
671	672	RXN00024	VW0127	64219	63275	POTASSIUM CHANNEL BETA SUBUNIT

## Lipoprotein and Lipopolysaccharide synthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
673	674	RXN01164	VW0117	15894	14260	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)
675	676	RXN01168	VW0117	14224	13415	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	gluB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glhA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M113774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an MtrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambda dacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambda dacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)



GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of $\phi$ phi304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

<sup>1</sup> A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCITC	DSMZ
<i>Brevibacterium</i>	<i>ammoniogenes</i>	21054							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19350							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19351							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19352							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19353							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19354							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19355							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	19356							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	21055							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	21077							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	21553							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	21580							
<i>Brevibacterium</i>	<i>ammoniogenes</i>	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							



Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							



Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419					11594		
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							



**TABLE 4: ALIGNMENT RESULTS**

<u>ID #</u>	<u>length</u> (NT)	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u> (GAP)	<u>% homology</u>	<u>Date of</u> <u>Deposit</u>
rx00051	1527	GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***; 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***; 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG7:AC009511	271896	AC009511	Homo sapiens clone RP11-860B13, *** SEQUENCING IN PROGRESS ***; 59 unordered pieces.	Homo sapiens	35,033	09-DEC-1999
rx00091	876	GB_BA1:D50453	146191	D50453	Bacillus subtilis DNA for 25-36 degree region containing the amyE-srfA region, complete cds.	Bacillus subtilis	54,452	10-Feb-99
		GB_BA1:SC151	40745	AL109848	Streptomyces coelicolor cosmid l51.	Streptomyces coelicolor A3(2)	36,806	16-Aug-99
rx00092	789	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,642	17-Apr-96
		GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	49,934	4-Jun-99
		GB_HTG3:AC011498_0312343	AC011498	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***; 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
		GB_HTG3:AC011498_0312343	AC011498	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***; 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
rx00104	879	GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	36,732	10-Feb-99
		GB_PL2:T24M8	68251	AF077409	Arabidopsis thaliana BAC T24M8.	Arabidopsis thaliana	37,150	3-Aug-98
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	42,874	10-Feb-99
rx00113	5745	GB_BA1:MAFASGEN	10520	X87822	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	68,381	03-OCT-1996
		GB_BA1:BAFASAA	10549	X64795	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	57,259	14-OCT-1997
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,870	17-Jun-98
rx00164	1812	GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	35,334	03-DEC-1999
rx00181	1695	GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_BA2:U32814	10393	U32814	Haemophilus influenzae Rd section 129 of 163 of the complete genome.	Haemophilus influenzae Rd	36,347	29-MAY-1998
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	37,454	8-Sep-97
rx00186	870	GB_PR3:AC004843	136655	AC004843	Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.	Homo sapiens	37,315	5-Nov-98

**TABLE 4: ALIGNMENT RESULTS**

GB_HTG2:HS745114	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745114 map q23.1-24.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces.	38,129	03-DEC-1999
GB_HTG2:HS745114	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745114 map q23.1-24.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces.	38,129	03-DEC-1999
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	37,297	1-Nov-98
GB_GSS1:CNS008ZZ	1101	AL052951	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR18L01 of Drosophila melanogaster (fruit fly), genomic survey sequence.	34,120	3-Jun-99
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	39,655	1-Nov-98
GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	34,520	23-Nov-99
GB_BA1:RCSECA	2724	X89411	R. capsulatus DNA for secA gene.	38,163	6-Jan-96
GB_EST34:AV122904	242	AV122904	AV122904 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610529H07, mRNA sequence.	38,889	1-Jul-99
GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	37,500	06-MAR-1998
GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	38,816	06-MAR-1998
GB_PR2:CNS01DS5	101584	AL121655	BAC sequence from the SPG4 candidate region at 2p21-2p22, complete sequence.	37,001	29-Sep-99
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	38,040	06-OCT-1999
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	38,040	06-OCT-1999
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	36,776	6-Sep-99
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	36,776	6-Sep-99
GB_PL2:YSCCHROM1	41988	L22015	Saccharomyces cerevisiae chromosome I centromere and right arm sequence.	39,260	05-MAR-1998
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459119, WORKING DRAFT SEQUENCE, in unordered pieces.	37,358	29-OCT-1999
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH0459119, WORKING DRAFT SEQUENCE, in unordered pieces.	37,358	29-OCT-1999
GB_BA1:AB017508	32050	AB017508	Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.	44,622	14-Apr-99
GB_BA1:SCOE8	24700	AL035654	Streptomyces coelicolor cosmid E8.	36,328	11-MAR-1999
GB_BA1:SCU51332	3216	U51332	Streptomyces coelicolor histidine kinase homolog (absA1) and response regulator homolog (absA2) genes, complete cds.	39,089	14-Sep-96
GB_HTG4:AC011122	187123	AC011122	Homo sapiens chromosome 8 clone 23_D_19 map 8, *** SEQUENCING IN PROGRESS ***, 27 ordered pieces.	38,658	14-OCT-1999
GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	100,000	20-Nov-98

**TABLE 4: ALIGNMENT RESULTS**

rx000346	813	GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
		GB_EST24:AI234006	432	AI234006	EST230694 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLU001 3' end, mRNA sequence.	Rattus sp.	46,552	31-Jan-99
		GB_BA1:SC2E9	20850	AL021530	Streptomyces coelicolor cosmid 2E9.	Streptomyces coelicolor	43,267	28-Jan-98
		GB_BA1:SC9B1	24800	AL049727	Streptomyces coelicolor cosmid 9B1.	Streptomyces coelicolor	44,613	27-Apr-99
		GB_BA1:ECU70214	123171	U70214	Escherichia coli chromosome minutes 4-6.	Escherichia coli	39,490	21-Sep-96
rx000368	1698	GB_BA2:AF065159	35209	AF065159	Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), japonicum SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/Spot homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc) gene, complete cds; GTP-binding protein Era (era) gene, partial cds; and unknown genes.	Bradyrhizobium japonicum	40,409	27-OCT-1999
		GB_BA1:AEOCHIT1	6861	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	Aeromonas sp.	38,577	13-Feb-99
		GB_EST4:D62996	314	D62996	HUM347G01B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-347G01 5', mRNA sequence.	Homo sapiens	41,613	29-Aug-95
rx000369	817	GB_BA1:YP102KB	119443	AL031866	Yersinia pestis 102 kbases unstable region: from 1 to 119443.	Yersinia pestis	35,396	4-Jan-99
		GB_GSS8:AQ012142	501	AQ012142	8750H1A037010398 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 8750H1A037010398, genomic survey sequence.	Rhodobacter sphaeroides	54,800	4-Jun-98
		GB_HTG2:AC005081	180096	AC005081	Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS *** , 18 unordered pieces.	Homo sapiens	45,786	12-Jun-98
rx000410	789	GB_BA1:ATPLOCC	8870	Z30328	A.tumefaciens Ti plasmid pTiAch5 genes for OccR, OccQ, OccM, OccP, OccT, OoxB, OoxC, OoxD, OoxE, OoxF, OoxG, OoxH, OoxI, OoxJ, OoxK, OoxL, OoxM, OoxN, OoxO, OoxP, OoxQ, OoxR, OoxS, OoxT, OoxU, OoxV, OoxW, OoxX, OoxY, OoxZ, OoxAA, OoxAB, OoxAC, OoxAD, OoxAE, OoxAF, OoxAG, OoxAH, OoxAI, OoxAJ, OoxAK, OoxAL, OoxAM, OoxAN, OoxAO, OoxAP, OoxAQ, OoxAR, OoxAS, OoxAT, OoxAU, OoxAV, OoxAW, OoxAX, OoxAY, OoxAZ, OoxBA, OoxBB, OoxBC, OoxBD, OoxBE, OoxBF, OoxBG, OoxBH, OoxBI, OoxBJ, OoxBK, OoxBL, OoxBM, OoxBN, OoxBO, OoxBP, OoxBQ, OoxBR, OoxBS, OoxBT, OoxBU, OoxBV, OoxBW, OoxBX, OoxBY, OoxBZ, OoxCA, OoxCB, OoxCC, OoxCD, OoxCE, OoxCF, OoxCG, OoxCH, OoxCI, OoxCJ, OoxCK, OoxCL, OoxCM, OoxCN, OoxCO, OoxCP, OoxCQ, OoxCR, OoxCS, OoxCT, OoxCU, OoxCV, OoxCW, OoxCX, OoxCY, OoxCZ, OoxDA, OoxDB, OoxDC, OoxDD, OoxDE, OoxDF, OoxDG, OoxDH, OoxDI, OoxDJ, OoxDK, OoxDL, OoxDM, OoxDN, OoxDO, OoxDP, OoxDQ, OoxDR, OoxDS, OoxDT, OoxDU, OoxDV, OoxDW, OoxDX, OoxDY, OoxDZ, OoxEA, OoxEB, OoxEC, OoxED, OoxEE, OoxEF, OoxEG, OoxEH, OoxEI, OoxEJ, OoxEK, OoxEL, OoxEM, OoxEN, OoxEO, OoxEP, OoxEQ, OoxER, OoxES, OoxET, OoxEU, OoxEV, OoxEW, OoxEX, OoxEY, OoxEZ, OoxFA, OoxFB, OoxFC, OoxFD, OoxFE, OoxFF, OoxFG, OoxFH, OoxFI, OoxFJ, OoxFK, OoxFL, OoxFM, OoxFN, OoxFO, OoxFP, OoxFQ, OoxFR, OoxFS, OoxFT, OoxFU, OoxFV, OoxFW, OoxFX, OoxFY, OoxFZ, OoxGA, OoxGB, OoxGC, OoxGD, OoxGE, OoxGF, OoxGG, OoxGH, OoxGI, OoxGJ, OoxGK, OoxGL, OoxGM, OoxGN, OoxGO, OoxGP, OoxGQ, OoxGR, OoxGS, OoxGT, OoxGU, OoxGV, OoxGW, OoxGX, OoxGY, OoxGZ, OoxHA, OoxHB, OoxHC, OoxHD, OoxHE, OoxHF, OoxHG, OoxHH, OoxHI, OoxHJ, OoxHK, OoxHL, OoxHM, OoxHN, OoxHO, OoxHP, OoxHQ, OoxHR, OoxHS, OoxHT, OoxHU, OoxHV, OoxHW, OoxHX, OoxHY, OoxHZ, OoxIA, OoxIB, OoxIC, OoxID, OoxIE, OoxIF, OoxIG, OoxIH, OoxII, OoxIJ, OoxIK, OoxIL, OoxIM, OoxIN, OoxIO, OoxIP, OoxIQ, OoxIR, OoxIS, OoxIT, OoxIU, OoxIV, OoxIW, OoxIX, OoxIY, OoxIZ, OoxJA, OoxJB, OoxJC, OoxJD, OoxJE, OoxJF, OoxJG, OoxJH, OoxJI, OoxJJ, OoxJM, OoxJN, OoxJO, OoxJP, OoxJQ, OoxJR, OoxJS, OoxJT, OoxJU, OoxJV, OoxJW, OoxJX, OoxJY, OoxJZ, OoxKA, OoxKB, OoxKC, OoxKD, OoxKE, OoxKF, OoxKG, OoxKH, OoxKI, OoxKJ, OoxKL, OoxKM, OoxKN, OoxKO, OoxKP, OoxKQ, OoxKR, OoxKS, OoxKT, OoxKU, OoxKV, OoxKW, OoxKX, OoxKY, OoxKZ, OoxLA, OoxLB, OoxLC, OoxLD, OoxLE, OoxLF, OoxLG, OoxLH, OoxLI, OoxLJ, OoxLK, OoxLL, OoxLM, OoxLN, OoxLO, OoxLP, OoxLQ, OoxLR, OoxLS, OoxLT, OoxLU, OoxLV, OoxLW, OoxLX, OoxLY, OoxLZ, OoxMA, OoxMB, OoxMC, OoxMD, OoxME, OoxMF, OoxMG, OoxMH, OoxMI, OoxMJ, OoxMK, OoxML, OoxMN, OoxMO, OoxMP, OoxMQ, OoxMR, OoxMS, OoxMT, OoxMU, OoxMV, OoxMW, OoxMX, OoxMY, OoxMZ, OoxNA, OoxNB, OoxNC, OoxND, OoxNE, OoxNF, OoxNG, OoxNH, OoxNI, OoxNJ, OoxNK, OoxNL, OoxNM, OoxNO, OoxNP, OoxNQ, OoxNR, OoxNS, OoxNT, OoxNU, OoxNV, OoxNW, OoxNX, OoxNY, OoxNZ, OoxOA, OoxOB, OoxOC, OoxOD, OoxOE, OoxOF, OoxOG, OoxOH, OoxOI, OoxOJ, OoxOK, OoxOL, OoxOM, OoxON, OoxOO, OoxOP, OoxOQ, OoxOR, OoxOS, OoxOT, OoxOU, OoxOV, OoxOW, OoxOX, OoxOY, OoxOZ, OoxPA, OoxPB, OoxPC, OoxPD, OoxPE, OoxPF, OoxPG, OoxPH, OoxPI, OoxPJ, OoxPK, OoxPL, OoxPM, OoxPN, OoxPO, OoxPP, OoxPQ, OoxPR, OoxPS, OoxPT, OoxPU, OoxPV, OoxPW, OoxPX, OoxPY, OoxPZ, OoxQA, OoxQB, OoxQC, OoxQD, OoxQE, OoxQF, OoxQG, OoxQH, OoxQI, OoxQJ, OoxQK, OoxQL, OoxQM, OoxQN, OoxQO, OoxQP, OoxQQ, OoxQR, OoxQS, OoxQT, OoxQU, OoxQV, OoxQW, OoxQX, OoxQY, OoxQZ, OoxRA, OoxRB, OoxRC, OoxRD, OoxRE, OoxRF, OoxRG, OoxRH, OoxRI, OoxRJ, OoxRK, OoxRL, OoxRM, OoxRN, OoxRO, OoxRP, OoxRQ, OoxRR, OoxRS, OoxRT, OoxRU, OoxRV, OoxRW, OoxRX, OoxRY, OoxRZ, OoxSA, OoxSB, OoxSC, OoxSD, OoxSE, OoxSF, OoxSG, OoxSH, OoxSI, OoxSJ, OoxSK, OoxSL, OoxSM, OoxSN, OoxSO, OoxSP, OoxSQ, OoxSR, OoxSS, OoxST, OoxSU, OoxSV, OoxSW, OoxSX, OoxSY, OoxSZ, OoxTA, OoxTB, OoxTC, OoxTD, OoxTE, OoxTF, OoxTG, OoxTH, OoxTI, OoxTJ, OoxTK, OoxTL, OoxTM, OoxTN, OoxTO, OoxTP, OoxTQ, OoxTR, OoxTS, OoxTT, OoxTU, OoxTV, OoxTW, OoxTX, OoxTY, OoxTZ, OoxUA, OoxUB, OoxUC, OoxUD, OoxUE, OoxUF, OoxUG, OoxUH, OoxUI, OoxUJ, OoxUK, OoxUL, OoxUM, OoxUN, OoxUO, OoxUP, OoxUQ, OoxUR, OoxUS, OoxUT, OoxUU, OoxUV, OoxUW, OoxUX, OoxUY, OoxUZ, OoxVA, OoxVB, OoxVC, OoxVD, OoxVE, OoxVF, OoxVG, OoxVH, OoxVI, OoxVJ, OoxVK, OoxVL, OoxVM, OoxVN, OoxVO, OoxVP, OoxVQ, OoxVR, OoxVS, OoxVT, OoxVU, OoxVV, OoxVW, OoxVX, OoxVY, OoxVZ, OoxWA, OoxWB, OoxWC, OoxWD, OoxWE, OoxWF, OoxWG, OoxWH, OoxWI, OoxWJ, OoxWK, OoxWL, OoxWM, OoxWN, OoxWO, OoxWP, OoxWQ, OoxWR, OoxWS, OoxWT, OoxWU, OoxWV, OoxWW, OoxWX, OoxWY, OoxWZ, OoxXA, OoxXB, OoxXC, OoxXD, OoxXE, OoxXF, OoxXG, OoxXH, OoxXI, OoxXJ, OoxXK, OoxXL, OoxXM, OoxXN, OoxXO, OoxXP, OoxXQ, OoxXR, OoxXS, OoxXT, OoxXU, OoxXV, OoxXW, OoxXX, OoxXY, OoxXZ, OoxYA, OoxYB, OoxYC, OoxYD, OoxYE, OoxYF, OoxYG, OoxYH, OoxYI, OoxYJ, OoxYK, OoxYL, OoxYM, OoxYN, OoxYO, OoxYP, OoxYQ, OoxYR, OoxYS, OoxYT, OoxYU, OoxYV, OoxYW, OoxYX, OoxYY, OoxYZ, OoxZA, OoxZB, OoxZC, OoxZD, OoxZE, OoxZF, OoxZG, OoxZH, OoxZI, OoxZJ, OoxZK, OoxZL, OoxZM, OoxZN, OoxZO, OoxZP, OoxZQ, OoxZR, OoxZS, OoxZT, OoxZU, OoxZV, OoxZW, OoxZX, OoxZY, OoxZZ.	Agrobacterium tumefaciens	46,490	10-OCT-1994
		GB_BA2:U67591	9829	U67591	OoxA and ornithine cyclodeaminase.	Methanococcus jannaschii	45,677	28-Jan-98
		GB_BA1:TIPOCCOMPJ4350	M80607	M80607	Plasmid pTIA6 (from Agrobacterium tumefaciens) periplasmic-type octopine permease (occR, occQ, occM, occP, and occJ) and lysR-type regulatory protein (occR) genes, complete cds.	Plasmid pTIA6	46,490	24-Apr-96
rx000419	882	GB_BA2:MSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds.	Mycobacterium smegmatis	57,029	12-MAY-1997
		GB_EST28:AI513245	471	AI513245	GH13311.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH13311 3prime, mRNA sequence.	Drosophila melanogaster	37,696	16-MAR-1999
		GB_HTG4:AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L72A4 clone RPC198-25O1, *** SEQUENCING IN PROGRESS *** , 70 unordered pieces.	Drosophila melanogaster	39,607	16-OCT-1999
rx000432	1608	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21), from 2795131 to 3013540.	Bacillus subtilis	49,810	26-Nov-97
		GB_PL1:CAC35A5	42565	AL033396	C.albicans cosmid Ca35A5.	Candida albicans	35,041	5-Nov-98
		GB_EST13:AA336266	378	AA336266	EST40981 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	39,733	21-Apr-97
rx000449	1704	GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPC1-98 01.K.8 map 94D-94D strain y; on bw sp, *** SEQUENCING IN PROGRESS *** , 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** 83 unordered pieces.	38,392	2-Aug-99
GB_RO:RATLTKP2	177	M22337	Rat link protein gene, exon 2.	40,678	27-Apr-93
GB_GSS1:FR0030597	476	AL026966	Fugu rubripes GSS sequence, clone 091C22aF9, genomic survey sequence.	47,407	25-Jun-98
GB_GSS5:AQ786587	556	AQ786587	HS_3086_B1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3086 Col=9 Row=P, genomic survey sequence.	38,406	3-Aug-99
GB_GSS14:AQ526586	434	AQ526586	HS_5198_B1_B03_SPE6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=774 Col=5 Row=D, genomic survey sequence.	36,951	11-MAY-1999
GB_EST17:AA610489	407	AA610489	np93e05.s1 NCL_CGAP_Tny1 Homo sapiens cDNA clone IMAGE:1133888 similar to Homo sapiens gb:M11353 HISTONE H3.3 (HUMAN), mRNA sequence.	41,791	09-DEC-1997
GB_PR1:HS33G4	1015	X05857	Human H3.3 gene exon 4.	38,182	24-Jan-96
GB_EST30:AI637667	579	AI637667	tt10g11.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240420 3', mRNA sequence.	35,417	27-Apr-99
GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** 12 unordered pieces.	38,769	3-Aug-99
GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** 12 unordered pieces.	38,769	3-Aug-99
GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS *** 12 unordered pieces.	36,797	3-Aug-99
GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	38,138	23-Nov-99
GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	38,138	23-Nov-99
GB_RO:AC005960	158414	AC005960	Mus musculus chromosome 17 BAC ctb20h22 from the MHC region, complete sequence.	38,712	01-DEC-1998
GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid i51.	40,284	16-Aug-99
GB_BA2:AF082879	3434	AF082879	Yersinia enterocolitica ABC transporter enterochelin/enterobactin gene cluster, complete sequence.	55,634	20-OCT-1999
GB_BA1:BSP132617	5192	AJ132617	Burkholderia sp. P-transporter operon and flanking genes.	40,793	13-Jul-99
GB_BA1:BSUB0008	208230	Z99111	Bacillus subtilis complete genome (section 8 of 21); from 1394791 to 1603020.	54,534	26-Nov-97
GB_BA2:AF012285	46864	AF012285	Bacillus subtilis mobA-nprE gene region.	54,534	1-Jul-98
GB_BA1:D90725	13796	D90725	Escherichia coli genomic DNA. (19.7 - 20.0 min).	51,481	7-Feb-99
GB_BA2:CAU77910	3385	U77910	Corynebacterium ammoniagenes sequence upstream of the 5-phosphoribosyl-1-pyrophosphate amidotransferase (purF) gene.	39,007	1-Jan-98
GB_EST4:H34952	382	H34952	EST108261 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCCCK07 similar to NADH-ubiquinone oxidoreductase complex I 23 kDa precursor (iron-sulfur protein), mRNA sequence.	39,267	2-Apr-98
GB_BA2:AE000963	22014	AE000963	Archaeoglobus fulgidus section 144 of 172 of the complete genome.	38,338	15-DEC-1997
GB_GSS12:AQ422451	563	AQ422451	RPCI-11-185C3.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185C3, genomic survey sequence.	38,767	23-MAR-1999

**TABLE 4: ALIGNMENT RESULTS**

GB_EST28:AI504741	568	AI504741	v16c01.x1 Stratagene mouse Toell 937311 Mus musculus cDNA clone IMAGE:972384 3' similar to gb:Z14044 M.musculus mRNA for valosin-containing protein (MOUSE);, mRNA sequence.	Mus musculus	37,900	11-MAR-1999
GB_EST18:AA712043	68	AA712043	vu29f10.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1182091 5' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);, mRNA sequence.	Mus musculus	42,647	24-DEC-1997
GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	38,468	17-Jun-98
GB_PR3:AC005788	36224	AC005788	Homo sapiens chromosome 19, cosmid R26652, complete sequence.	Homo sapiens	36,911	06-OCT-1998
GB_PR3:AC005338	34541	AC005338	Homo sapiens chromosome 19, cosmid R31646, complete sequence.	Homo sapiens	36,911	30-Jul-98
GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	37,242	30-Nov-99
GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	36,485	30-Nov-99
GB_BA1:MSGB26CS	37040	L78816	Mycobacterium leprae cosmid B26 DNA sequence.	Mycobacterium leprae	39,272	15-Jun-96
GB_IN1:CEK09E9	30098	Z79602	Caenorhabditis elegans cosmid K09E9, complete sequence.	Caenorhabditis elegans	34,092	2-Sep-99
GB_PR4:AF135802	4965	AF135802	Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds.	Homo sapiens	36,310	9-Apr-99
GB_PR4:AF104256	4365	AF104256	Homo sapiens transcriptional co-activator CRSP150 (CRSP150) mRNA, complete cds.	Homo sapiens	36,617	4-Feb-99
GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	34,321	02-MAY-1998
GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.	Homo sapiens	35,739	02-MAY-1998
GB_PR1:HUMCBP2	2047	D83174	Human mRNA for collagen binding protein 2, complete cds.	Homo sapiens	40,404	6-Feb-99
GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	40,862	23-Jun-99
GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv complete genome; segment 119/162.	Mycobacterium tuberculosis	38,833	23-Jun-99
GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv complete genome; segment 107/162.	Mycobacterium tuberculosis	60,552	17-Jun-98
GB_BA1:RSPNGR234	34010	Z68203	Rhizobium sp. plasmid NGR234a DNA.	Rhizobium sp.	51,992	8-Aug-96
GB_BA2:AE000101	10057	AE000101	Rhizobium sp. NGR234 plasmid pNGR234a, section 38 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	51,992	12-DEC-1997
GB_HTG5:AC008338	136685	AC008338	Drosophila melanogaster chromosome X clone BACR30J04 (D908) RPCI-98 30.J.4 map 19C-19E strain Y; on bw sp, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Drosophila melanogaster	35,341	15-Nov-99
GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999
GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999



TABLE 4: ALIGNMENT RESULTS

rx00733	1008	GB_EST30:AU054038	245	AU054038	AU054038	Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
		GB_EST30:AU054038	245	AU054038	AU054038	Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
rx00735	692	GB_BA1:MTCV50	36030	Z77137	Z77137	Mycobacterium tuberculosis H37Rv complete genome; segment 55/162.	Mycobacterium tuberculosis	36,819	17-Jun-98
		GB_BA1:D90904	150894	D90904	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	52,585	7-Feb-99
		GB_BA1:D90904	150894	D90904	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	39,699	7-Feb-99
rx00796	298	GB_GSS14:AQ579838	651	AQ579838	AQ579838	T135342b shotgun sub-library of BAC clone 31P06 Medicago truncatula genomic clone 31-P-06-C-054, genomic survey sequence.	Medicago truncatula	37,153	27-Sep-99
		GB_PR4:AC007625	174701	AC007625	AC007625	Genomic sequence of Homo sapiens clone 2314F2 from chromosome 18, complete sequence.	Homo sapiens	38,014	30-Jun-99
		GB_EST14:AA427576	580	AA427576	AA427576	zw54b04.s1 Soares_total_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773839 3' similar to gb:M86852 PEROXISOME ASSEMBLY FACTOR-1 (HUMAN);, mRNA sequence.	Homo sapiens	42,731	16-OCT-1997
rx00801	756	GB_BA1:MTV022	13025	AL021925	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	59,350	17-Jun-98
		GB_RO:AC002109	160048	AC002109	AC002109	Genomic sequence from Mouse 9, complete sequence.	Mus musculus	39,398	9-Sep-97
		GB_BA1:MTV022	13025	AL021925	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	36,842	17-Jun-98
rx00802	837	GB_GSS14:AQ563349	642	AQ563349	AQ563349	HS_5335_B2_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=911 Col=18 Row=B, genomic survey sequence.	Homo sapiens	37,649	29-MAY-1999
		GB_BA1:DIHCLPBA	2441	M32229	M32229	B.nodosus clpB gene encoding a regulatory subunit of ATP-dependent protease.	Dichelobacter nodosus	41,140	26-Apr-93
		GB_GSS3:B61538	698	B61538	B61538	T17M17TR TAMU Arabidopsis thaliana genomic clone T17M17, genomic survey sequence.	Arabidopsis thaliana	36,946	21-Nov-97
rx00819	1452	GB_HTG3:AC008691_1	110000	AC008691	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***; 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC008691_1	110000	AC008691	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***; 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
		GB_HTG3:AC009127	186591	AC009127	AC009127	Homo sapiens chromosome 16 clone RPCI-11_498D10, *** SEQUENCING IN PROGRESS ***; 49 unordered pieces.	Homo sapiens	38,947	3-Aug-99
rx00821	966	GB_HTG1:HS32B1	271488	AL023693	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,565	23-Nov-99
		GB_HTG1:HS32B1	271488	AL023693	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	36,565	23-Nov-99
rx00827	876	GB_PR3:AC004919	75547	AC004919	AC004919	Homo sapiens PAC clone DJ0895B23 from UL, complete sequence.	Homo sapiens	34,346	19-Sep-98
		GB_EST6:W06539	300	W06539	W06539	T2367 MVAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	40,000	12-Aug-96
		GB_PR4:AC008179	181745	AC008179	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	35,903	28-Sep-99
		GB_EST18:AA710415	533	AA710415	AA710415	v53f08.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1166823 5', mRNA sequence.	Mus musculus	41,562	24-DEC-1997
rx00842	1323	GB_PR2:AC002379	118595	AC002379	AC002379	Human BAC clone GS165104 from 7q21, complete sequence.	Homo sapiens	36,321	23-Jul-97
		GB_PR2:AC002379	118595	AC002379	AC002379	Human BAC clone GS165104 from 7q21, complete sequence.	Homo sapiens	37,284	23-Jul-97

**TABLE 4: ALIGNMENT RESULTS**

rx00847	1572	GB_IN1:CEF02D8	31624	Z78411	Caenorhabditis elegans cosmid F02D8, complete sequence.	38,163	23-Nov-98
		GB_OV:XELRDS38A	1209	L79915	Xenopus laevis rds/peripherin (rds38) mRNA, complete cds.	36,044	30-Jul-97
		GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPC11-208N14, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces.	33,742	21-OCT-1999
rx00851	732	GB_HTG4:AC007920	234529	AC007920	Homo sapiens chromosome 3q27 clone RPC11-208N14, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces.	33,742	21-OCT-1999
		GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	39,833	9-Jul-98
		GB_HTG2:AC004064	185000	AC004064	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	39,833	9-Jul-98
		GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	39,833	23-Nov-99
		GB_HTG3:AC010120	121582	AC010120	Drosophila melanogaster chromosome 3 clone BACR22N13 (D1061) RPCI-98 22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	36,855	24-Sep-99
rx00856	1635	GB_HTG3:AC010120	121582	AC010120	Drosophila melanogaster chromosome 3 clone BACR22N13 (D1061) RPCI-98 22.N.13 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	36,855	24-Sep-99
		GB_HTG2:AC006898	299308	AC006898	Caenorhabditis elegans clone Y73B6x, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	36,768	24-Feb-99
		GB_BA1:STMMSDA	3986	L48550	Streptomyces coelicolor methylmalonic acid semialdehyde dehydrogenase (msdA) gene, complete cds.	63,743	09-MAY-1996
		GB_PAT:192043	713	I92043	Sequence 10 from patent US 5726299.	38,850	01-DEC-1998
		GB_PAT:178754	713	I78754	Sequence 10 from patent US 5693781.	38,850	3-Apr-98
rx00875	690	GB_BA2:AF119715	549	AF119715	Escherichia coli isopentenyl diphosphate isomerase (idi) gene, complete cds.	54,827	22-Apr-99
		GB_BA2:AE000372	12144	AE000372	Escherichia coli K-12 MG1655 section 262 of 400 of the complete genome.	51,416	12-Nov-98
		GB_BA1:ECU28375	55175	U28375	Escherichia coli K-12 genome; approximately 64 to 65 minutes.	51,416	08-DEC-1995
		GB_HTG2:AC007472	114003	AC007472	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98 30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	36,592	2-Aug-99
		GB_HTG2:AC007472	114003	AC007472	Drosophila melanogaster chromosome 2 clone BACR30D19 (D587) RPCI-98 30.D.19 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	36,592	2-Aug-99
rx00880	1968	GB_HTG2:AC006798	207370	AC006798	Caenorhabditis elegans clone Y51F8, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	36,699	25-Feb-99
		GB_EST4:H22888	468	H22888	ym54e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52158 5', mRNA sequence.	37,179	6-Jul-95
		GB_GSS13:AQ426858	516	AQ426858	CITBI-E1-2578F1.TF CITBI-E1 Homo sapiens genomic clone 2578F1, genomic survey sequence.	38,447	24-MAR-1999
		GB_PR1:AB002335	6289	AB002335	Human mRNA for KIAA0337 gene, complete cds.	35,799	13-Feb-99
		GB_BA1:NGU58849	2401	U58849	Neisseria gonorrhoeae pilS6 silent pilus locus.	40,623	20-Jun-96

**TABLE 4: ALIGNMENT RESULTS**

rx00902	1333	GB_BA1:PLPDHOS	3119	L06822	Plasmid pSa (from Escherichia coli) dihydropteroate synthase gene, 3' end.	Plasmid pSa	38,966	20-MAR-1996
		GB_BA1:PDGINTORF	6747	L06418	Integron In7 (from Plasmid pDGO100 from Escherichia coli) integrase (int), aminoglycoside adenyltransferase (aad), quaternary ammonium compound-resistance protein, dihydrofolate reductase (dhfrX), and dihydropteroate synthase (sulI) genes.	Plasmid pDGO100	38,966	20-MAR-1996
		GB_GSS15:AQ606873	581	AQ606873	HS_5404_B2_H05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=10 Row=P, genomic survey sequence.	Homo sapiens	37,900	10-Jun-99
		GB_GSS9:AQ163442	658	AQ163442	nbxb0007A07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0007A07f, genomic survey sequence.	Oryza sativa	41,885	12-Sep-98
		GB_PL1:PSST70	4974	X69213	P.sativum Pss170 gene for heat-shock protein.	Pisum sativum	36,866	3-Jul-96
		GB_GSS1:FR0025208	612	AL018047	F.rubripes GSS sequence, clone 145D10aA8, genomic survey sequence.	Fugu rubripes	37,815	10-DEC-1997
		GB_GSS1:FR0021844	252	AL014715	F.rubripes GSS sequence, clone 069K22aG5, genomic survey sequence.	Fugu rubripes	37,698	10-DEC-1997
		GB_GSS12:AQ403344	593	AQ403344	HS_2257_B1_B03_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=5 Row=D, genomic survey sequence.	Homo sapiens	31,552	13-MAR-1999
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	37,902	17-Jun-98
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	39,140	17-Jun-98
		GB_BA2:MSGKATG	1745	L14268	Mycobacterium tuberculosis ethyl methane sulphonate resistance protein (katG) gene, 3'end.	Mycobacterium tuberculosis	42,517	26-Aug-99
		GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95f16, *** SEQUENCING IN PROGRESS ***; 17 unordered pieces.	Homo sapiens	39,497	08-DEC-1999
		GB_GSS1:GGA340111	990	AJ232089	Gallus gallus anonymous sequence from Cosmid mapping to chromosome 2 (Cosmid 34 - Contig 15), genomic survey sequence.	Gallus gallus	37,970	25-Aug-98
		GB_HTG6:AC010998	144338	AC010998	Homo sapiens clone RP11-95f16, *** SEQUENCING IN PROGRESS ***; 17 unordered pieces.	Homo sapiens	38,226	08-DEC-1999
		GB_BA1:ECTTN7	2280	AJ001816	Escherichia coli left end of transposon Tn7 including type 2 integron.	Escherichia coli	38,822	4-Nov-97
		GB_IN2:AF176377	8220	AF176377	Caenorhabditis briggsae CES-1 (ces-1) gene, complete cds; and CPN-1 (cpn-1) gene, partial cds.	Caenorhabditis briggsae	39,921	09-DEC-1999
		GB_GSS10:AQ196728	429	AQ196728	CIT-HSP-2381F4, TR CIT-HSP Homo sapiens genomic clone 2381F4, genomic survey sequence.	Homo sapiens	39,019	16-Sep-98
		GB_BA1:U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	58,303	01-MAR-1994
		GB_BA1:SYCGROESL	3256	D12677	Synechocystis sp. groES and groEL genes.	Synechocystis sp.	34,593	3-Feb-99
		GB_BA1:D90905	139467	D90905	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915.	Synechocystis sp.	34,593	7-Feb-99
		GB_BA1:PSEFAOAB	3480	D10390	P. fragi faoA and faoB genes, complete cds.	Pseudomonas fragi	51,919	2-Feb-99
		GB_BA1:AB014757	6057	AB014757	Pseudomonas sp. 61-3 genes for PhbR, acetoacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds.	Pseudomonas sp. 61-3	50,573	26-DEC-1998
		GB_BA1:SC8D9	38681	AL035569	Streptomyces coelicolor cosmid 8D9.	Streptomyces coelicolor	42,200	26-Feb-99
		GB_EST11:AA244557	379	AA244557	mx07a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	39,050	10-MAR-1997
		GB_EST14:AA407673	306	AA407673	EST01834 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus musculus cDNA clone C0014F02 3', mRNA sequence.	Mus musculus	38,562	26-Aug-98
		GB_EST26:AI390328	604	AI390328	mx07a01.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	33,136	2-Feb-99

**TABLE 4: ALIGNMENT RESULTS**

rx01138	540	GB_OV:XLXINT1 GB_PR4:AC006054	1278 143738	X13138 AC006054	Xenopus laevis int-1 mRNA for int-1 protein. Homo sapiens Xq28 BAC RPC11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Xenopus laevis Homo sapiens	40,038 37,996	31-MAR-1995 1-Apr-99
rx01172	1578	GB_PR4:AC006054 GB_BA1:SCE39 GB_BA1:MSU50335	143738 23550 5193	AC006054 AL049573 U50335	Homo sapiens Xq28 BAC RPC11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence. Streptomyces coelicolor cosmid E39. Mycobacterium smegmatis phage resistance (mpr) gene, complete cds.	Homo sapiens  Streptomyces coelicolor Mycobacterium smegmatis	36,053  62,357 37,853	1-Apr-99  31-MAR-1999 1-Feb-97
rx01191	1713	GB_BA1:BACTHRTRNA15467 GB_PR2:HS1191B2	60828 60828	D84213 AL022237	Bacillus subtilis genome, trnI-feuABC region. Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Bacillus subtilis Homo sapiens	53,807 38,366	6-Feb-99 23-Nov-99
		GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	39,595	23-Nov-99
rx01205	554	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 57/162.	Mycobacterium tuberculosis	57,762	17-Jun-98
rx01212	1047	GB_PL1:ATY12776 GB_PL2:ATT6K21 GB_BA2:SCD25	38483 99643 41622	Y12776 AL021889 AL118514	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus. Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSA project). Streptomyces coelicolor cosmid D25.	Arabidopsis thaliana Arabidopsis thaliana Streptomyces coelicolor A3(2)	32,971 35,273 39,654	7-Sep-98 16-Aug-99 21-Sep-99
rx01219	1005	GB_BA1:SLGLYUB GB_BA1:SCH10 GB_PAT:A68024 GB_PAT:A68025 GB_PAT:A68027 GB_PR3:HS512B11	2576 39524 520 193 193 64356	X65556 AL049754 A68024 A68025 A68027 AL031058	S.lividans tRNA-GlyU beta gene. Streptomyces coelicolor cosmid H10. Sequence 19 from Patent WO9743409. Sequence 20 from Patent WO9743409. Sequence 22 from Patent WO9743409. Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.	Streptomyces lividans Streptomyces coelicolor unidentified unidentified unidentified Homo sapiens	54,493 44,638 42,553 43,229 38,342 35,478	20-DEC-1993 04-MAY-1999 05-MAY-1999 05-MAY-1999 05-MAY-1999 23-Nov-99
		GB_EST6:N99239	424	N99239	zbf76h11.s1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:309573 3', mRNA sequence.	Homo sapiens	39,623	20-Aug-96
		GB_EST16:AA554268	400	AA554268	nk36c09.s1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1015600 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);, mRNA sequence.	Homo sapiens	36,111	8-Sep-97
rx01221	849	GB_PR4:AF179633 GB_V1:EHVU20824 GB_BA2:AE000407 GB_PAT:AR068625	96371 184427 10601 28804	AF179633 U20824 AE000407 AR068625	Homo sapiens chromosome 16 map 16q23.3-q24.1 sequence. Equine herpesvirus 2, complete genome. Escherichia coli K-12 MG1655 section 287 of 400 of the complete genome. Sequence 1 from patent US 5854034.	Homo sapiens Equine herpesvirus 2 Escherichia coli Unknown.	40,199 37,001 39,471 40,574	5-Sep-99 2-Feb-96 12-Nov-98 29-Sep-99

**TABLE 4: ALIGNMENT RESULTS**

GB_BA2:SSU51197	28804	U51197	Spingomonas S88 sphingan polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase (spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase (spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26, ATP-binding cassette transporter (atfD), ATP-binding cassette transporter (atfB), glucosyl-isoprenylphosphate transferase (spsB), glucose-1-phosphate thymidyltransferase (rfsA), dTDP-6-deoxy-D-glucose-3,5-epimerase (rfsC) dTDP-D-glucose-4,6-dehydratase (rfsB), dTDP-6-deoxy-L-mannose-dehydrogenase (rfsD), Urf 31, and Urf 34 genes, complete cds.	Spingomonas sp. S88	40,574	16-MAY-1996
GB_IN1:BBU44918	2791	U44918	Babesia bovis ATP-binding protein (babo) mRNA, complete cds.	Babesia bovis	39,228	9-Aug-97
GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	99,923	1-Feb-99
GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	59,056	17-Jun-98
GB_PR3:AC005618	176714	AC005618	Homo sapiens chromosome 5, BAC clone 249h5 (LBNL H149), complete sequence.	Homo sapiens	36,270	5-Sep-98
GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS *** 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-17C17, *** SEQUENCING IN PROGRESS *** 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	56,071	01-DEC-1999
GB_BA1:AB002668	24907	AB002668	Actinobacillus actinomycetemcomitans DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.	Actinobacillus actinomycetemcomitans	46,679	21-Feb-98
GB_BA1:AB010415	23112	AB010415	Actinobacillus actinomycetemcomitans gene cluster for 6-deoxy-L-talan synthesis, complete cds.	Actinobacillus actinomycetemcomitans	46,679	13-Feb-99
GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999
GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999
GB_HTG3:AC006445	174547	AC006445	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS *** 7 unordered pieces.	Homo sapiens	34,812	15-Sep-99
GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21); from 3197001 to 3414420.	Bacillus subtilis	37,802	26-Nov-97
GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	42,021	26-Jun-98
GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	40,323	26-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

rx01339	1111	GB_PL1:MGU60290 GB_HTG3:AC011371	4614 189187	U60290 AC011371	Magnaporthe grisea nitrogen regulatory protein (NUT1) gene, complete cds. Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Magnaporthe grisea Homo sapiens	38,707 39,741	3-Jul-96 06-OCT-1999
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
rx01382	1192	GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
rx01399	1142	GB_PR3:AC002416 GB_EST9:AA096601	128915 524	AC002416 AA096601	Human Chromosome X, complete sequence. IMAGE:552473 5' similar to gb.L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN); gb.L04280 Mus musculus ribosomal protein (MOUSE);, mRNA sequence. pat.pk0074.e9.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence.	Homo sapiens Mus musculus	37,521 40,525	29-Jan-98 15-Feb-97
rx01420	1065	GB_EST37:AI982114 GB_OV:GGU20766 GB_HTG2:AC005690	626 1645 193424	AI982114 U20766 AC005690	gb.L04280 Mus musculus ribosomal protein (MOUSE);, mRNA sequence. pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence. Gallus gallus vacuolar H+-ATPase B subunit gene, complete cds. Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Gallus gallus Gallus gallus Homo sapiens	37,785 38,244 37,464	15-Sep-99 07-DEC-1995 11-Apr-99
		GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
rx01467	414	GB_HTG1:CEY102G3_2110000 GB_HTG1:CEY102G3_2110000 GB_HTG1:CEY113G7_4110000 GB_BA2:AF030975	22092 2511	AC006637 AL020985 AL020985 AL031113 AF030975	Caenorhabditis elegans clone F41B4, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces. Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces. Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces. Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces. Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Caenorhabditis elegans Aeromonas salmonicida	37,488 35,437 35,437 35,437 41,516	23-Feb-99 3-Dec-98 3-Dec-98 12-Jan-99 2-Apr-98
rx01576	882	GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	38,171	2-Apr-98
rx01580	840	GB_EST22:AI068560 GB_GSS14:AQ554460	965 681	AI068560 AQ554460	mgae0003aC11fMagnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0003aC11f 5', mRNA sequence. RPC1-11-419F2.TV RPC1-11 Homo sapiens genomic clone RPC1-11-419F2, genomic survey sequence.	Pyricularia grisea Homo sapiens	40,073 36,522	09-DEC-1999 28-MAY-1999
		GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	36,609	23-DEC-1998
		GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	33,612	23-DEC-1998
rx01584								
rx01604	771	GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999

**TABLE 4: ALIGNMENT RESULTS**

rx01614	1146	GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
		GB_HTG3:AC011402	168868	AC011402	Homo sapiens chromosome 5 clone CIT978SKB_38B5, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
		GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	42,284	11-Aug-98
		GB_EST17:AA608825	439	AA608825	af03g07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030620 3' similar to TR:G976083 G976083 HISTONE H2A RELATED. ; mRNA sequence.	Homo sapiens	40,092	02-MAR-1998
		GB_PR4:AC005377	102311	AC005377	Homo sapiens PAC clone DJ1136G02 from Tq32-q34, complete sequence.	Homo sapiens	37,811	28-Apr-99
rx01629	1635	GB_BA1:CGPROPOGEN	2936	Y12537	C. glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
		GB_BA1:CGPROPOGEN	2936	Y12537	C. glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
		GB_PR4:AF191071	88481	AF191071	Homo sapiens chromosome 8 clone BAC 388D06, complete sequence.	Homo sapiens	35,612	11-OCT-1999
rx01644	1401	GB_BA1:MSGB577COS37770	35615	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	55,604	14-Jun-96
		GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	36,416	27-Aug-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	55,844	24-Jun-99
rx01667	1329	GB_BA1:CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds.	Corynebacterium glutamicum	100,000	13-MAR-1997
		GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPC198-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
		GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3L/77E1 clone RPC198-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
rx01722	1848	GB_GSS1:FR0022586	522	AL015452	F. rubripes GSS sequence, clone 077P23aB10, genomic survey sequence.	Fugu rubripes	40,192	10-DEC-1997
		GB_GSS1:FR0022584	485	AL015450	F. rubripes GSS sequence, clone 077P23aB11, genomic survey sequence.	Fugu rubripes	35,876	10-DEC-1997
		GB_IN1:CET26H2	37569	Z82055	Caenorhabditis elegans cosmid T26H2, complete sequence.	Caenorhabditis elegans	34,759	19-Nov-99
rx01727	1401	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein YhbW (yhbW) gene, partial cds.	Corynebacterium glutamicum	99,929	4-Jun-98
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	36,903	30-Nov-99
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	35,642	30-Nov-99
rx01737	1182	GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3.	Streptomyces coelicolor	38,054	8-Jul-99
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
rx01762	1659	GB_BA1:MTCI28	36300	Z97050	Mycobacterium tuberculosis H37Rv complete genome, segment 10/162.	Mycobacterium tuberculosis	49,574	23-Jun-98
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	44,049	24-MAR-1999
		GB_BA1:SCE29	26477	AL035707	Streptomyces coelicolor cosmid E29.	Streptomyces coelicolor	40,246	12-MAR-1999

**TABLE 4: ALIGNMENT RESULTS**

rx01764	1056	GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	37,084	6-Sep-99
		GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	34,890	6-Sep-99
rx01801	1140	GB_EST38:AW066306	334	AW066306	687009D03.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.	Zea mays	46,108	12-OCT-1999
		GB_GSS13:AQ484750	375	AQ484750	RPC1-11-248N4.TV RPC1-11 Homo sapiens genomic clone RPC1-11-248N4, genomic survey sequence.	Homo sapiens	32,000	24-Apr-99
		GB_GSS13:AQ489971	252	AQ489971	RPC1-11-247N23.TV RPC1-11 Homo sapiens genomic clone RPC1-11-247N23, genomic survey sequence.	Homo sapiens	36,111	24-Apr-99
rx01823	900	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	35,779	16-Aug-99
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	39,211	15-Jan-97
		GB_BA1:BSUB0018	209510	Z99121	Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.	Bacillus subtilis	36,999	26-Nov-97
rx01853	675	GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	37,612	17-Jun-98
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPC111-296K13, *** SEQUENCING IN PROGRESS ***; 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPC111-296K13, *** SEQUENCING IN PROGRESS ***; 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
rx01881	558	GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***; 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***; 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	37,893	18-Jun-98
rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPC1-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01897	666	GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY53F4_2	110000	Z92860	Caenorhabditis elegans chromosome II clone Y53F4, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	33,333	15-Oct-99
rx01946	1298	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	65,560	17-Jun-98
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	50,648	24-MAY-1999
		GB_BA1:SCARD1GN	2321	X84374	S.capreolus ard1 gene.	Streptomyces capreolus	44,973	23-Aug-95



**TABLE 4: ALIGNMENT RESULTS**

rx01980	756	GB_PL2:AC008262	99698	AC008262	Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome 1, complete sequence.	Arabidopsis thaliana	35,310	21-Aug-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	35,505	20-Nov-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	39,973	20-Nov-99
rx01983	630	GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	32,367	27-OCT-1999
rx02020	1111	GB_BA1:CGDNAAROP 2612	X85965	X85965	C.glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum unidentified	100,000	30-Nov-97
		GB_PAT:A58887	1612	A58887	Sequence 1 from Patent WO9701637.	Salmonella typhimurium	100,000	06-MAR-1998
		GB_BA1:STYCARABA 4378	M95047	M95047	Salmonella typhimurium transport protein, complete cds, and transfer RNA-Arg.	Salmonella typhimurium	50,547	13-MAR-1996
rx02029	1437	GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:HS118B18	104729	AL034344	Homo sapiens chromosome 6 clone RP1-118B18 map p24.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,355	03-DEC-1999
rx02030	1509	GB_PR4:AC007695	63247	AC007695	Homo sapiens 12q24 BAC RPC111-124N23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	38,681	1-Sep-99
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,445	22-OCT-1999
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,968	22-OCT-1999
rx02073	1653	GB_BA1:CGGDHA 2037	X72855	X72855	C.glutamicum GDHA gene.	Corynebacterium glutamicum	39,655	24-MAY-1993
		GB_BA1:CGGDH 2037	X59404	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	44,444	30-Jul-99
rx02074		GB_BA2:SC2H4 25970	AL031514	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	38,452	19-OCT-1999
rx02095	1527	GB_EST18:AA703380 471	AA703380	AA703380	zj12b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450035 3' similar to contains LTR5.i3 LTR5 repetitive element ; mRNA sequence.	Homo sapiens	36,518	24-DEC-1997
		GB_HTG6:AC009769 122911	AC009769	AC009769	Homo sapiens chromosome 8 clone RP11-202112 map 8, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,473	07-DEC-1999

**TABLE 4: ALIGNMENT RESULTS**

rx02099	373	GB_EST7:W70175	436	W70175	zd52c02.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344258 5' similar to contains LTR5.b2 LTR5 repetitive element;; mRNA sequence.	Homo sapiens	34,174	16-OCT-1996
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum ampP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***; 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***; 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
rx02115	1197	GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	36,717	13-Nov-99
		GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	36,092	13-Nov-99
		GB_PR1:HUMHM145	2214	D10925	Human mRNA for HM145.	Homo sapiens	39,171	3-Feb-99
rx02128	1818	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	38,682	17-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	35,746	17-Jun-98
		GB_GSS10:AQ161109	738	AQ161109	nbxb0006D03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0006D03r, genomic survey sequence.	Oryza sativa	38,482	12-Sep-98
rx02133	329	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	32,317	18-Nov-96
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPCI-98 10.M.16 map 93C-93D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
rx02150	924	GB_EST37:AW012260	358	AW012260	um06e09.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:2182312 5' similar to SW:AMPL_BOVIN P00727 CYTOSOL AMINOPEPTIDASE ;; mRNA sequence.	Mus musculus	39,385	10-Sep-99
		GB_GSS3:B87734	389	B87734	RPCI11-30D24.TP RPCI-11 Homo sapiens genomic clone RPCI-11-30D24, genomic survey sequence.	Homo sapiens	37,629	9-Apr-99
		GB_PR4:AC005042	192218	AC005042	Homo sapiens clone NH0552E01, complete sequence.	Homo sapiens	36,901	14-Jan-99
rx02171	1776	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	53,714	12-MAY-1998
		GB_EST24:AI170522	367	AI170522	EST216450 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCO75 3' end, mRNA sequence.	Rattus sp.	44,186	20-Jan-99
		GB_PL1:PHVDLECA	1441	K03288	P.vulgaris phytohemagglutinin gene encoding erythroagglutinating phytohemagglutinin (PHA-E), complete cds.	Phaseolus vulgaris	39,103	27-Apr-93
rx02173	1575	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	44,118	17-Feb-95
		GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	36,189	17-Feb-95

**TABLE 4: ALIGNMENT RESULTS**

rx02224	1920	GB_BA2:AE000104	10146	AE000104	Rhizobium sp. NGR234 plasmid pNGR234a, section 41 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	38,487	12-DEC-1997
		GB_BA2:GXU21300	8990	U21300	Corynebacterium striatum hypothetical protein YbhB gene, partial cds; ABC transporter TetB (tetB), ABC transporter TetA (tetA), transposase, 23S rRNA methyltransferase, and transposase genes, complete cds; and unknown genes.	Corynebacterium striatum	37,264	9-Apr-99
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248019, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
		GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248019, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
rx02225	905	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	35,498	18-Nov-96
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ; mRNA sequence.	Homo sapiens	35,589	18-MAR-1999
		GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS. ; mRNA sequence.	Homo sapiens	42,786	18-MAR-1999
rx02233	1410	GB_BA1:ERWPNLB	1291	M65057	Erwinia carotovora pectin lyase (pnl) gene, complete cds.	Erwinia carotovora	37,780	26-Apr-93
		GB_EST30:AV021947	313	AV021947	1190024M23, mRNA sequence.	Mus musculus	39,423	28-Aug-99
		GB_EST33:AV087117	251	AV087117	AV087117 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310028C15, mRNA sequence.	Mus musculus	47,410	25-Jun-99
rx02253	1050	GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ; mRNA sequence.	Mus musculus	36,136	12-MAR-1997
		GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1 ; mRNA sequence.	Mus musculus	36,202	12-MAR-1997
rx02261	1479	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE	2028	X93513	C.glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
		GB_BA1:CORPEPC	4885	M25819	C.glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
rx02268	1023	GB_PL2:AF087130	3478	AF087130	Neurospora crassa siderophore regulation protein (sre) gene, complete cds.	Neurospora crassa	39,268	22-OCT-1998
		GB_EST30:AI663709	408	AI663709	IMAGE:1449010 5' similar to TR:O75585 O75585 MITOGEN- AND STRESS-ACTIVATED PROTEIN KINASE-2 ; mRNA sequence.	Mus musculus	41,523	10-MAY-1999
		GB_RO:AF074714	3120	AF074714	Mus musculus mitogen- and stress-activated protein kinase-2 (mMSK2) mRNA, complete cds.	Mus musculus	38,347	24-OCT-1998
rx02269	1095	GB_GSS4:AQ742825	847	AQ742825	HS_5482_B2_A04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1058 Col=8 Row=B, genomic survey sequence.	Homo sapiens	37,703	16-Jul-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_L_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_L_06 map 18, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99

**TABLE 4: ALIGNMENT RESULTS**

rx02309	1173	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	52,344	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	52,344	03-DEC-1998
		GB_HTG2:AC007163	186618	AC007163	Homo sapiens clone NH0091M05, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	37,263	23-Apr-99
rx02310	1386	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	36,861	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	36,861	03-DEC-1996
		GB_PR3:HS279N11	169998	Z98255	Human DNA sequence from PAC 279N11 on chromosome Xq11.2-13.3.	34,516	23-Nov-99
rx02321	1752	GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dlsR1 and dlsR2 genes, complete cds.	99,030	19-OCT-1998
		GB_PAT:E17019	4961	E17019	Brevibacterium lactofermentum dlsR and dlsR2 genes.	98,973	28-Jul-99
		GB_BA1:AB018530	2855	AB018530	Corynebacterium glutamicum dlsR gene, complete cds.	99,030	19-OCT-1998
rx02335	1896	GB_BA1:CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds.	99,947	16-Jan-97
		GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	40,247	30-Jan-96
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	67,568	10-Feb-99
rx02364	750	GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	36,130	8-Feb-99
		GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	34,543	8-Feb-99
rx02372	2010	GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***; 4 ordered pieces.	36,138	07-OCT-1999
		GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***; 4 ordered pieces.	36,138	07-OCT-1999
		GB_EST21:AA992021	279	AA992021	ot36c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618848 3', mRNA sequence.	41,219	3-Jun-98
rx02397	1119	GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	38,566	12-OCT-1999
		GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	38,566	12-OCT-1999
		GB_BA1:D90826	19493	D90826	E.coli genomic DNA, Kohara clone #335(40.9-41.3 min.).	39,600	21-MAR-1997
rx02424	723	GB_EST13:AA334108	275	AA334108	EST38262 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.	38,603	21-Apr-97
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	36,111	14-Aug-98
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	33,427	14-Aug-98
rx02426	1656	GB_PAT:A06664	1350	A06664	B.stearothermophilus tct gene.	39,936	29-Jul-93
		GB_PAT:A04115	1361	A04115	B.stearothermophilus recombinant tct gene.	40,042	17-Feb-97
		GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus tct gene encoding L-lactate dehydrogenase, complete cds.	40,338	26-Apr-93
					Bacillus		
					stearothermophilus		

**TABLE 4: ALIGNMENT RESULTS**

rx02487	1827	GB_BA2:AF007101	32870	AF007101	Streptomyces hygroscopicus putative pteridine-dependent dioxygenase, PKS modules 1,2,3 and 4, and putative regulatory protein genes, complete cds and putative hydroxylase gene, partial cds.	Streptomyces hygroscopicus	43,298	13-Jan-98
		GB_BA1:MTCI364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	44,352	17-Jun-98
		GB_BA2:AF119621	15986	AF119621	Pseudomonas abietaniphila BKME-9 DtlI (dtlI), dioxygenase DtlA oxygenase component small subunit (dtiA2), dioxygenase DtlA oxygenase component large subunit (dtiA1), DtlH (dtiH), DtlG (dtiG), DtlF (dtiF), DtlR (dtiR), DtlE (dtiE), DtlD (dtiD), aromatic diterpenoid extradiol ring-cleavage dioxygenase (dtiC), DtlB (dtiB), and dioxygenase DtlA ferredoxin component (dtiA3) genes, complete cds; and unknown genes.	Pseudomonas abietaniphila	43,611	28-Apr-99
rx02511	780	GB_PR4:AC002470	235395	AC002470	Homo sapiens Chromosome 22q11.2 BAC Clone b135h6 in BCRL2-GGT Region, complete sequence.	Homo sapiens	37,971	30-Nov-99
		GB_PR4:AC002472	147100	AC002472	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.	Homo sapiens	38,239	13-Sep-99
		GB_EST34:AI806938	118	AI806938	wf24b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356501 3' similar to SW:PLZF_HUMAN Q05516 ZINC FINGER PROTEIN PLZF ; mRNA sequence.	Homo sapiens	38,983	7-Jul-99
rx02512	1086	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	37,407	17-Jun-98
		GB_BA1:MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	43,193	24-Jun-97
		GB_OV:GGU43396	2738	U43396	Gallus gallus tropomyosin receptor kinase A (ctrka) mRNA, complete cds.	Gallus gallus	38,789	18-Jan-96
rx02527	1452	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rmb-dnaB genomic region.	Bacillus subtilis	37,395	4-Feb-98
		GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rmb-dnaB genomic region.	Bacillus subtilis	36,218	4-Feb-98
		GB_HTG2:AC005861	112369	AC005861	Arabidopsis thaliana clone F23B24, *** SEQUENCING IN PROGRESS *** , 6 unordered pieces.	Arabidopsis thaliana	38,407	29-Apr-99
rx02547	2262	GB_PL1:AB006530	7344	AB006530	Citrus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrus lanatus	35,449	20-Aug-97
		GB_PL1:CNASA	5729	D85624	Citrus vulgaris serine acetyltransferase (Sat) DNA, complete cds.	Citrus lanatus	35,449	6-Feb-99
		GB_PL1:AB006530	7344	AB006530	Citrus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrus lanatus	34,646	20-Aug-97
rx02566	1332	GB_EST32:AI727189	619	AI727189	BNLGH17498 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AB020715) KIAA0908 protein [Homo sapiens], mRNA sequence.	Gossypium hirsutum	35,099	11-Jun-99
		GB_BA1:CGPUTP	3791	Y09163	C. glutamicum putP gene.	Corynebacterium glutamicum	38,562	8-Sep-97
		GB_PL2:SPAC13G6	33481	Z54308	S. pombe chromosome I cosmid c13G6.	Schizosaccharomyces pombe	35,774	18-OCT-1999
rx02571	1152	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,872	9-Apr-97
		GB_EST35:AI857385	488	AI857385	wf55e03.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2428828 3', mRNA sequence.	Homo sapiens	39,139	26-Aug-99
		GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	38,552	9-Apr-97

**TABLE 4: ALIGNMENT RESULTS**

rx02578	1227	GB_PL1:AB016871	79109	AB016871	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence.	Arabidopsis thaliana	34,213	20-Nov-99
		GB_PL1:AB025602	55790	AB025602	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone: F14A1, complete sequence.	Arabidopsis thaliana	36,461	20-Nov-99
		GB_IN1:CELF36H9	35985	AF016668	Caenorhabditis elegans cosmid F36H9.	Caenorhabditis elegans	35,977	8-Aug-97
rx02581	1983	GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	38,517	17-Jun-98
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	39,173	17-Jun-98
rx02582	4953	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	38,548	24-Jun-99
		GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	46,263	17-Jun-98
		GB_BA1:SEERYABS	20444	X62569	S. erythraea eryA gene for 6-deoxyerythronolide B synthase II & III.	Saccharopolyspora erythraea	45,053	28-Feb-92
rx02583	1671	GB_BA2:AF113605	1593	AF113605	Streptomyces coelicolor propionyl-CoA carboxylase complex B subunit (pccB) gene, complete cds.	Streptomyces coelicolor	58,397	08-DEC-1999
		GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	52,916	15-Jan-99
		GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	58,809	19-OCT-1998
rx02599	600	GB_BA1:AEMML	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	35,264	22-Jan-98
		GB_EST15:AA508926	422	AA508926	MBAFCW1C08T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCW1C08 5', mRNA sequence.	Brugia malayi	43,377	8-Jul-97
rx02634	1734	GB_BA1:AEMML	2585	X99639	Ralstonia eutropha mmlH, mmlI & mmlJ genes.	Ralstonia eutropha	41,148	22-Jan-98
		GB_BA1:SYNPOO	1964	X17439	Synechocystis ndhC, psbG genes for NDH-C, PSII-G and ORF157.	Synechocystis PCC6803	38,145	10-Feb-99
		GB_GSS9:AQ101527	184	AQ101527	HS_2265_A1_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=21 Row=I, genomic survey sequence.	Homo sapiens	38,798	27-Aug-98
		GB_IN1:MNE133341	399	AJ133341	Melarihaphe neritoides partial caM gene, exons 1-2.	Melarihaphe neritoides	39,098	2-Jun-99
rx02638	999	GB_BA2:AE001756	10938	AE001756	Thermotoga maritima section 68 of 136 of the complete genome.	Thermotoga maritima	40,104	2-Jun-99
		GB_GSS12:AQ423878	689	AQ423878	CITBI-E1-2575E20.TF CITBI-E1 Homo sapiens genomic clone 2575E20, genomic survey sequence.	Homo sapiens	36,451	23-MAR-1999
		GB_HTG2:AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Caenorhabditis elegans	39,072	23-Feb-99
rx02659	335	GB_EST36:AI900317	436	AI900317	sc04a02.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:Gm-c1012-1155 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ., mRNA sequence.	Glycine max	41,566	06-DEC-1999
		GB_GSS12:AQ342831	683	AQ342831	RPCI11-122K17.T.J RPCI-11 Homo sapiens genomic clone RPCI-11-122K17, genomic survey sequence.	Homo sapiens	34,762	07-MAY-1999
		GB_EST36:AI900856	779	AI900856	sb95c11.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:Gm-c1012-429 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ., mRNA sequence.	Glycine max	39,063	06-DEC-1999
rx02676	1512	GB_IN2:CELB0213	39134	AF039050	Caenorhabditis elegans cosmid B0213.	Caenorhabditis elegans	35,814	2-Jun-99

**TABLE 4: ALIGNMENT RESULTS**

GB_GSS1:CNS00PZB	364	AL085157	Arabidopsis thaliana genome survey sequence SP6 end of BAC F10D11 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	38,462	28-Jun-99
GB_RO:RNITPR2R	10708	X61677	Rat ITPR2 gene for type 2 inositol triphosphate receptor.	Rattus norvegicus	37,543	21-OCT-1991
GB_RO:D89728	5002	D89728	Mus musculus mRNA for LOK, complete cds.	Mus musculus	38,829	7-Feb-99
GB_GSS8:AQ062004	362	AQ062004	CIT-HSP-2346O14, TR CIT-HSP Homo sapiens genomic clone 2346O14, genomic survey sequence.	Homo sapiens	36,565	31-Jul-98
GB_GSS14:AQ555818	462	AQ555818	HS_5230_B1_G06_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=806 Col=11 Row=N, genomic survey sequence.	Homo sapiens	36,534	29-MAY-1999
GB_IN1:DME9736	7411	AJ009736	Drosophila melanogaster Idefix retroelement: gag, pol and env genes, partial.	Drosophila melanogaster	36,522	19-Jan-99
GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	39,341	2-Feb-99
GB_PR4:AC004801	193561	AC004801	Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	37,037	2-Feb-99
GB_EST34:AV132028	258	AV132028	AV132028 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA clone 2700087F01, mRNA sequence.	Mus musculus	43,529	1-Jul-99
GB_GSS10:AQ240654	452	AQ240654	CIT-HSP-2385D24, TFB.1 CIT-HSP Homo sapiens genomic clone 2385D24, genomic survey sequence.	Homo sapiens	40,044	30-Sep-98
GB_GSS11:AQ309500	576	AQ309500	CIT-HSP-2384D24, TFD CIT-HSP Homo sapiens genomic clone 2384D24, genomic survey sequence.	Homo sapiens	38,869	22-DEC-1998
GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (mh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds, and unknown genes.	Zymomonas mobilis	39,024	4-Nov-98
GB_BA1:SYCSLRB	146271	D64000	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999.	Synechocystis sp.	34,573	13-Feb-99
GB_BA2:AE001306	13316	AE001306	Chlamydia trachomatis section 33 of 87 of the complete genome.	Chlamydia trachomatis	38,940	2-Sep-98
GB_BA2:AF126953	1638	AF126953	Corynebacterium glutamicum cystathionine gamma-synthase (metB) gene, complete cds.	Corynebacterium glutamicum	100,000	10-Sep-99
GB_BA1:SC15	6661	AL079332	Streptomyces coelicolor cosmid i5.	Streptomyces coelicolor	37,486	16-Jun-99
GB_PR3:HS90L6	190837	Z97353	Human DNA sequence from clone 90L6 on chromosome 22q11.21-11.23. Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens	34,149	23-Nov-99
GB_BA2:AF099015	5000	AF099015	Streptomyces coelicolor strain A3(2) integrase (int), Fe-containing superoxide dismutase II (sodF2), Fe uptake system permease (firE), and Fe uptake system integral membrane protein (firD) genes, complete cds.	Streptomyces coelicolor	36,721	1-Jun-99
GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,787	17-Apr-96
GB_HTG3:AC011361	186148	AC011361	Homo sapiens chromosome 5 clone CIT-HSPC_482N19, *** SEQUENCING IN PROGRESS ***; 69 unordered pieces.	Homo sapiens	43,577	06-OCT-1999
GB_PR4:AC005998	96556	AC005998	Homo sapiens clone DJ0622E21, complete sequence.	Homo sapiens	37,298	29-Jul-99
GB_PR4:AC006008	57554	AC006008	Homo sapiens clone DJ0820A21, complete sequence.	Homo sapiens	36,638	17-Jun-99
GB_PR3:HSDJ73H14	95556	AL080272	Human DNA sequence from clone 73H14 on chromosome Xq26.3-28, complete sequence.	Homo sapiens	39,726	23-Nov-99

**TABLE 4: ALIGNMENT RESULTS**

rx02809	375	GB_RO:MUSPCTLT	3172	M22527	Mouse cytotoxic T lymphocyte-specific serine protease CPPII gene, complete cds.	Mus musculus	47,518	19-Jan-96
		GB_RO:MUSGRC	894	M18459	Mouse granzyme C serine esterase mRNA, complete cds.	Mus musculus	44,939	12-Jun-93
		GB_RO:RNU57062	880	U57062	Rattus norvegicus natural killer cell protease 4 (RNKP-4) mRNA, complete cds.	Rattus norvegicus	41,554	31-Jul-96
rx02811	484	GB_GSS6:AQ832862	476	AQ832862	HS_5261_A2_E10_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=837 Col=20 Row=I, genomic survey sequence.	Homo sapiens	35,610	27-Aug-99
		GB_GSS5:AQ784593	515	AQ784593	HS_3248_A2_F02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3248 Col=4 Row=K, genomic survey sequence.	Homo sapiens	38,956	3-Aug-99
		GB_GSS13:AQ473140	397	AQ473140	CITBI-E1-2589G6.TF CITBI-E1 Homo sapiens genomic clone 2589G6, genomic survey sequence.	Homo sapiens	34,761	23-Apr-99
rx02836	678	GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	40,604	28-Nov-98
		GB_EST18:AA696785	316	AA696785	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster	38,281	28-Nov-98
rx03212	1452	GB_BA1:CGBETPGEN	2339	X93514	C. glutamicum betP gene.	Corynebacterium glutamicum	99,931	8-Sep-97
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor A3(2)	57,557	24-MAY-1999
rx03220	725	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rnb-dnaB genomic region.	Bacillus subtilis	40,000	4-Feb-98
		GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	45,328	17-Feb-97
		GB_EST38:AW048153	383	AW048153	UI-M-BH1-alq-h-05-Q-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alq-h-05-Q-UI 3', mRNA sequence.	Mus musculus	41,758	18-Sep-99
		GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.	Chlorella kessleri	38,106	17-Feb-97



## APPENDIX A: DNA SEQUENCES

>RXA00051-upstream

CAGTAAAAGTGCACCGACACTAAGAATCCTTATCCTTCAGAGTAAGGTGATCTGCGTCAA  
AAAATGTCCGCTATTACCCGAAACGAGGTGAGCATCTCG

>RXA00051

ATGAATGCCTCCCTGCCCAACCCGATCTTTTAAAGGATTGCGGGCTCGACACATTAC  
TTCATCGCGCTGGGTTCGCGATCGGCACCGCTTGTCTACGGTTCCGCTGGCGCAATC  
CAAGCAGCTGGTCCATCTGTACTCTTGGTCTACCTTCTCGGTGGCGCCGTCGTGTACTTC  
ATGCTGCGCGCACTCGGCGAGATGGCTGTGCATCACCAGTCCGTGGTTCCCTTCGCGGTC  
TACACCCGCGCACACCTTGGCGGATGGGCAGGCTACATCACCAGTGGATGTTTCGCGTTT  
GAGATGCTCATCGTCTGCCTGGCTGACCTCACAGCCATCGGCATCTATATGAACCTCTGG  
TTCCCGGCGACCCCAACAATGGACTTGGGTGGTAGCCACCCTTCTTATTGTGCGGTGGCGCA  
AACCTCGCATCAGTGCCTGGTTCGGTGAGCTCGAGTTCATCTCACCATCATTAAGGTC  
ACCGCAGTTGTGCGCATGATCGTTCGGCGGCGCAGCCATCCTCGCATTCGGTCTCGGCGCC  
AACGCTGAAGTTGCCGGCGTATCCAACCTCTGGGAGCACGGCGGATTCTTCCCAACGGT  
GTTGAAGGCATGATCGCAGCCTTCATCCTTGTCTCTTCGCATTTCGGTGGCACCGAAATC  
ATCGGTGTTGCAGGCTCTGAAGCTGAAGATCCTGAGAAGTCCATCCCCAAGGCTGTTAAT  
ACTGTCCCAGTACGCATCCTCCTCTTATGTGGGTGCCATCCTGGTGATCCTTGCCCTT  
AATCCTTGGCCTTCCATCACCAGGCGAAGAATCCCCATTTCGTCCAGATCTTCGACACCCTC  
GGCGTCAACTGGGCTGCTGGTCTCCTCAACGCCGTGGTCATCACCCTGCACTGTCTGCC  
ATCAACGCTGACCTCTTCGGCGCTGGCGCGTTCCTCACTGGTCTTGCGAAGGAAAACCTC  
GCACCAAGGCCATGGGCAAGATCGCCAAGAAGCGGCTTCAGTCATGACCACCACCATC  
ATGATCATCGTCTTGATCGTGGGAGTAATCCTCAACGCAGTGCTTCCCGAGCGCGTCTTC  
GAGATCGTCGCTTCCCTAGCAACCTTCGCCACAGTTTACGTCTGGCTGATGATCCTGCTC  
GCACAGGTGGGATCCCGCCGAAACATGCCTGCCGACGAGGTCAAGTCCCTGAAGTTCCCT  
GTCCCTTCTACCCCTTCGGACAATACTTCGCGATCCTATTTATCGCCTTACCTTCGGC  
ATCATGGTCTGGTACGACAACCTACCACCTGCCACTCGCCGTCGGCGTTGGATTCTTGTC  
CTGATGACAATCCTTTACTACGCCACAGGCCGACCAAAAGGCGATCGCTCCGATCGATTAT  
GAAGAGCTAGATCCGCGACGCGAT

>RXA00051-downstream

TAATCTAGACTCGCACGAAAAAG

>RXA00091-upstream

TCATGAACCACGTGTTCCGCGCACAAGGCGTCGTGTCCATCATTATTGAGATGGTCGGCG  
GTACCGTCTTCTCATCGTCATCCTCAGAAAGGGCAGACT

>RXA00091

GTGATTACGTTAACTAATGTCCGCAAGGAATACTCCAGCGACGTTGCCATCGGCCCGTC  
AACCTTGAGATCCCAGCCGGCGGCATCACCAGCTTGGTTCGGCCAAACGGTGCAGGCAAG  
TCAACACTGCTCACCATGATCGGTGACTCCTCGGCATCGATGAAGGCAACATCACCCTA  
GCCTCCTACGATGTCACCTCAACCGCATCCAAAGATCTGGCCAAGATCATCTCCATCCTG  
CGCCAGGAAAACCACTTTGTTACCAAGCTGACCGTGCGCCAGCTCGTAGGTTTTCGGACGC  
TTCCCATATAGCAAGGGCCGGCTGACGGAAGAAGACGAGGGAATCATCTCCCGCTACATC  
GACTTCTTCAATCTCACCCTCAAGACCGCTACCTCGACCAGCTTTCGGCGGCCAG  
CGCCAGCGCGCTATGTGCGCATGGTGCTGTGCCAAGAGACGACTACGTGCTTCTCGAC  
GAACCCCTCAACAACTTTGATATCGCACACTCGGTGGAAATGATGAAACACCTCGAGAAT  
GCTGCAGCCCAATTTGGCCGCACCATCATCGTGGTTCTTCACGACATCAACTTCGCCGCG  
CGCTACGCCGATTACATCGTGGCCGTAAAGCACGGAATGATCGAAAAAGAGGGAACACCT  
GAACAGATCATGAAAAACGAGATCCTTTAGAAATCTTCAATACAGAGATCGAAGTTATT  
GAAGGACCACACGGCAAGATTGCTTGCTACCAC

>RXA00091-downstream

TAAATGAAGAGAAATAAGCCGAC

>RXA00092

ATCGCGAGAGCCCTCATCGGCCCCCGAAAAATCTTGCTTGCCGACGAACCCACCGGCGCC

CTCGACACCTCCACCGGCGACGCAGTCCTCCGCGTCTCCGCCAAAGAATCGATTCCGGT  
GCCGAGGCCTCCTTGTACCCACGAACCCCGCTTCGCCGCGTGGGCAGACCGAACAATC  
ATGCTTAGGGATGGTGAAATCCAG

>RXA00092-downstream  
TGACCACACTTCTAGCAGCAACC

>RXA00104-upstream  
TGCAAAGACATCCCGGAACCACTCCGCTACTTGAGGTCGGAATCGGGAAAGAATGCTTTT  
AGCCATGCCTTAATGTAACCAAACATCTAGAATTGAGAAC

>RXA00104  
ATGACTGTCTCAGATTGATGATTGATCCTCACCCATCGTCTCGCCCAAGGCACCGGAGAA  
ATCCTCAAAGGTGTCCGCAATGTTGGGGTGTAAAGAGGTCGGAATCTCGGTGATGCCGCG  
GACGAACTCGCACAAAGTTGGATTGCTCGAGTGTGGAGCAGCACCGCCCCAACGATGGA  
TTCCTGTCTGAAGAAGCCGCGGACAACCCAGACCGCCTATCCAAGGACCGCGTGTGGATC  
ATCGATCCCCCTCGACGGCACCAAGAATTGCGCCACCGCGCCGAGGACTGGGCAGTACAC  
ATCGCACTGGTAGAAAACGGTGTTCACCCACGCGCTGTTGGCCTCCCCGACCTTGGC  
GTGGTGTTCCTACTCCGCTGATGCCGCGCGCTGACTGGCCCTTACTCCAAGGTCATCGCC  
ATCTCCCAACCGCCCAACAAAGGTTGCTCTATCTTGCGCAGAGCAGCTCGGCTTTGAA  
ACCAAGGCCCTTGGATCCGCAAGGCGCTAAAGCAATGCACGTTCTCCTCGGTGACTACGAC  
GCCTACATCCACGCGCGGCGCAATACGAGTGGGATTCCGCAGCACCAGTCGGCGTCTGC  
AAGGCAGCAGGCTTGCACTGCTCCAGGCTCGACGGTTCCGAGCTGACCTACAACAACAAA  
GACACCTACATGCCAGACATCTTGATCTGTCGCCCTGAACTTGAGATGAACTTCTCGAG  
ATGTGCGCAAGTTCTACGAGGAGAATGGAATTAC

>RXA00104-downstream  
TAACGCTGTTATGATGACGGCAT

>RXA00113  
GCTTCAGGTGGCGGAGTTGTTGATTCCGCAGCACTTGATGCCTACGCATCCACCGTCACT  
GGTGAAGAAGGCGTCTGGCAAACGTTGCTCGCGGCATTCTGTCTCAGCTTGGTCTCGAC  
ACCAAGGACGAGGTTGAAGGCGCAGAGATCGACACCGAATCTACGACGCTGTGAAGCA  
GAACTGGGCACCGGCTGGCTGAAGCTTGTACCCCAAGTGTCTCCGCTGATCGTGCGATC  
TTGTTGACGACCGTTGGGCATCTGCACGTGAAGATCTGGCACGCCTTGCCAAACGGCGAG  
GATATTGCCGTCGAGCGCTTTGCTGGAACGGGGGAGACCGTCGTCAAGCAAGCTGCATGG  
TGGGCTGAGCACGTTGAAGACACCGCTCTCGCTGCAACCCCTGAAGCAGGTTTCCGAGGTG  
GCTGCGAAGCCAGCCAACGAGCCACACATCGACGATGTTGCGCTGGTTACCGGTGCGGCT  
CCTGAGTCGATCGCCGGTGCAGTTGCGGCTCGCCTGCTGTCCCAGGGCGCGACCGTCATT  
CTCACCGCATCGAACGTCTCCAGGCGCGTAAGGAATACGCACGCAAGCTCTACGCTGCG  
AACGCAACCCCTAACGCAAAGCTGTGGATTGTTCTGCGAATATGCTCTCTACCGCGAT  
GTTGATGCAGTCATCGATTGGATCGGCAACGAGCAGCGCGTCACCGTCGGCAGCACCGTC  
ACCGTGACCAAGCCAGCTCTGACCCCAACCTTGCGTACCCATTTCGACGCTCCATCCGTA  
TCCGGTACCTTGGCGGATGCAGGCCCACAGGCTGAAAACAGGCACGCTGCTCCTCTGG  
TCCGTGGAGCGCACCATCGCAGGACTTGCAGATCTTGCATCCCGCGGTGTCGATGGACGC  
GTCCACGTTGTACTCCCAGGTTCCCCGAACCGCGGAATGTTCCGGTGGCGACGCGCTTAC  
GGCGAAGTCAAGGCTGCTTTGACGCCATCCTTGCCAAGTGGGGCTCCGAGACCGGCTGG  
CCACAGTTTGTCTCCCTCGCACAGGCACGCATCGGCTGGGTGCGAGGCACCGGCCTCATG  
GGTGCGAACGACGTGCTCATCCCTGCCGCTGAAAAGCTGGGCATCCACGTCTACACCCCT  
GAAGAGATCTCTCCGAACTGCTGGGTCTTGATCCGCGAATCCCGCGAAAAGGCTCTG  
GAAGCACCGATCGATTACGACCTGACCGGTGGACTTTCCGGTGGCGTATCCATCGCAGCA  
CTGGCAGCATCCCTCGAGTCCGACGCAGTAGAGACCACCTCTGCAGCAGAAGACACCATC  
AAGGCGCTTCCATCACCTAAGCACCCAGAGCAGCCAGTGGGCACGCCAGTTGGAGAGGTC  
AAGACCGATCTCGAAGACATGGTTGTATGTTGGCGTTGGCGAAGTCTCCTCATGGGCG  
TCCGGACGTACCCGCTTCAAGCTGAGTACGGCATCCAGCGCGACGGCTCCGTTGACCTC  
ACCGCAGCAGGCGTCTTGAGCTTGATGGATGATGGGTCTGATCTCTGGAGCGAAGAT  
CCAAAGCCAGCTGGTACGACGCTGACGGCACCGAAGTGCTGAAGAAGAGATCTACGAG  
CGCTTCCGCGACGAAGTCATCGCACGATGCGGTGTTTCGTGAGCTTGTCGACGACGCATTC  
CTCGTCGACGGCGGCTCCCTCGACGCAGCTGAAGTCTTCTCGACCGCGACATCTCCTTC  
TCCGTAACCTCTGCTGAAGAAGCACAGGCCTACGTCGATGCAGATGCTTCCGTGACCGTT  
GAAGAAGCAGACGGCGAATGGATCGTGACCAAGAAGAAGGGCTCCACCTCCTTCGTGCCA

CGCAAGGCAACCCGTGACCCGCTCCGTAGCAGGCCAGCTGCCAACCGACTTCGACCCCTGCC  
AAGTGGGGTATCCAGCCTCCATGATCGATGCACTCGACAACATCGCAGCGTGGAACTTG  
GTCAGTGCAGTCGACGCCTTCTGTCTCCGGCTTCAGCCCAGCAGAACTCCTGCAGTCC  
ATCCACCCAGCTGACGTGTCTCCACCCAGGGCACCAGGTATCGGTGGCATGCAGTCCCTA  
CGCAAGCTGTTTCGTCAACCGCTTCTCCGGCCAGGATCGTCCATCCGACATCCTCCAGGAG  
ACCCTGCCAAACGTTGTGGCTGCACACACCATGCAGTCTACGTCCGTGGCTACGGCCAG  
ATGATCCACCCAGTGGCAGCATGTGCAACCGCAGCTGTCTCCGTGGAAGAAGGCGTGGAC  
AAGATCCGCCTCAACAAGGCAGATTTTCGTTGTGCGCGGTGGTATCGATGACATCCAGGTT  
GAATCCCTGACCCGCTTCCGTGACATGAACGCCACCGCAGACACCCAGGCAATGCTGGAC  
AAGGGCATCGACCCACGCTTCATCTCCCGCGCAAACGATCGACGTCGCGCAGGCTTCCTC  
GAAGCAGCAGGTGGCGGTACCGTCTCTGGCACGTGCATCCGTTGCTGCTGAAGTGGGA  
CTGCCAGTTCTCGCAGTTGTTGCACACGCACAGTCTACGCCGATGGTGTCTCACACCTCC  
ATCCCAGCACCCGGGACTTGGCGCACTGGGTGCAGCACGTGGTGGCAAGAAGTCCGTACTT  
GCTCGCGAAGTGAACAAATTGGGTCTGACCCAGATGACGTTTCGCGTGGTCTCGAAGCAC  
GACACCTCCACCAACGCCAACGATCCAAACGAGTCCGAGCTGCACAACCTGCTGTGGAAG  
ACCATTGGACGCGAAGCCGACAACCCGATGTTTCGTCGTCTCCAGAAGTCCCTTACCGGA  
CACTCAAAGGGCGGTGCAGCACTCTCCAGATCGGTGGACTTGCTCTCCATCCTGGAAACC  
GGCAAGCTGCCACAGAACGCATCCCTTGACTGCGTTGACCCAGAGATGGAAGCAAAGGGC  
GAGAACTTCGTCTGGCTGCGCAAGCCACTGGATCTCGGCGCAGGCTCCATTAAGGCCGGC  
GTACTTACCTCACTGGGCTTCGGCCACGTGGCTGCAGTCGTCTGCTGGCAACCAGCGGC  
ATCTTCGAGCAGGCAATGCGCAACGCAGGCCTCGACGTCGAAGCATGGCGTGCACGCGCA  
ACCCAGCGCCTGCGCACCGGTGCAAACCGCTAGAAGCTGGCATGGTTGGCCGAGCACCA  
TTGTTTCGAGCAGGTGACGCGACGTGCGCTGCCAGAGCATGGCGCTCACCAGCAGAGATC  
AAGTTGCTTATCGACGCTGACGCTCGCCTCGGTGCTGACGGCATCTACCAGGGC

>RXA00113-downstream  
TAAACGTTAGATAGCTAAGAAAG

>RXA00158-upstream  
CGTGCCATTTTCTTTACAAAAGAGTATTAACCGAACTTCAGGTCAGGATCCACGCCCTG  
CGTTTCATCCCGGCTAAGTTATACAAGGAGCGAGTTCTCAC

>RXA00158  
GTGACCGAATTGAGCAGGAACCTTCGGGGCCAGCCGACTGATTAACCGCTTTGGCCAGGAG  
CCTTTTGCCTTCGCTTTCGCGGCCAAGGATATGACTGGTTGAAGACCCCTTCGTGCCGCG  
GTTGCCGCGAGGTGCAGGCACCAATGTTAGTGACATCGTCGAGCGCGCAAATGCGCTGCTT  
GCACTAGTTGCAGATGATCTCATTTGGCACCCTTCCATTTGGTTTCGATCCAGTGGCTTGG  
GCTAACAACTCCGAAGATCCAGCTTTCGATACTGCACAATCTGCAGTGAGCGTGCCGGGT  
ATCTTTGTCTCCAGATCGCAACCCCTGGATTCCCTTGAGGCGCAGCGCCTTGATGTGGAT  
CAGGCTGTGTCCAGCATTGGTTCATTTCCAGGGCGTATTGGGCGTGACCTGCTCAATGAT  
GCGACTCGTGCTGATGAACTCGTTGCCATTGCGCAGTTGATCGGTGCAGCGATCACCCGC  
ACCGCACGCATGACGGGCTGATCGCGCAGGGCGACAACATGCCGATGCTGTGATCGCC  
GGAATTTCCCGCGAACAGCTTCAGCAAGCTATCGACGCGGCCTGCGCCGAAGTCCCTGCG  
GAGATCCGCCCCGTTATCGGTCTGCGCAACTCACGCGATTCTTATGTTTTGGTTGGCCGC  
CCAGACGACAACGCTCGCGTTGTTAAGGTCATTGAGGCAATGGCTGCCAAGGATAAGAAG  
GCCATTGAAGATAAGCTGCGCGGCGGTTCCGCGTTCAGCCCCCGTATTACTCCGCTGAAG  
GTGCAGGCTGCTTTCCATCACCCAGCTATGAACATGGCTGTGGAGCAGACCGTGGCGTGG  
GCAACCACTGCTGGTTTGGATGTGGAACCTCACCCGCGAGATCGCCGCTGATGTTTTGGTT  
AACCCTGTCGATTGGGTAGCACGCGTCAACGAAGCGTATGAGGCTGGCGCTCGCTGGTTC  
CTCGACGTTGGACCAGATGGTGGCATCGTTAAGCTGACTGCCAACATCCTTGAGGGCGGC  
GGCGCGGATTCTTCTATGTTGGTGACGCCGCGAGGCCAGGCCAAGATATTTGATGCTGGC  
ATGGCACCTGAACTTCCAGTGGATTACCAGGAGTTCGCACCACGCGTTGAGCACGTTGAT  
GGAACCCACGCTGGTTACCAAGTTCACTGAGCTGACCGGCCGACCCCAATGATGCTG  
GCTGGCATGACCCCAACCAACCGTTGACCTTGCCATTGTTGACGCGCGTGCACAACCGTGA  
CACTGGGCTGAGCTCGCTGGTGGCGGACAGGTTACCCAGAGCTGCTGGAAACCCACATC  
GCACAGCTCACCGACATGCTTGAGCCAGGTATCAACGCCAGTTCAACTCCATGTTCTTG  
GATCCATACCTGTGGAAGATGCAGATTGGTGGCAAGCGCCTTGTTCCTAAGGCCCGCGCT  
AATGGTGATCCATCGACGGCATCGTCATACCGCCGGCATTCCTGAAAAGGATGAAGCT  
GTTGCATTGGTCAAGGAACCTGATGCGTGATGGTTTCCCTTGATCGCATTCAGGCCAGGT  
GCCATCAAGCAGGTTAACTCTGTGTTGGCTATCGCTAAGGAAGTTCCAGAAGTCCCCATC  
ATCATTCAGATTGAGGGTGGCGTTGCAGGTGGACACCACTCTTGGAAGACCTCGATGAG

CTGCTGATCGCCACCTACGGCAAGGTCCGCGCACTGGATAACGTGGTGCTGTGTGTCGGC  
GGTGGCATTGGCTCACCTGAGCGCGCTGCTGATTACGTACCGGTTCTTGGTCCACTTCC  
TACGGCCTGCCAGCTATGCCGTGTTGATGGCATCTTGGTGGGTACCGCTGCGATGGCAACC  
AAGGAAGCAACCACCTCCAGGCCGTCAAGGAACCTTCTGTTTCCACCCAGGGCTCTGAT  
GAATGGGTTCTGCTGGTGGCGCAAAGAACGGAATGGCATATGGCCGTTCCAGCTTGGC  
GCAGACATCCAGAGATCGACAACCTCCTTTGCTAAGGCTGGACGCCTTCTTGATGAGGTT  
GCAGGCCATGAAACGGATTTGCAAGCGCGCCCGGATGAGATCATT

>RXA00164-upstream

CTGCTTTGCGGGAGGTTATGAAATGAGTGGGGAGACGTGAAAAGCATGCGCTTTCCGTT  
GGCCAGCCTGCCGCAAGTGCGGCGCGAGGTGGCCCGGCAG

>RXA00164

GTGGGTTCGTATTCCGCGGGCGAAGTGGTGGTTTTTAGGCGCGCTGGTGTGCTGAGTGGC  
GGCGCTTATGCGTCGGTGCTGGTGCCGAGGTGCTGGGGCGGATTGTGGATCTGGTGTCC  
GATGGCGCGCAGATGCCGTGATTTTGTGAGCTCAGTGTGATTCTCATTGCGGTGGCAATT  
GCCGGCGCGGTGCTCAGTGCCTGCGGGTTCTATGTGGTGTGCGGGATTCTGAGAAGATT  
ATCGCCAATTTGAGGGAAGATATGGTGGGCACCGCGCTTGGGTTGCCACGCACCAGGTG  
GAAGATGCGGGCTCTGGCGATTTGGTGAGCCGCTCCACCGATGATGTCTCCGAGCTATCC  
GCAGCGGTGACAGAGACCGTCCCGATTTTAAAGTTTCTCACTGTTTACCATTGCCGCGACG  
ATCATTGCGCTGTTTTCTTTGGACTGGCAATTTGTGCTCATTCTGTCGTGGTGGCGCCG  
GTGTACTACTTCGCGTCCAAGCACTATTTAGCAAGGCGCCGGATCGGTATGCGGCAGAA  
CGCGCGGCGATGGCGGAGCGTGCGCGAAAGGTACTTGAGGCTATTCGCGGGCGTGCAACT  
GTGCGGGCGTATTCCATGGAAGATGCCATGCATAATCAGATTGATCAGGCGTCTGTTGCT  
GTGGTGGTCAAGGGTATTCTGTCGCGCACCAACCATGTTGATTTTGAACATGTGGATGCTG  
TTTGCGGAATTCCTCATGCTCGCGGTGCGGTTGGTGATCGGCTACAAGCTGGTCATTGAT  
AATGCGCTGACGATCGGCGCGGTTACCGGTGCGGTGCTGATGATTATTCGTCTGCGTGGC  
CCGATGAATATGTTTCATGCGCGTGTCTGACACCATTCATCCGGCTATGCGTCTGCTGGCG  
CGCATCGTGGGAGTTGTTGCGGATCCGCGGATTCTGTGCCCCGACAGCGGTGTGAAAGCA  
CCTCAGGGCAAAGTGGAAATGCGCAACGTGAGCTTTAGCTATGGCGATTCTTGGGCGGTG  
AAAGACATCGACATCACGATCAATTCGGCGGAACTGTGCGGCTCGTGGGCGCATCTGGC  
GCAGGTAAGACGACGCTGCGCGCCTTGCTGGCGGGCTTGCGGGTGCCAGATCAAGGGCAA  
GTGCTTGTCGACGACTTCCCGTCTCTCACCTCTCTGACCGCGAGCGTATCGCCCGCTTG  
GCCATGGTCAGCCAGGAGGTTTCATGTTTTCTCCGGCACGCTGCGCCAGGATCTCACCTTG  
GCTAAACCAGATGCCTCCGATGAGGAATTAGCGCATGCTCTTGGGCAAGTTAATGCCCTT  
GACTGGTTGGAGAGTCTTCCAGAAGGACTGGACACGGTCGTTGGTGCGCGAGGAATCCAG  
CTAGAACCAGTGGTGGCTCAGCAGTTGGCGTTGGCCCCGGGTGTTGTTGCTCAATCCGGCG  
ATCGTCATCATGGATGAAGCCACGGCAGAAAGCAGGATCGGCGGGTGCCAGCGCACTGGAA  
GAGGCTGCAGATGCAGTGAGCAAGAACCGTTCCGCATTGGTGGTGGCGCACCGGTTGGAT  
CAGGCATCGCGGGCTGATCAGATTCTGGTGATGGATAAGGGGGAGGTTGTGGAATCCGGT  
ACTCACCAGGAGTTATTGGATCACGGGGGTATTTATCAGCGTCTGTGGACTGCGTGGAGT  
GTCCGAAGA

>RXA00164-downstream

TAGTTGACTGTTCAATGCGTTGA

>RXA00181-upstream

GTATATTACAGACACCCACGTGATTAGTGTTGTAGTTACAGTGCTTATTTTTTATTTGT  
ATCTTTGCACGTTTGTCCCTACCCAAAAGAGAAACCTC

>RXA00181

ATGAGCGATAACACCTGGTTCATCATAGCCATCGTTATCTATATGTTGGTGATGGTGCTC  
ATCGGCTATTGGAGTTACCGCAAGACAGAAAAATACGACGACTACATGCTCGCCGGCCGC  
GGGCTCAACCCTTTTGTGCGGCAATGTCCGCAGGTGCCTCAGATATGTCAGGTTGGCTG  
CTCATGGGTCTGCCGGCGCGCTGTTGTACCCGGCATGTCCGAGTTGTGGATCGCAGTC  
GGACTCACCATTTGGTGCATGGGCGAACTGGATGTGGGTGGCACCTCGTCTTCTGTTCTTAT  
TCCGAAATCTGGCCAACTCAATCACCTGCCTTCAATCTTTGAGAACCAGACTTCGCGAT  
AAATCTCGCGGCTTCGCATCATTCGAGCACTAATTATCATTGTGTTCTTCACTTCTAC  
ATTTCTTCAGGCATGGTTGCTGGTGGAGTGATTGGGAGTCCACGTTTGGTGGAGATTAT  
CTACTCGGTATGGCCATTGTGCGAGGTGTGACAGTGCTGTATACCTTCAATGGAGGATTC  
CTTGCTGTGTCTTATACAGACGAGTTACGGGGACTATCATGTTCTTCTCGTTGATCATC

GTGCCAGTCATGGCATATTTTCGCACTGGCGAACCCCATGGATATTTGGAGCTTTGCAAAC  
TCTAATGATTACGGCCCGCACACCGATGGAATTGGCAATCCCACCTACTTCTCCATGATC  
AGTGGCATTCTGCAGCAGCAATCATTTGGTAACTTAGGTTGGGGTCTTGGATACTTCGGC  
CAGCCACACATTGTGGTTTCGTTTCATGGCACTTCGCACACCAGCTGAAGCAAAGCAAGGT  
CGTCGCATCGGTATTTCTCGGATGATAATCTGCCTGATTGGTGCAACCTTTACCGCAATT  
ATCTCCACAGTTTTCTTTGCACAAAACCCCGACGCCAACATCACTGACACAAGGGCTTAT  
GAGTCCATCTTCTAGATCTTGCCCGGATGCTGTTCCACCCATTGATCGCTGGACTTATT  
CTGACTGCTGTTCTCGCGGCCATCATGTCTACCATGTCTGCACAGCTGCTGGTCAACCGCA  
TCTTCCCTGATTGAGGACCTGCTGAAGGTAGTTAAAAGGACTCGCTGAGCGAACGCACC  
CTGATCATGCTGTCTCGTGCCACAGTCATCATTCTGGCGATCATTGCAGCAGCCATGGCT  
ATTAACCCGTCTGATTCCATCCTCGGATTGGTGGGATTTGCGTGGGCAGGATTCGGCTCT  
GCATTTGGTCCGATCATACTTGCTAGCCTTTATTGGAAGCGTCTCAACGCCCGCGCGCT  
ATCTCCGGCATGATTACTGGTGCTATTGTCTCATCGCGTGGGGTATGTCCCCACTAAGC  
GATACGTTGTATGAAATCATCCCAGTTTCGCCTTGGCAACCATCGTGATGGTCGTTGTT  
TCCCTCCTGACAAAGGAACCCCTCCGAAGAAATCCTCAACGAGTTTGAAACCGCCAAGGAT  
CTTGCTGCCGCTGTGGAATCAAACGAGGATGTTGATTTTCGCTGACGCAGCTCAGAAGCTT  
TCGAAAGAAAGT

>RXA00181-downstream  
TAAGCCTTAGAGGGAACCAAACG

>RXA00186-upstream  
AGAAGCCCAGCATTTTGTCTTAGCTCACCTCTAAAGCTCCTGATCTGGATACGAGGACTCC  
TGCGGAAAACCGTGTGGCTAGTGAAGCTACCCGGCATCTC

>RXA00186  
ATGGGGGAGAAGACTTCTGTGCGGTATGTTACGATGTTCTGATCAAGGGCGTGCCAGTG  
CGGATATACAATCCGCACCCCAACGACGGGCGCTTCCTGTCTTTATCTACTTCCATGGT  
GGCGGATGGGTTTTTGGGGGACCTTGAATCAGTGGATTCCACCGTGCGGATATTGCCGTT  
GCTTCAGGCGCCCTGTGTATCAGTGTGGATTATCGCCGTGCACCGGAACATCCTTTTCTC  
GCTGCATTGGATGATTGCCAAGTGGTCACGGAAGCTGTCTCAATGGTGAACCTGCCAGT  
GCTAACCAGCATCTAGTGGCAGTCGGCGGGGACAGCGCCGGTGGCAATATTGCGGCGGTC  
ATCGCTCAACAGCTGCGCGATCAGATCACCCACCAAGTTCTTGTGTATCCGGTGATGGAC  
GTAATCTTGCTGGTGATTGTTCTATCATTACCACTGGTTTTGCGCTGCTCATGCATCCA  
AAGAGCAAGGACAAGACGGAGACGATTTCTGATGAATTCCTCGCAGAGATCCAAGCGGGA  
AGTGAAAAGATCTCCATTCTGCGTTTCGACCCCTGCTGAAAAAGCCAATGCGAGCCGTTGG  
ATCATGTACTTTCGTTGGCGGAATTGGCCTGCTCTACAGCGTGTTACGCCGTGTGGACAGGT  
GGCGTAACCGGACTGACGTTGAACTCCTTCAACTTCTGTTCTGTCCTCGGCATGGTG  
CTCACCGCTAATTACGGGCCAGAGTAT

>RXA00186-downstream  
TAAGCAAAGCTTATTCGCGAAGG

>RXA00187-upstream  
GCTTATTCGCGAAGGCATCCAAGGAACGTGGGGATTCATTCTTCAATTCCCGTTCTACGC  
AGGCATTTTCGGGTTGATTTCTTACCGGTCTGGGTGTT

>RXA00187  
GTGATCTCCGGATTTTTCACCTCGATTTCCACGGCAACCACGTGGCCTGTCATCGCGTTC  
CTCTACTCTGGACTGCTCAACATCGCGGTGCCTTCAGGTGGCTCGAAATTCATCATCGAA  
GCCCGGTACATCATCCCAACCCAGTGGATCTTGGCGCTGACATGGGCCTTGTCTGACG  
GCTTATCAAATGAGTGATGGCGCGACCAACCTGCTCATTCCGTTCTTCGCGCTGCCATAT  
TTGGCCAATTTCAAGATCAAATTCAGCCAAGTGGTGGGCTATACAGTTCCGCCTGTCTCTC  
GTTGTTATCGCCGTGATCTGCATTTACCTGTTCTGCGAGCATCAATCATT

>RXA00187-downstream  
TAAAAAGATGCTTCTCG

>RXA00201-upstream  
ACGTCGCGGACTTCAAGTAGTCGGCGATGAAAAAGTCCGTTTACTAAACCCCGATCTGTG

TTACGCCATCGCGGGCTCGGGCACACCGATACCTGGGCA

>RXA00201

GTGGCAGATTGCGGATTACCCATCCCAGAACACGTAGAGATCATCGATTGGCACTCGTG  
TTTGGGATCCCCACCTTTGAACAAGTACTGAATGCTCTCAAGCCGGAAGTAGTTGTGGAA  
GGCGCGGTGATTGCCGAAGGGGACCCCAACGTATCCGCGAAATGGTGGATACGGATGTG  
GAAGTT

>RXA00228-upstream

CCGCATGGCATCCGCCGAAAGAATTCCCCTCCGGAGGAATGGCACGCCTCATGGGAGAAC  
GCATCGGCAAAAACTGAC

>RXA00228

ATGCGCGACCTCCGCTCCATGATCGGCGTCAGCTCCTCCGCATTAGGCAACCGAATCCCC  
TCCGAAGAAAAAGTCTCTGACCTAGTCATCTCCGCAGGCTACGCAATCCTCGGCCGCTGG  
CGCGAAGACTACGACGAAATGGACTTCGGACAAGCCACCGAAATCCTCGAACAAGTCGGA  
GCCATGCACCTAGCCGACCGCACCTGGGGAACCTCTCCGAAGGCGAACGAAACGAGTC  
CTGGTCGCACGCGCACTCATGACCAACCCGGAACCTCCTCATCCTTGACGAACCAACCGCA  
GGAATGGACCTCGGCGGACGCGAAGACCTCGTCGGCTACCTCGGAGAACTCGCCATGGAC  
CCAGACGCACCTGCCATCGTCATGATCACCACACGTCGAAGAAATCCCCGCCGGATTTC  
ACCCACGCAATGCTCCTCGACGAAGGTGAAATCGTAGCCCAAGGCCTGATCAACACCGTC  
ATGACAAACGAGAACCCTATCCAAAGCATTCCACCAGCCAATCCAAGTAGACCGCATCGGG  
GAACGCTACTTTGCCCCGCCGTGTGAGAACCGCCAGGAGTCATAGGGCTCAG

>RXA00228-downstream

TAGGTTTTTTGGAGTTGTGGGCC

>RXA00243-upstream

CACTGCGCCAGATTTTTGATGCCGACACTGTGGCAGGTGTGCGCGCTGAGTACGAAAAAT  
TTAACAAAGCAGCCCATGATGGAAATGAAGAGGAACAGAA

>RXA00243

GTGACCAGCGAACAAGCTTTAGATCCTATCCACCCAGGTCAGTTCGGTCTTTCTCGGATT  
CAGTTGATCAACTGGGGAACCTTCCACGGAACGGTGGACATTCTGTGACCAGGGAAGGA  
ATCTTAGTTACCGGTGGTTTCGGGATCAGGAAAATCCACGCTGATTGATGCGATCACGGCG  
GTATTGCTTCCGCAAGGAAAGCTGAGGTTTAACTCTGCCGCACAGGCTAATACTCCGCGG  
AATAAGGGACGCAGTTTGTTTACCTATATCCGTGGCGCTTGGCGTGCGCAGGAGGATCCG  
CTGCAGGATCAGATTGTCTCCACGTACCTACGTCCCCGCGCAACCTATTTCGCTGGTTGGA  
TTGACTTATTCCAACGGTGAAGGCGTCGAGCACACCTTGGTGGCTATTTTCTATCTGAAA  
TCGGGACACAATTTAACCTCCGATATTTCTTCATATTATGGTGTGTTTCCCGTTGATCAA  
GACATCAATGCGCTGCTGGATTTCTGAAAGAGGGCATCGATAAACGCCAGATCAGAGCT  
GCTTTCAAGGAAGCCATCTTTAGCGAGCAGCATTCTGTATTCTCCGGCAGGTTTAGAAGC  
CGTTTGGGGATCTCCAGTGAGGAAGCTTTGCTGTTGTTGCACCGCGCGCAGTCGGCGAAA  
GATCTTCAAAGCTTGGATGATCTATTTCCGGGATTACATGCTGGTGGAAACCGGATACGTTT  
AGCATTGCCAAAACCTGCCGTGGAACAATTTCAAGACCTTGAAGGTGCTTATGAGCAGGTC  
GAAGATATTAAACGGCAGATCCACACCCTGGATCCTTTGGTGCAGCTGAAGAATCGGCGA  
GAGAAAGCGCAACAGTCCAAAGATCATGCCAATGCACTGAAGAAGGCGCTGCCGACTGTC  
GGGAATCGCATTAAGAAGGAAGAGCAA

>RXA00259-upstream

GGCCTTATTAAACATACGGCGGTTCTAGCACACAGCGATGGATGATGTGTCCCACCGATAT  
TGCTGCATGTGCCAAGATTTAGCACGGTACAGTGCTAGAA

>RXA00259

ATGAGCGGACTGTTTTACCCCATTTTCAGATGCGGCAAAAAACAACACGGTAAAAACTGAT  
GGAGATTCAAGTATCTGGTCGAGACTTGCCATTACTAAGATCTCTGAGGATCGTTTCGAG  
CGTTCTGCGTATTTCAGCCCAGCTGGCAAATATAATCTGCGATGTGGCACCTTGGGGAGCG  
AGCACTGTTTTCACTCTTACTGGTCAGTGGGGCAGTGGTAAGACATCTCTTGTTAATTTG  
ATTTCGCTCGGAAGAATCTCTATCGAACGAAAAATGGACAATCGTTGATTTCAACCCGTGG  
GTGGCCTCTGACCCGCAATCTTTGATTGAGGAGTTTACCGAGTAATCGTTGGGACGGTA  
CCTGATGATAAGACCGGCCAAAAGATCAAAACTGTTCTGCAGAAAACCTTTAGCACGATT

GGGTCAATTGCAGGTGGGGTCGGAGGGTTTGGTGTCTAGAAAGCACTTGCGCTCTCAAAA  
 GGAGTAGATGCTGCAAACGCTGTATATAAGACATGGAAACAGGAGCAAGATTCGTGGCCA  
 ACGCTGTATACAGTGTGCGAACCATTTTAAAGATCTGAACAAGCGAATTCTCATTGTC  
 GTCGATGATATTGATCGCCTCCATACTGATGAATTGGCGCTGTTAATGAAAGTAATACGC  
 TTGCTTGGACGATTCCCGCAGGTGAATTATCTTTTGGTTTATGAAGAAGAATCACTGTTA  
 ACGACGCTAGCCAGATCGACAGCTGTAGGTGGTAGCGAAGATGATGCTTTGCGTTTTCATG  
 GAGAAAATCGTGCAGTATCCTTTTCGATGTTCCGCTCTGACATCATTTCAAATAGAGAAA  
 GAGCTCAGTGCATTATTTGACAAGCTTTTCCAGGGTGTTCGCTATCGGGTGATCCTGAA  
 GACTTTGCACTAGTGAAGTCGAGAATGTTTCGATGTCTGGGAAAAGACTCTGGTCACGCCG  
 AGGCTGTTGCACCGTTTTGCTGCTCTACTAACCAACTGGACTCGGATATATGGATCAGGT  
 GAAGTTAACGGCGTTGATCTCACAATACTTGGCACCATTGCAATTGTTTTTCCGTCTGTG  
 TATAAACGCTCTTTCTCGAGCGAAGGAAGTATTGCTTCAAGGAGGTGGAACGACAGGCTCG  
 CAGAAACCCGGTTGGGAAAAGCAATTATGTGAGGGGATGAACAACGAGCAGATGGATCTT  
 TTAAAGACCATGCTTTTGTTCCTTTTCCACGCTTTTCGGATCACCTAGTACGAGAATG  
 CATCGTGAGAGGGGGATCTCGACGGAAGTTTATTTTGACACGTACCTCATGTTTCAAAGA  
 CCTGGACATGTCATAAGTGATGAACAGTTGGATAAGTATCTATCTAATGCGGACGATGCT  
 ATGGGTTTTCGTCGATTTAATTAACCTCCGATGACAATGACATGGTGGCATCAGTGATGAAA  
 AAGCTTCTCTAGCAATTGATCGACTTGATGGAGAGGGTGTAGGCACATGGCAGTTGAG  
 GTGTTATTACCCGTGCTAATGGTATGCATGATAAAGGTCGTCAAGTGCGTATGAGCGGC  
 ATATTAGTGACCTGTATTCCCATGCGTGCTCGATTCTTGGTGCATTGCCTCAATTACCA  
 GTGAACAACACTCTATGAGAAATTTCTTTCTGAGATGACGCTTAATGAGGCTGCTTTCTGG  
 TTAAACCAAGTGGGGGAAAGGGCTAGAGCCTGTGGTAATGATGTAAGTGGCCTTGAGCTT  
 TTTTCGTAAAGTTAATATAAAGACCGAAGCTAGAATTTTAAGTGATTGAAGAATCAGGAC  
 CCCTCAGATTGGGATTTAGGTCCATATTGCTTGGTATTTTGGCGAAAAGCTCGAATTTT  
 TCTTCAGTGCTGAAGTCTCTGCAAAGTGGTATAGAGGAACATCAGTTTGATGTGATAGAT  
 ATTGGAGTGCTTTTCTTAACGACTGTGTATTCTTCGCGACAGGGACCAAGCGGTGGTGCA  
 TGGATAGATTCTTTTCAGCATAGTCTGTTTTACGGTACGTACCTGATTCTCTACGGGCT  
 ATAACCAAGTCTGAAGTAGATGTAGAATAAGTAAGATACAGTTCACGGATTTTAGCTGG  
 GAAGGGAAGCGAAAAGTTGTCGCATATGACTGGAGACTGGAAGAAGTGATTTCACTCGA  
 GAACGATTAGGGGGCTACAGTATCGCAGATTCTATAGTCGAT

>RXA00259-downstream  
 TGATGAGGCTGAGGTCATGACTT

>RXA00269-upstream  
 TGCGATCTTGGTGGTTGTTCGCCATGCTGCTGCCGAGGTGGCGTGCGAAGTTCTCCAAGGC  
 ACCGAAGCCTAAGCAACCAGTAGCAGTGGAGGCTTAAGAC

>RXA00269  
 ATGTTATCCATCAACGGAATTTCTAAGACGTTCTTCCCCGGCACTGTGAATGAGCGCCGC  
 GCGTTGCAGCAGCTCAAACCTCGATATGGCTGAGGGCGATTTTGTACCGTCATCGGTTCT  
 AACGGTGCAGGTAATCCACGCTGCTCAACGCTGTTTCTGGCCGTTTGCTTGTGATTCC  
 GGCGAGATTTCCATCGACGGCAACAAGGTAAACAAGATGTCAGAGCACAGCGTGCCCCGC  
 TACATCGGCCGCTTTTCCAGGATCCTCTGGCCGGCACCGCGCCGAATCTCACCATTGAA  
 GAGAATCTGGCCATCGCGTTGCTGCGCGGCAAGCGCCGTGGATTGGGCTTTGCACTGACC  
 TCGAAGCGCCGTGAGCAATTCAAGCAGGAACCTTGAGCGCCTTGAGCTGGGTCTGAAAAC  
 AGGCTCACTGCCAAAGTTGGTTTGTCTCTGCGGTCAGCGTCAGGCATTGTCCCTGCTG  
 ATGGCTGGTTTTACTCAACCTAAAATCATGCTGTTGGATGAGCACACCGCAGCGCTTGAT  
 CCACAGCGTGCAGAGCTTGTGACCACCTTGACCGAAAAGATCGTGGCAGATGGAAATCTG  
 ACTACGCTTATGGTCACGCACAACATGGAACAGGCAATTCGCCTGGGCAATCGCCTGATC  
 ATGATGCATGAAGGCCAGATTGTCTACCAGGCAGATCAGGCTACCAAGTCGAAGTTGACT  
 GTGCGGATTTGCTGTCAGGAGTTCCGCAACATCAAGGGCGCAACATTGTCTGACAAGGCG  
 TTCTTCGGC

>RXA00269-downstream  
 TAAAAAGAGCTTGCTTTACGACG

>RXA00281-upstream  
 GGTTGACTCTTTGGCTTTGATGCCAGCATTCCGCCAAAGCGTGGCCCTCTTTAAGAAAGCT  
 ACTGAACACAACAGAGTAGGTTTATGCGACACTGGTGCGC

>RXA00281

ATGATCAACGTTGAAGGCCTCACCAAACAATATGGTCAGGTCCGCGCAGTCGATGATCTG  
AGCTTCGAAGTAAAACCCGGAATAGTCACCGGATTTCTCGGCCCCAACGGCGCCGAAAA  
TCCACCACGATGCGGCTGATCCTTGGCTTAGATAATCCAAGTCAGGGCATGCCACGATC  
GAAGGACAACCCCTACCGATCGCTCAAAAATCCCTGACCAAAGTGGGAGCACTGCTTGAT  
GCCAAAGCAACACACCCAAATAGAACAGCAGAAAACCACTCAAGTGGATCGCCCGTGCA  
AATGGGCTGTCCACCAAAAGAGTCGATGAAGTTCTCACCTCGTGGGACTGACTGGTGT  
GGGTCAAAGAAGACCGGTGGGTTTTCTACTAGGCATGGGCCAACGTCTAGGACTTGCTGCA  
GCATTGCTCGGCGATCCGGAATACTTAATTCTCGACGAACCCGTCAACGGCCTTGACCCA  
GAAGGCATTCACTGGGTGCGCACCTTGTTGCAAAACATCGCCAAGCAGGGCAGAACCGTG  
CTCGTGAGTTCCCACTGCTGTCCGAGATGGCGCAAACCTGCGGAACATTTGATCGTGATT  
GGGCGTGGCAAGCTGGTCCCGATATGCCCATGCATGAGTTTGTGCGCTCCCATTCGCT  
TCCACAGTTGTGGTGCGGGCAGCA

>RXA00298-upstream

TTTAGACAAGTTCTGGTTAAAATTCTTCATGAAGGTGAGAATCTGGGAATTTCTCGGTAC  
TCTTTCAGATTCTGTAGTTATCCACTGATTGGAAGAATGAG

>RXA00298

ATGAGCTCAAATATAGCTATCACGACCGAGCCTGAAGGGAAAAATAAAAAGGGTCTCAAA  
TCAGACCCGTTCAATTTTTCCATTTCTGTGCGTTTTATCGTGGTGTGTCATCGCCACA  
AATTGCGCTAGGCGAGAAAGCTCGAACAACTTTTCCGCGATTGCCGGCTGGCTCTTAGAA  
AATTTAGGGTGGATGTATATCGGGGGTGTCTCCTTGGTTTTCAATTTCCCTCATGGGTATC  
TTTGCGTCCCGGTATGGCCGGGTAAACTTGGTGATGACGATGATGACCCCGAGCACACC  
CTAATCGTGTGGTTCTGTATGCTTTTTGCTGGCGGTGTCGGTGCAGTCTTAATGTTTTGG  
GGTGTGTCGGAACCGATTAAACCACGCGTTCAACGTGCCAATGGCTAATGAAGAATCCATG  
AGTGAAGCCGCAATTGTGTCAGGCTTTTGCTTATACTTTCTATCACTTCGGTATTCACATG  
TGGGTAATCATGGCACTCCCAAGATTATCATTGGGATACTTTATTTACAAACGTAAGCTA  
CCTCCCCGTCTATCCTCTGTGTTTTCTCCGATCTTGGGTAAGCACATTTATTCACACCC  
GGCAAGCTCATCGATGTACTGGCCATCGTAGGCACCAACGTTTGGTATTGCTGTGTCAGTA  
GGTCTTGGTGTGTGCAAAATCAATGCAGGTATGAACAAACTATGGAGCACCCCGCAAGTA  
TCGTGGGTTCAGCTTTTGATCATCTTGATCATCACCGCGGTGTCATGTATTTCCGTTGCT  
TCCGGTTTGGATAAGGGCATTAAAGTTACTGTCCAACATTAATATTGCAATGGCCGTTGCG  
TTGATGTTCTTCATCTTGTTCACTGGTCCAACCCCTCACATTGCTGCGCTTTCTCGTAGAA  
TCCTTCGGAATCTATGCATCCTGGATGCCTAATCTGATGTTTTGGACTGACTCTTTCCAA  
GATAACCCAGGCTGGCAGGGCAAATGGACGGTGTCTATTGGGCATGGACTATTTGTTGG  
TCGCCATATGTCGGCATGTTTCGTGGCGCGTATTTTCGCGTGGACGTACCGTCCGTGAATTT  
ATCGGTGGGGTTCTAGCTCTGCCAGCGATCTTTGGCGTAGTTTGGTTCTCTATCTTTGGT  
CGTGACGGCATCGAAGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT  
GAAGGTGACGTGCCAGCAGCGCTTTTAAATGTGCTGCAAGAGTATCCGCTGACTGGAATT  
GTCTCCGCGTTTGCACCTGTAATTATTGTGATTTCTTTATCACCTCCATCGATTCCGCA  
GCGCTAGTTAACGATATGTTTCGCTACCGGTGCAGAAAATCAAACACCGACTAGTTACCGC  
GTGATGTGGGCTGCACCATTTGGGGCGGTGCGAGGTTCCCTGCTGATCATTTCCCATCC  
TCTGGTATTGCCACGCTGCAAGAAGTGGTTATCATCGTGGCTTTCCCATCTTCTCGTG  
CAATTTGTGATGATGTTTTCTTTGCTTAAAGGCATGAGTGAAGATGCTGCTGCGGTTTCGT  
CGTGTGCAGACTCGTCAGTGGGAAAAGACTGATACACCAGAAAACTTGAAGAGCATTCG  
TCCCAACCAGCCCCGGGCTATGATGACGAGGGCAACCCCTTGCCAATGCCTGCCCTCGAA  
CATGATGAGGACGGTAACATTGTTATCCAGGCAACGTAGTCATTGAAGGTGATCTTGGG  
GTAGTTGGTGATGTGGTTCGACGATCCTGAGGAAGCCCAAGAGATGGGGTCTCGTTTTAAG  
ATCGTCGAGCAAACCTCGGCCCCAGTCCAGGGACGAATACGATATT

>RXA00298-downstream

TAAACGATTGCTTTTCGACGCAC

>RXA00346-upstream

ATCTATGAGACCCCTCAAAACACCGAGAATTTCTCGATGCATTACCAAGGCAGTTGAT  
GATCTCACCGCTGCCACTAACCAGGTTTAGAATTATTTAA

>RXA00346

ATGCTGTTGACTTTCAATGATGCTGCGGTGGATCCCCTCTGGAGGGGCTGAATTTAGAG  
CTCCGACAGGGGAATTTCTTGCGGTTTTAGGCCCAACGGCGTGGGAAAATCCACGCTC



ATCGGTACGATTTTGGGCACCCGAAACTCACCCACGGTTCGGTTAAAACTGATGCCCGG  
GTGGGTTATATTCCGCAACAACGAATTTTCGATGTCCCGTTGCGTGCCCGCGATATGGTT  
TCGCTGTCCGCGGCGCATGGCGTGGTTTCCAAAAGGGGACCCGCGAAGGGTGACGTCGAT  
AAGCTTCTTGCCCGCGTGGGCGCTTCCGGAATCGCCGATCGACGCGTCGGCGAGCTCTCC  
GGCGGGCAGCAGACGCTCGTCCGCCAAGCCCAGGCCCTTGCCACGCGCCCGCAATTATTG  
CTTGCCGACGAACCCCTCCTCAGCCTTGACCCCGGCGTCGCGCAGCGCACGGTGTCCCTA  
TTTGGTGAATTGAAGGCCGAAGGCGTCGGCGTTGTTGTGGTCACCACGATGTCAATCCA  
CTAATGGGCCTGGTAGATCGCATTTTGTACCTCGCCCCAACGGCCACACCATCGGCACG  
GTTGGCGATGTATGCAGTCCGAAAACTCAGCGAACTCTACAACGCACCCGTCACGGTG  
GCTCGCATCAACGACAGAATCGTGGTGGTT

>RXA00346-downstream  
TAAGTGGATCTATCCACCTGGCT

>RXA00368  
TCCCTCATGTTATCCCTGGGTGCAGCCCTAATCTGTGGGGTGCTGGGATGGCTGATCGGA  
GTGCTCATCACCCGAACCCAGCATTTCCGCAACGTACCGTTGACACTCACTGTGCTGCTT  
CCCACCGCACTGCCGGGCATGATCATCGGCGTCGGCTGGCTCATTTTGGGCAGATACACC  
GGAATTTACAACACACCTTGGGTGATTTTGGGTGCATATGTGTGTGCTTTTACCGCGCTG  
GTTGTCCAAGCTGTACGCGGACCACTCAGTCAAGCACCCGAAGCAATCGAAGAAGCCGCA  
CGAATCAGCGGCGCAGGCAGATTACGATCCATCATGGACACCACCGGAGCGATGGCAATT  
CCCGCAGCTTTCCGCGGCGCAGTGTGTTGCGGTAACGCGGTCGAGAGTTAACCGTG  
TCCATTTTGTCTCATCGCGCCGGGCACCACCACCTGGGTGTGCAGGTGTTCAATTTGCAG  
CAGGCGGGAATTACAATCAGGCATCGGCGTTGTGCTTGATGTTTGCATTATCGGTATC  
GTGGCGCTCGCGTTGACGGTGCGCAGCCAGAAGGAGTTT

>RXA00368-downstream  
TAGGTGTCATCGATCAAAATTGCG

>RXA00369-upstream  
GGCGGGAAATTACAATCAGGCATCGGCGTTGTGCTTGATGTTTGCATTATCGGTATCGT  
GGCGCTCGCGTTGACGGTGCGCAGCCAGAAGGAGTTT

>RXA00369  
GTGTCATCGATCAAAATTGCGCGATTTAAGCGTGAGCTTCCGCGACGGAACCTTCGGGCTG  
CAAGATATCAATTTGAAAATTGAGCCGGAAGAATTTGTGGTGCTCATCGGGCCGTCGGGG  
TCCGGTAAACCACCATGTTGGGCACCATCGCGGGGTTGTGGAGCCAAGTTCGGGCAGT  
GTGCTCATCGCCGGCGAAGAAATGACGCATGTCCCGCCGAGCGCCGTCGCATGGGCATG  
GTGTTTTCAGCAGCATGCGGTGTGGCCGCATATGTGCGTCGCCAAGAATGTGGGATACCCG  
CTGGCGCGAAGTGGTCAGAAGGGGGCGTCGATAAGCAAACGCGTGGAGCGCACGCTCGCG  
CTGGTGGGGCTTGAGGGGTTCCGCGAGTCGCAGACCGGCCAGCCTGTCTGGTGGTCAACGT  
CAGCGGGTGGCGCTTGCGCGCGCCATCATCGCCGACCCACCGTGCTGCTTCTCGACGAG  
GCCCTCTCCGCCCTCGACGAACCGCTGCGAGACGCTTTACGACGCGAACTCGTATCTTTG  
ACCCGGCGCGAAGGCCCTCACTACTGTGCACGTGACGCATGACCGCGCCGAAGCGATCTCC  
ATCGCTGACCGCATCGTCTACTCGGCAACGGTCAATCCAACAGGTAGCCACCCCTACT  
GAGCTCCTTTCCGCCCCCGCTACTGCCGATGTTGCCGATTCATCGTCGACGCCACC

>RXA00370  
GGCAAAGCCCTATGGAATTCGCGCTATACAACAGTGCTTTCTGCGGTGGGCGCGACCATT  
ATCGGCACGATCATGGCTCTCAGCTGGACCGAACTGATGTTTTCGGGCGCACCGCGTTG  
CGGTTATTTTGTATCCCGCTGTTGATCCCTCCGTTTATTGGGGCTATTGCGTGTTG  
CAGCTGTTCCGGGAAGAACCAGGGCATCAACCGGTTTTCGGCACGGAAGTGTGGGATATT  
TACGGCGCTGATGGTGTGACATTTTGTGATTGTGCACTCCTATCCACTGTGTACATC  
ATTGTTTCGGCAGCTCTGAGGCAACTTCTAGTGATTGAGCAAGCTGCACGGATCGCG  
GGGGCGGATACTTTTACGGTGTGCGCACCATCACACTCCCACTGCTCAAACCTGCATTG  
TTGTGCGCGTTTACTCTTACCACAGTGGCGAACCTCGCCGACTTTGGCATTCCAGCTCTG  
TTGGGATCGCCAGCGCGTTTGAACCTTAGCCACCATGATTTATCGCTTCATGGAATCC  
GGCACCGTGAGCAATCCATTGCAGGTGGTATCCACCATTGGCATCGTGTGTTGTTCTG  
GGAATCGCAGCAGTAACCGCGGATTATCTGGTGTCTTGTACGCGGCATCAAAGTTGCAA  
GACGCAGGAACACCGCATCGCTTTACTCTCAACAAATCACGAATCCAGTCAGCGTGATC  
ACGTGGATCATCGCGTTGATCATACCGCCGCCCCGCTGCTGGGTCTGGCATAACAGAGCA

TTACTGCCTGCCCCAGGT

>RXA00410-upstream

GTGTTGATGCGTTAGTCCACCCACGCAGCTACGCCCCAAAGGAATAATCTTGAACCCCTGC  
CACAGATAACGCTCCGCCGGTCTTTTCAGCCCAAGATCTC

>RXA00410

ATGATGATCTATGGAAAAGGATCAACAGAAGTTCGGGCTCTCGATGGCATTCTGTACAG  
ATTCAGTCCGACAAATGGACCTCCATCATGGGGCAATCAGGCTCTGGCAAAACAACTCTG  
TTGCAGTGCCTTTCCGGATTGGCGCAGCCAACCTCAGGCAGAGTGACACTGAACAAAAAC  
AACATCACGTTGAGCTCCCTGTCAGAAAATAAGCGTGCCAAGCTGCGTCGCACGCACATC  
AGCATGGTGTTCAGGATTTCAACTTGGTGCCTATTTTGTGCGGTGAAGGACAATATTTTG  
CTGCCGTTGCGTCTTGCGCATCGCAGGGTGGATAAGCAGTGGTTTGAACACATCACCAGT  
GTGTTGAAGATTGATAATCGTATGCGCCATTTGCCTGGGGAGCTGTCTGGCGGTGAGCAA  
CAACGCGCCGCGATTGCCCCGGGCGTTGATGTCTAGGCCCGATATTGTCATTGCGGATGAG  
CCAACAGGAAGTTTGGATTCCGTCACCAGCGATGCAGTGTGAATTTGTTCCGCAGCATT  
GTTGATGATTTTGGGCAGTCACTTGTGTTTGTACCCACGATAAAGATGCTGCTCACCCT  
GGTGACGTGTTGATCACAATGCGTGATGGCAAGATCATCGATACGGCAGATTTGCGGGTG  
GGCGT

>RXA00410-downstream

TAATGTTTCAGGCTTGCTTTTCGCT

>RXA00419

GACAACGAAGCACAGTGGCGCGACCAAGCACTAGCAGTGGGAAGCAACCACCGTGAACCTAC  
ACCGCCGGCGTTTCCGTAGGTGTACTGCTGGGCCAGAAATTTGAGCAGCAGGGCCACGGC  
ACCATCGTGGCATTGTCTCTGTGGCAGGCCAGCGAGTCCGCCGCTCCAACCTTTGTCTAC  
GGCTCCGCCAAGGCAGGTTTTCGACGGTTTCTACACCCAGCTCGGCGAAGCCCTGCGTGGA  
TCCGGTGCCAACGTATTGGTGGTTTCGCCCAGGCCAGGTACGCACCAAGATGTCCGCAGAT  
GGTGGCGAAGCCCCACTGACCGTCAACCGCGAAGACGTGGCAGATGCTGTTTATGATGCA  
GTGGTGAACAAGAAGGACATCATCTTTGTCCACCCACTGTTCCAGTACGTCTCTTTTGCG  
TTCCAATTCATTCCGCGAGCAATCTTCCGCAAGCTGCCGTTT

>RXA00419-downstream

TAACGGAAGTTACGGAAGTTACG

>RXA00421-upstream

GCTGGTTGAAGACTCGAAATGAGATCGACCCAAACCGGAGTCTTTGCATCTGACATGTCCC  
GCCGACTTGAGCTTTCTTAAGAAAGGGCTTGAACATAACA

>RXA00421

ATGCTTAACGCAGTGGGCAAAGCCCCAAACATTCTCCTTCTTGGTGGAACCTCTGAGATC  
GGTATTTCCATTGTCTCCCGCTTCTCAAGCAGGGTCCATCCCATGTGACCTTGGCAGCG  
CGTAAAGATTCCCCACGCGTGGACGCAGCAGTCGCAGAG

>RXA00432

TTGTCTGCGCTGGTTATTTTTGGCGGCGTGCAGCGTATCGCAAACGTGACGCAGTGGATG  
GTTCCGTTTCATGGCGGGTGCCTACATCATTGTGGGTGTGGTGGTGATTGTGATTAACATT  
CAGCAGGTTCCGACCATGATCAACGACATCATTGCTGGTGTCTTTGGTTTCCGTCCGGTT  
GCTACTGCGTGGTGTGGGGCGCGTTCTGGTTGGCGTTTATGAACGGTATGCGCCGTGGA  
CTGTTCTCCAATGAGGCTGGTGAGGGTTCTGTCCCGAACGCTGCTGCTACCGCGACTGTG  
TCTCACCCTGTGAAGCAGGGTTTGGTTTCAGACTCTGGGCGTATATTTTCGACACCCTGCTC  
GTTTGTAGCATTACCGCTTTTGTCTATCCTGCTGTCTGGAGTGGAGTACGCGACCGGCGAT  
ATTCAGTCTTCTTCTTTGACTCAGTCCGCGCTGGCTAGCGTTGTTGGTGGTTGGGGAACC  
CACTTCATTACCGTAGTGATGTTCTTCTGGCGTTTCTTCCGTGCTGGGTAACACTACTAC  
TTGGCACAGGCGAATATTCACTACTTACCGATTTCGAAGACTGTGATGACTGTTTTCCGA  
CTCTGGTGTGCTGCTCAGCGTGTCTCTGGCGCGGTTGCTTCGGTGCCGTTGATCTGGGCT  
TTGGGTGATACTTTTCGCTGGCATCATGGTGTCTATTAACCTGGCGGCGATCATTCCGCTG  
GGTGGCGTTGCAGTGAAGTTGCTTAAGAATTACACCATTCAGAAGAAGGCTGGTCTGGAT  
CCTGTGTTCCACCGCGACATGATGCCAGAGGTTTCGTAATATTGCGTGCTGGAACGGCAA  
GATGCAGCTACATCCAATATCACGAAGCGATGGAAGTGATCAAGAAGAGC

>RXA00432-downstream  
TAGTCATCGAAGGAACAGTGGTA

>RXA00436-upstream  
GGGATTTACTAAAAATCGGGTAACACGCGCTAGTATTTTTTCGC

>RXA00436  
ATGGAATTATTGGAGACCTTCATCACTGATGTCATTAATGACAATTTGTGGATGATCTTG  
CCCTTCTTGCTCGTTGCTGCTGGCCTCTATTTTCGGTGGGCGTACGTTGCTGGTTCAGATT  
CGGATGATTCCGGAGATGTTCAAAGCGGTTCGTCGAGAAGCCTGCGAAGGATGGGGAGTTC  
GCGGACAAGCAGGACATTTTCGGCTTTTAAGGCGTTCACGATTTCTGCGGCGTCGCGAGTT  
GGTACGGCGAATGTTGCGGGTGTGCGCTGGCGATCACTCTGGGTGGACCGGGTGCAGTG  
TTCTGGATGTGGATCATTGCGCTGGTTGGCGGTGCGACATCGTTCATTGAGTCGACTCTT  
GGACAGTTGTGGAAGGTGAAGGACGGCGACAGCTATCGCGGTGGCCCTGCGTACTACATG  
ACGCTTGGTTTTGAATGCTCGGTGGCTTGGCGTTGTTTTTCGGTGTGCGCCATCACGTTGACC  
TTTGGTTTTGTGTACAACGCTTTGCAGTCCAACGCGTTGTTGAG

>RXA00449  
CTGGCACTGACCGCTGAGACTGTGGGCGGAATGAAAAACCAAAGAAATTCGCCACTGGA  
CTCATGCTGTCCATTGCTTATTCTGCTTCCATCGGTTCACTCGGCACCTTAATTGGCACG  
CCACCCAATGCCTTGCTTGCTGCGTATATGTCTGAATCGCATGATATCCACATCGGATTT  
GGTCAGTGGATGATTCTTGGTGTACCAATTGCTGTCTTCCACATCATCGCGTGGCTT  
GTGTTGACCACCGTGTTCAGCCAGAAATGAAAGAAATCCCTGGCGGACGTGAACGATC  
AAACGTGAAATCGCTGAAATGGGGCCGTGGACTGCACCTCAGGTACAGTGGGTGTTATT  
TTTGGCGCAGCTGCACTGGCTTGGGTCTTCATTCCATTAACCTCTAGATTGGACCGGTTCC  
CAGCTCTCTATCAATGACTCCCTCATTGGCATCGCTGCCGGCCTGCTGATGTTTATCGTT  
CCCCTAACTTTAAAACCGGCGAACGCATTCTTGATTGGCGTACTGCAGGCGAACCTTCCA  
TGGGATGTTCTCTTGCTTTTTTGGTGGCGGGCTTTCACCTTCTGCGATGTTTACCAGCACG  
GGACTTTCCCTATGGATCGGTGAACAGTAAAGGACTTGATGCCCTTCCAATCTTCATT  
CTCATCTTCGCCATTGCTGTCTGTTGTTCTTGACCGAGTTCACCTCCAACACCGCA  
ACAGCGGCAACCTTCCCTGCCAATCATGGGTGGCGTCGCCGTAGGTATCGGACTGACCGCA  
GGTGGCGAGCAGAATGTTCTGCTGCTGACCATCCAGTCGCACTGTCCGCAACCTGTGCG  
TTCATGCTTCCAGTGGCAACGCCTCCAAACGCGATTGCATTCCGGCTCCGGCTACATTAAG  
ATCGGCGAAATGGTCAAGGGTGGTCTGTGGCTGAACATCATCGCAGTCATCCTCATTACG  
ATTTTCACCTACTTCGTAGCGATCCCACTCTTTGGCATCATGCTT

>RXA00449-downstream  
TAAAAGTTAACAGGCCCGCAGTC

>RXA00456-upstream  
CTACCAACCCGGAGATCGTCACAGCGGTGCTAACGGATCATGCCTAGCTTATGGCGTGC  
TCGTGCGAGACTTTTGCTCATTGCCCTAGGTGTACTTGGT

>RXA00456  
GTGCTGCAGGCACTGCTGGCGATCATGGTGTGCTTGAGCGTAGCCGCCATACTTGAGGGA  
AACCGAGCACTTGTTGGATTGCTGCTTGCTACCACGTTGGGTTTGGGGGTGGCGCAGTGG  
ATTCAAAAAGTAGTGGCAGAAGATCTAGGCCAGCATTATGTGCATGAGGTGCGTCGTGAA  
TTGGTGGGTGCTGCGCTGGTGCCTGGAAATACGGCCTCGTTGGGCGTGAAGTGTACCCGA  
GCCAGCAATGATCTACCGCGGTGCGCAATTGGGTGGCTTTGGGCATTGTTCCGATGGTC  
ACCGGGCTGCCG

>RXA00459-upstream  
AGGCGTGGCTGTTACTGTGCCACTGCTCAT

>RXA00459  
GTGTGTACCCGTGCTGCCGGTGGTGGCGCGGTGACTTTGAAAAGAGCACGTGAACTACGC  
AAAAAACGTGGACGCATGGCTGCGCGGATCGCAGATTCTGTGATGGCTGGAGAATTACTG  
CACGCAACAGGAGCAATAGACCGTGAGCTCAATGCAGTCACCCGAGATTCCGACCGAGTG  
GTGATAGCTGCTGTAAGACGTTCCCTGGGCCACCGGTTTTAGCCGCGCATTGATGGCCATG  
GCAGCCTCGCTTGGCACTGTGAGCATTGTGATTTCTGGCCACCTGGAAGTAAGTGAGGTT

GCGGGAATAATGATGCTTCTTGCGGTTCTTGCCACTCCAGTTGCAGAACTTGGCCGCGTG  
GTGGAATATCGCCAAAATTATAAAGCCGCGACACGCATCCTGATTCCACTTCTGCAACGA  
GGCTCAGAATTTAAACACTCCCAACAAAACTACCCGGGTTGCAAGCAACAGAAGGAATC  
CCCGGTGTCTATGTCAAAGGTATTTCCGCCCTTCTGGAGAACGGATCTACCTCCACGGC  
TCTGCAGATGCGACGAGAAAATGGGTCACCTCGTTGTCTGCAATGGAGGAAGGCACAGAT  
GTAATAGTCAACGGTCAAAGGCTTTCGCAGCTTCCTTTGAAACAACGACGCGCCCTCATC  
GGAATCGCCTCAGCACACCACCACTTAAGCCGTGGTTTCAGTATCGCGCCTGGTTGGTTG  
CGAGTGCCGGATGCCACCGTGAAGAAATTGAGCAAGCACTGGAACAAGTTGGTCTGAAC  
AACACCGGGAACAACGCTTGAAAAACGGCGGACACCCCTGGAGTACTTCGCAGATCAAC  
AAACTGAAAATTGCCAGCGCCACCTTCGAACCCACCGCTTTTGGTACTTGAAGGCATC  
ACCCCTGAAAACCTCCTCAACTATCCCGGAGTGATCATCTCCACCGTTTCAAGGAAACCA  
TCCGAAACATGGCGGCAAGTGAACATC

>RXA00459-downstream  
TAATCTAGAAACATGGCAGGACG

>RXA00477-upstream  
TGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACCTCTCTACACTCGCTAGAGCCACGA  
TGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTTCGTG

>RXA00477  
ATGAAGGTCTCGACTAAAACCTCCACGCTCCTCAGGTACCGCCGTAGTCATAGGCGCAGGT  
GTTGCTGGTTTAGCCACTTCTGCACCTTTAGCACGTGATGGCTGGCAAGTAACTGTTTTG  
GAAAAAATACTGATGTGGTGGCCGAGCTGGATCGCTTGAAATATCAGGCTTTCTGGC  
TTTCGATGGGATACCGGACCTTCTTGGTACCTCATGCCCCGAGGCCTTGACCATTTCTTC  
GCACTTTTTGGTGCATGTACTTCTGATTATCTCGATTTGGTAGAATTAACGCCTGGTTAT  
CGAGTTTTTTCTGGCACACATGACGCTGTGATGTCCCCACTGGGCGTGAAGAAGCAATT  
GCGCTATTGCAATCCATCGAACCCGGCGCGGGTGCAAACTAGGAAATTATCTTGATAGC  
GCGGCAGACGCCTATGACATTGCCATTGATAGATTCCCTTTATAATAATTTCTCCACGTTA  
GGCCCGTGCTTACCGGGATGTACTGACCCGAGCTGGCCGACTGTTTTCTCTACTGACC  
CGTTCTTTACAAAAGTACGTAAATAGTCAATTTCAGTAGCCCGGTGTTGCGCCAGATCCTA  
ACCTATCCAGCAGTCTTCTGTCTTCCCGACCCACTACTACCCCATCGATGTACCACTTG  
ATGAGTCATACCGATTTGGTGCAGGGAGTGAAATACCCCTATAGGTGGTTTTACTGCAGTG  
GTTAACGCTCTGCATCAGTTAGCGCTGGAAAACGGGGTTGAGTTTCAACTCGATTCTGAG  
GTCATTTCCATCAACACTGCTTCATCGAGGGGCAACACAAGCGCCACAGGTGTGAGCTTG  
CTTCAACAGAAAAGTGCAAAATCTAGATGCGGATCTTGTGGTTTCAGCAGGCGACCTA  
CACCATACAGAAAATAATCTGCTTCCCCGGGAACCTTCGAACCTATCCCGAACGATATTGG  
TCCAATCGCAATCCTGGAATTGGAGCGGTATTAATCCTCCTGGGCGTAAAAGGAGAGTTA  
CCCCAGCTCGACCATCACAACTTTTCTTTCAGTGAAGATTGGACAGATGATTTTGTGTGA  
GTTTTCGACGGGCCTCAACTTACCCGCCCCCACAATGCATCAAATTCCATTTATGTCTCC  
AAGCCTTCAACGTCCGAAGACGGCGTTGCACCTGCTGGATACGAAAACCTTTTTGTTTTA  
ATTCCGACCAAGGCCTCTAGCAGCATCGGCCACGGTGATGCGTATATGCAGTCGGCTTCA  
GCATCCGTGGAACAATCGCGTCACATGCAATCAATCAAATTGCTACGCAAGCCGGCATC  
CCTGACCTCACTGACCGAATTGTGGTCAAACGCACCATTTGGCCCTGCGGATTTTGAGCAC  
CGCTACCATTATGGGTAGGCAGTGCCTGGGTCCAGCACATACCCCTCAGACAGTCCGCT  
TTCTTAAGAGGGCGCAATAGCTCCCGCAAGGTCAATAACCTCTCTATTCCGGTGCCACC  
ACCGTCCCGGGTGTAGGAATACCCATGTGTTAATTTCTGCCGAGAATATTATTAAGCGT  
TTACATGCCGATACAGTGCAGGACCACTGCCCCGAACCATTGCCGCCTAAAACGACACCA  
TCTCAAAGACCTCATACGATCAT

>RXA00477-downstream  
TAAATTTTGATCCCTATCATCGA

>RXA00478-upstream  
ACCAGAAGCAGCCTCAGCTATGACACACCAAAATTCGCCCTCTCTTCTTAAAAGTGCAT  
GAGACTTTACAATCGGGCCTCATTCAAGGCTTCACATAAA

>RXA00478  
GTGATCGAAGAATATTCCACGAGCTTCAGTCTGTCTACGTGGTTGCTATCCCCACGCATA  
CGAAATGACATACGAAATCTCTATGCAGTAGTTTCGTATCGCCGATGAGATTGTGACGGC  
ACTGCACATGCCGCTGGTTGCTCAACTGCCAAAATCGAAGAGATTCTCGATGCCTATGAA

ATTGCGGTTCTTGCAGCACCACAACAACGCTTCAACACAGATCTTGTTTTACAAGCTTAT  
GGTGAAACTGCCCGACGCTGTGATTTTGAACAAGAGCATGTAATAGCCTTCTTTGCATCA  
ATGCGTAAGGACCTCAAAGCTAATACACACGACCCAGATAGCTTCAACAGTATGTCTAT  
GGCTCCGCGGAAGTTATAGGCCTGCTTTGTCTCAGCGTTTTCAACCAAGGTAGAACGATT  
AGCAAAAAACGGCTAGAGATTATGCAAAACGGAGCCCGCTCATTGGGAGCGGCATTCCAG  
AAAATTAACCTTTCTCCGTGACTTGGCAGAAGATCAGCAAAATTTGGGCGGATTTTATTTTC  
CCCAAAACCAGCCAAGGAACCTTTACTAAAGAACAAAAAGAAGATCTCATCGCTGATATC  
CGTCAAGACCTAGCAATTGCCACGATGCATTTCCAGAAATACCAGTGCAGGCTCGCATC  
GGAGTGATCTCTGCTTATTTGCTCTTTCAAAAACCTCACTGACCGAATTGAGGCTACTCCT  
ACCGCCGATTTATTGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACCTCTCTACACTC  
GCTAGAGCCACGATGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTCTG

>RXA00478-downstream  
TGATGAAGGTCTCGACTAAAACT

>RXA00480-upstream  
TTTATGGACCCAAATTCACACTTTCTGTACTTCATCAAAATAAAGCGCCATATACAACGA  
TTGGGAATTTTTCGAGATAACTGGCCGTGTGATACTCGA

>RXA00480  
ATGGACAATGGCATGACAATCACCACAGAACATTCAACTCATCCTGATCTTGATTTCAAT  
GATGAGATTTATCGGGAACTAAACCGCATCTGCGCTTCGCTATCTCAACAGTGCAGCACA  
TATCAACCAGAGTTCCGTACCTGCCTAGATGCTGCTTTCCAAGCTTTGCGAGGTGGCAAG  
TTAATCCGCCCTCGAATGCTACTGGGGCTATACAACACGCTTGTAGACGATGACATTGAG  
GTCAAACTCAACACCGTTTTACAGGTAGCAGTGGCTTTAGAACTACTGCATTTTTCCCTT  
TTGGTTCATGACGATGTTATTGACGGAGACCTCTATCGCCGAGGCAAACCTAATTTTATT  
GGGCAGATTCTCATGCATCGCACACCTGAAAGTTTTGCACAAATCCAGCGCGATCCAGAG  
CATCTAGATTGGGCACAATCTAATGGACTGCTTATGGGAAATCTTTTTCTTGCTGCCACC  
CATCAAATCTTCGCGCGCCTTGACCTTCCACATCACCAACGGGTTGACTTTTAGATTTA  
CTCAACCACACGATAAATGACACTATTGTGGGTGAGTTTCTTGATGTGGGATTAAGCAGC  
AAAGCCATCAGCCCCAATATGGACATTGCTCTAGAAATGAGTCGGCTAAAAACAGCCACA  
TACACTTTTGAACCTCCAATGAGAGCAGCGGCAATTCTCGCGGAACTACCTCAGGAGATT  
GAAACAAAGATAGGTGAGATAGGCACAACTTGGGCATCGCTTATCAATTGCAGGACGAT  
TACTTATCTACTTTTGGTGACGCAGCCGAACACGGCAAAGATGCCTTTTCTGACCTTCGA  
GAAGGAAAAGAACTACAATTATCGCCTTCGCTCGAGATACTGCTAAATGGACTGATATT  
CAAGACAACCTTCGCGCAGATCTGAGACCTCTCAGGCAGAGCGAATTCAACATCTT  
CTCATACAGTGTGGAGCAAAGAATCACTCCTTGAATGCCATCTCCGACCACTTAAATATC  
TGCCGTTTCGATGATCAAAACACTAAGCCCCCAGGTAGATCCCAAGGCTCAAATTTATTA  
CTTAAACAAGTTGAGCAACTAGCCAGCCGCAATCT

>RXA00480-downstream  
TAGAACTAACCTTTACGCCTTTA

>RXA00524-upstream  
TCCTCGGCACCCGCTACCCCGTCGGAGTTGTACCGGCGCATTCGGCGCCCCATTCTTTA  
TCTATTTACTCATTCGTTCCAACCGCGCGGGAGTAACCTT

>RXA00524  
GTGACCACCAACCATCAACTATCCGCCGAAGAAATTTCCCTGGCGTACGGCGAGCGCACC  
ATCATCGATTTCGCTCAGCGTCGACATCGTCCCCGGCAAATCACCTCCATCGTCGGCCCC  
AACGGATGCGGCAAATCAACGCTGCTGCGCGCCTTTGCGCGCCTCCTTAAACCTAGCGCC  
GGGCAAGCGCTTATCGACGCCCACCCCTTCTTCACTGCCAGGCAAAGAAGTACTCGC  
ATGCTCGGGCTGTTACCGCAATCCCCACCGGACCTGAAGGCATCGTCGTCGCCGACCTC  
GTGGGCCGCGCGCGCCACCCCAAGGACTC

>RXA00526-upstream  
GGTGGAGCAGGCGGCGGCTCCTTTTAGTCCTGCGGCCCCCTTTGACCCTGCAGCCCCCTGC  
CGTTTCTGCCAAGCAAACCGTGGGCCAGGTGATTTAGCCT

>RXA00526  
ATGAGCCTCATCGAAATGCGAAATATTGTCAAGACCTACAACATTGGATCTGAAGGTGAA

CTCACCGTGTGTCACGGTGTGGATTTCCATGTGGACCGTGGCGAATTCGTGTCGGTTGTG  
GGTACGTCCGGCTCAGGTAAATCAACGATGATGAACATCATTTGGGTTGTTGGATAAGCCA  
ACTGATGGCACGTACACCTTGGATGGCGTGGATGTGTTGGATATCAGCGATGATGCTTTG  
GCGAGCCACCGCGCTAAATCGATTGGTTTTGTGTTTCAGAACTTCAATCTGATTGGCCGG  
ATCGATGCGTTGAAGAATGTGGAAATGCCCATGATGTATGCGGGCATTCCGGCTAAGCAG  
CGGAGAAGTCGTGCGGTTGAATTATTGGAAATGGTCGGGATGGGTGAGCGTCTCAACCAT  
GAGCCCAATGAGCTTTCGGGTGGTCAGAAGCAGCGCGTGGCCATTGCTCGCGCGTTGGCG  
AACGATCCTGAGATCATTTCTTGTGATGAACCAACTGGTGCGTTGGATTCTGCAACGGGC  
CGGATGGTGTATGGATATTTTCCACCAGCTCAACAAGGAGCAGGGCAAACCATCGTGT  
ATTACTCACAACCCTGAGCTTGTGATGAATCTGATCGGGTGGTCACCATGGTTGACGGG  
CGCATCATTTGGGTCTGAGGTGAAACACTCA

>RXA00526-downstream  
TGAGCCTTGCAGAATCAATTCTT

>RXA00559-upstream  
CCCTTCAATCCAGTCTTTGACGGCCAATACGGCTTGCCGGGTTTCCAGCGGATCAATCCT  
CATGAAGCATCAGCCTAGTACGAACCGTTAAAGTGCCAT

>RXA00559  
ATGTCTGATAATCCGCATGAGAATCCCCGTGAGAATCCACACCGCTCCCCAGAAGTCGTC  
CTTCGTTTCATGGCTGCCCTACTGACGTTTTGATGGCTGGTAGCCATGGCGTTGGCGGT  
GGCCGAGTCTTGAATGGATCGATAAGGCTGCTTATGCTTGTGCTACCCACGGGTCTGGA  
ACCTACTGCGTCACTGCTTATGTTGGTCACATT

>RXA00570  
CCAACCATCGTGATGGCCATGGTCGCAGGCATTTTCCCTCCGCTTCGGACTCGACCTCATC  
GACGCCAGCGTGACCGACCCGCTCATTGCACTTCCCATGGTCATAGTTTTTGTGGCATTG  
AGCATGAGTCCCCGCTTGGCAAGCATCGCCCCACCCGTTGCAGTAGCCGAGTAGGGGA  
ACCATCGTTGCCATCGCATCCGGCAAACCTAGCGTCCGGAATTCTAGACAACGGAATTATC  
TCCCCGCCCCGCTTTTACCGCCCCAGAATTTTCCCTTCGCCGCCATCATGGAACCTCGTTGTT  
CCCTTGGCGATCACCGTAGTCATTGTCCAAAACGGCCAAGGCGTCGCAGTGCTTAAAGCA  
GCAGGTCAACGCCCCGAGTAAACCTTGCCGCCGCGGCTCCGGACTGTGGTCCCTACCC  
ATGGCGTTGATCGGCAACATCACACCTGCCTCACCGGCCCCACCAACGCGCTGATCGTC  
GCCGGAGCAAAATCACAC

>RXA00571  
CAGATCGGTGCGCTCAGCCCAGCAGTCGCCGGCACCCCTTGGTTCCTACGCCATGATCGGC  
GTGATGATCGGTGCTCTATCTGCAGGTGCCGTTGGTGACCGCCTTGGTCGTCGCAAAGTT  
ATGCTCACCGCAATCGTCTGGTTCTCTGTGGGCATGGCGCTGACCGGCTTCGCGTCTCG  
ATTGCGCTGTTTCGGTTTCTTGCCTTCCCTCACCGGACTTGGCGTGGGCATGATCGTTGCA  
ACCGGCGGCGCAATCATCGCGGAGTTTCGCTCCAGCGAATAGGCGCAACTTGTTCACGCA  
ATCGTGTACTCCGGTGTCCCAGCCGGTGGCGTGCTGGCTTCTATCCTTGCACTGCTCTTT  
GAAGATGTATCGGCTGGCGCGGACTTCTCCTCATCGGTGGATCCCCACTACTGTTCCCTC  
CTGCCACTTGATATCTTCTCCTCCAGAGTCCCCGCGCTGGCTCACCTCCCGCGGCGGT  
GCTGCGGACGCCAAAGCCCTCTGCGCACGCTATGGGCTGCCGACGGAGGAATTTGTGCTC  
GAAAAGCAGCAGGAAACAAAGGGCACCGGATTTCGCTGGAATTTTCTCCTCCAAGTACCTC  
ATGGGCACCATTTCTCATCGGCGCAATGAGCTTCATCGGGCTGCTTTCGACCTACGGCCTG  
AACACCTGGTTGCCAAAGATCATGGAATCCAACGGCGCAACCTCACATGATTCCCTGTAC  
TCCCTGCTGTTTCTCAACGGCGGCGCAGTGTTTCGGTGGCCTCATCGCATCCTGGTTGCT  
GACCGCATCGGCGCAAGACCGTGATCACCTCCACCTTCGCTCTCGCCGCGATCTGCCTC  
GGAGTCTGCTGCCAAACATCTCTCCTGGCCAATGATGTACACCGCAATCGCATTTCGAGGC  
GTCGGCGTCTTGGGCACCCAGGTTCTCACCTACGGCTGACCTCGAATTCTTCGGAACC  
GAATGCCGCGCAGCGGGAGTTGCATGGTGTGCAGGATTTCGGCCGACTCGGCGGAATCGTC  
GGACCAGCAATCGGTGGCCTGATCATCGGCGCAGGATTTCGGACCAAGCTCCGCATTCTC  
ATCTTCGAGCAGCTGCCGCAATCGGCGCGGTCTGCACCTTGCTGATCCCGCGCTCCCCA  
GCAGAAGTAGAGGTCAAGGTGCGCGAGGAACCACTTGCACGTGTC

>RXA00571-downstream  
TAACCCCAATTAATTCGAAACAA

&gt;RXA00572

CAGTGGCTCAACCGCTACCTCGAGCTGTCTGGCCCTGTTGATGGTCAGTGGATTGATGCT  
TCCTGGGCTGCACGTTTTTGCCAGATGCTGGAGCGTGCCGAGGCGCGTTTTGATCGAGCAG  
GATCATGGCCAATTTGAGCCAAGCCTGACGGTGGAGGATGGCGTCGACAAGCTTGTGCT  
GCTTACCCGCATGCCGCAACCGACCTGCTCACCCCGGCTGATGTCGCCTGGTTCTTGGGC  
CTGTGCCGACGCGGGCAAGCCTGTGAACCTTGTGCCCGTCATTGATAAGGACGTGCGT  
CGCTGGTGGCGCTCGGACTCCCTGTGGCAGTCCCACGATGATCGCTACACCGCTGATCAG  
GTGGCTATTATCCCTGGTGTGCTCGCCGTTGCTGGCATCACCAAGGCCAACGAACCTGTC  
GCTGACCTGCTTGATCGCTTTGTGACGCCACCATCGAGCGCATCGATGAGCACGATTCC  
CGCTCCCGCGACATCATGGGCAAAGTGCTTTCTCACCCTGGCACATTCTGGGCTGGCCGC  
AACATCCCATCGGTGATCCACAGCCTTGGGCATGCTGACAAGTGGTCCCGCTCCGAATTC  
GAAGCATTCATAGCCCCAACCGGCGCCAACCTGGTGTACGAAGACGCCGAGCACGCGATG  
CTGACTGTGCCTTTGGCGGGTTCCACCGCATTCGGCACCACCGCTGAGCTGAAAATCCGT  
TTCACCGCCCATCGACGCTCTGCCAAGCGCTGTCCCACTGGTCACCCAGGAAGACGCT  
GAAGCCGCGATGGGTGAAGTGAACCGCATCGCAGCTGGCGGCACCCCTGGCAACTGTGAAC  
AATGGCACCGCTACCTGGGAAACCTCCGTCGATGCCGGCGTCATCGCTGACTACAACAAC  
GTCACCGCAGGCTACCTGCCAGCATCCGTTGTTCTGTCACACACCGCACCTGACGTGCTG  
GTTGGCCGCGCATGGCCAGCAGTTTTCGCTGCCGTAAAGTCCGCAGTCATCCAGGCACC  
GATTCCGCATCCGTTGTGGAAGGCATGCTGTCCCTGGTTCACCTGGAGCACACATTGTG  
CTCAAGTCCGATGTCCCAACCGACGGCGCGCTGAAGGTTTCCGCGACTGCCGATGAGGTA  
GTCGATACCGACCTGGGTGCGCTCGTGATCGTGCGCGCAGAAATCGCCGACGCAGAAGGC  
AACCTGATTGTACGTTGGCTGAGCTTTCCGATCCGCGGACGCAAGGGCAACGCTGTC  
GCACGCACCAACACCTCCGCACTGCCAACCACCGTGGACACCCACGCTCAGCTCGCGCA  
GTGGCAACCGTTGTTGCACCTGAATCCATGCGCCCATTCGCTGTGATCTCCGGTGACCGC  
AACCCAATTACGCTCTCTGATGTTGCGGCTTCCCTGGCTGGTCTGCCAGGTGTGATCGTG  
CACGGCATGTGGACCTCTGCCATCGGTGAAGTATCGCCGGTGACGATTCAACGATGAG  
CAGATCCAAACTCCCGCAGCCAAGGTGCTGGAATACACCGCAACCATGCTGGCACCAAGTT  
CTTCCAGGTGAAGAAATTGAGTTTACGCGTTGAGCGCTCCCGCAGTGGACAACCGCCCAGGA  
ATGGGAGAGGTCCGCACCGTTACCGCAACCGTCAACGGCAACTTAGTGCTTACCGCCACC  
GCTGTTGTGGCAGCTCCATCTACTTTCTACGCATTCAGGCGCAGGGCATTGAGTCCAG  
GGCATGGGTATGGAAGCACGCCGTAACCTCTCAGGCAGCTCGCGCTATCTGGGACCGCGCC  
GATGCACACACCCGCAATAAGCTGGGCTTCTCCATCGTGGAATTCGTGGAAAACAACCCA  
CGCGAAGTAACCGTGGCAGGGGAGAAGTTCTTCCACCCAGACGGCGTTTTGTACCTCACC  
CAGTTCACCCAGGTGGGCATGGCAACTCTGGGCGTTGCTCAGATCGTGAAATGCGTGAA  
GCACATGCCCTTGAACCAGCGTGCATACTTTGCTGGACACTCCGTTGGTGAGTACAACGCG  
CTTGCTGCATATGCTGGTGTGCTGTCCCTGGAATCCGTTCTGGAGATCGTTTACCGTCGT  
GGCTTGACCATGACCGCTTGGTGGATCGCGATGAAAACGGTCTGTCCAACACGCGCTC  
GCAGCTCTTCGCCCAACAAGATGGGTCTGACCGCAGACAACGTTTTCGATTACGTTGCG  
TCTGTTTCCGAAGCTTCCGGTGAATTCCTGGAGATCGTTAACTACAACCTTGGCTGGCCTG  
CAGTACGCAGTTGCTGGAACCCAGGCTGGTCTTGCCGCCCTTCGTGCCGATGTTGAGAAC  
CGTGACCCAGGTGAGCGTGCCTTCATTTTGATCCCTGGCATTGACGTGCCATTCCACTCC  
TCCAAGCTGCGCGACGGTGTGGGCGGTTCCGTCGAGCACCTTGATTCCCTGATCCCAGCT  
GAGCTGGATCTGGATGTGCTGGTTGGCCGCTACATTCCAAACTTGGTGGCTCGCCCATTC  
GAACTCACTGAAGAGTTCTGTGGCATCCATGGCAGAAGTGGTGGAGTCCACCTATGTCAAT  
GAGATCTTGGCTGATTTCAAGGCTGCTTCCGCCGATAAGCAGAAGCTTGCCCGCACGTTG  
CTTATTGAGCTGCTTGATGGCAGTTTCGCATCACCTGTGCGCTGGATCGAGACTCAGGAT  
CTGTTGATCAAGGGCCTTCAAGCTGAGCGTTTTCGTGGAGGTCGGTGTGGCTCTGCTCCA  
ACGCTTGCCAACATGATGGGCCAGACCCTGCGCCTTCCTCAGTACGCGGACGCCACCATT  
GAGGTGTTAAACATTGAGCGCGATCGCCAGTTGTGTTTCGCTACCGATGAGGTTGTGCGT  
GAAGTGGCGGTTGAAGAGACCCAGCAGCTCCTGCAGAAACCACTGAAACCCAGCAACC  
CCAGCAACCCAGCCCTGTTGCAGCTGCAGCCCTGCCACCGCGCGCCCTCGCCAGAT  
GACATCAGCTTCACTCCTTCTGATGCCACTGAAATGCTCATCGCTATCTGGACCAAGGTT  
CGCCAGATCAGATGGGTGCCACTGATTCCATCGAGACCCTGGTTGAGGGCGTGTCTCT  
CGCCGTAACCACTCCTGCTGGATCTTGGTGTGGAGTTTCGGCTCGGCGCAATTGACGGA  
GCAGCCGATGCTGAGCTCGGTGATCTAAAGGTACCGTGTCCAAGATGGCTAAGGGCTAC  
AAGGCGTTTGGCCCTGTGCTCTCCGATGCTGCAGCTGATGCCCTGCGTCGCTCACTGGT  
CCTACCGGTAAGCGCCCGGGATACATCGCAGAGCGGTCACCGGCACGTGGGAATTGGGC  
CAGGGCTGGGCTGACCACGTGGTCTGAAGTTGTGATCGGCGCCCGCAAGGCGCATCC  
CTGCGCGGCGGCGACCTGGCGTCACTGTCTCCTGCAAGCCCAGCGCTGTCATCAGATCTT  
GATTCGCTTATCGACGCAGCCGTCCAGGCCGTAGCCTCCCGCCGCGCGGCTTGCGGTCTCC  
CTGCCTCAGCAGGCGGCGCTGCCGGTGGCGTGGTTGATTCCGCAGCTCTTGGCGAGTTT

GCAGAGCAGGTCACCGGACACGATGGTGTGCTTGCTCAGGCAGCCCGCACCATCTTGACC  
CAGTTGGGTCTTGATAAGCCAGCAACCGTTTCCGTGGAAGACACCGCAGAGGAAGACCTC  
TACGAGTTGGTCTCCAAGGAACCTCGGTTCTGATTGGCCACGTCAGGTTGCACCAAGCTTC  
GATGAAGAAAAGGTTGTTCTGCTTGATGACCGTTGGGCTTCTGCGCGTGAG

>RXA00590-upstream

TACGCTGGCGCACACCGCATGCTGGACTCCGGACGAACCGGCCCAACACGTCAAAGCTG  
TTTCCAATTCTCTATCACCGGCATCCTGATCACTGGCCTC

>RXA00590

ATGCGCGTGGTGTCTTCTCGCGGTTCTCGGTGTTGTGCGAGGTGGCGTCACCCTATCC  
ACCACGGGCAACCCAGCCGCGGAAGCATTCAGCACGCTGCAGGCGATATCGGACTACGC  
ATCTTCGGCGCCGTGCTGTGGGCAGCGTCCATTTCCTCAGTCATCGGCGCCAGCTACACC  
TCTGCAACCTTCTGGTGGAAACAAGCCAGAGAAGAAGCGTCTGCAAAACTGGGTGACC  
ATCATCTTCATCCTGATTTCTTGCTCCGTGTTTCATCATGCTCGGCACGGCACCAGCAATC  
CTCTTGGTCTTCGCCGAGCATTTCAACGGTTTGGTCCTCCCCGTAGGCTTTACCCTGATG  
ATCTACGTAGCGATCTTCGCCAAAAA

>RXA00591-upstream

GCAACGCCACAGGCAAAATCCAAAAGAACATCCTGCGAGACTTCACCATCCCCGTTTCAT  
AAACCCCCCAACGTCACTTTGAAAACACTTGGAGAACGCA

>RXA00591

ATGACTACATCTTCCACAGCTTCGCCGATCGCTGAATTACAAAACCTCAGCCCGAAGCAA  
AGAAAATCAGAATCCCGGCGCGCGATTATATCCAGCTACTTGGGCTCCACGATCGAGTTC  
TATGACTTCCTGTTATATGCCGCGAGCCTCCGCGACGGTATTCCCCGAGTGTTCTTTACC  
AATCTCGATCCGCTGGCTGGAACCATTCGCCGCTACGGAACCTTCGCCGCGAGTTATTTA  
GCTAGGCCACTTGGTGGAGCAATCTTCGGACACTTCGGTGACCGTCTTGGACGCAAGAAG  
ATGCTTGTGTTGTCCATGCTCATCATGGGTGTGGCATCCACATGCATCGGCCTTGTCCCA  
AGCGCTGAAATGATCGGAAGCATGGGCGCGGTAATCCTGATCATGCTGCGCATCTGCCAA  
GGCATCGCTGTGCGTGGCGAATGGGGCGGAGCTGCCCTCATGGCGCTCGAGCACTCAGAT  
TCCAAGAAGCGCGGATTTCGCCGCTCCTTCACCAACGCTGGTGCACCAACCGGCGCTGCA  
CTGGGAACCTTCGCGCTCGGTACCGCATCTGCTGTTCTCAGGAGCAATTCTTTCA  
TGGGGTTGGCGCATCCCATTCCTGCTCTTTCTGTTCTGCTGATTGTGCGCTTGGTTATC  
CGCGCGAAAGTTAGCGAATCACCAGTGTTCGCGAGCTGCAGCGGCCGCCGAAAAAGCCAAG  
CCAACCGAACGTAAAGTCCCCCTCTTCGAGGTTCTTCGCCGACCAAGGCACTGATCTTG  
ACCATGCTTGGCGGCGCATCAGGATTCGGACTTCAAGTTCTCTTGTCACCTTCTCCATC  
AGCTACGCAACACAATCCGGCATCGAAAGATCCAGCGTCTCTACGCCTTCGAGTCGCC  
TCAGTGTTCTCTGTCTTCTTTGTGATCCTTTCGGTTCGCGTATCCGACCTCTTCGGACGC  
CGACCCGTCATGATCATCGCGCTCGTACTGTTTCGTGGCCTACCTGCCGGCATTCTTCCGG  
ATGCTCACCTCAGACAACCTGGTTCATCCTGCTCTCGGCATTACCATCGCGCTCGCACTC  
CACGCCATGCTTTACGGCCCACTAGCAGCGTTTATCTCCGAACAATTTCGGAACCTCCGCG  
CGCTACACAGGCGCATCCCTGGGTACCAGTTGGCCACGCTCATCGGTGCAGGATTACCC  
CCAACCATCCTGGCTAGCCTCTACGCGGGACCAGGCGGGCGGAACCTCTGTACCCCCAGTC  
ATCGTCTTCTCGCAACGATGTCCCTAGTGTCCATCATCGCCATCGCAATCACCAGAGAA  
TCAAAAGACCACGATCTTTCTACTTACGAACAC

>RXA00591-downstream

TAAGGGGACGATAGGGTCAATTT

>RXA00596-upstream

CCGCCACCGACGGCCTCTTGAACACCGATGCATACCAACAGGCTGTGCTCGGTGAAAATG  
CCATCGGAGTGCCAAGCCCTAGCTACCAGGGAGGAACTA

>RXA00596

ATGCTTAACGCCCTGAAATTCATCCCATGGCTGATCGGCCAGATTTTCTCTCTGGCTTC  
AGCGTGATCACCGCTGCGGTAAAAAAGGACACCGGCTTCAACCCCGTTGTTATCCGCTAC  
CCACTTCGAGTGACCACGGACTTCCAGATCGCAGCCCTGTCAACGTGCATCACCAGGACT  
CCTTCCACCCTGTCCCTTGGCCTACGCGAACCCCGCAAGCCCGGCGACCCACCATTTTG  
CTGATCCAAGCAGTGTTTGGTTCGGATCCAGTAGAAGTTTTTGAATCCATCGCCGATATG  
GAACAACGCCTCGTCCCTTCGGTCGCTTCAATTGACCACGGCGTCCCAGGCCAAGGCCCT



TACAAGGAGATCCGCCCCAGCGATGCTGAGTGGCCAAGTCGCGAGATCGCTGACACCGCC  
CAAAACACCGTCAGCCAAGACAAGAGGGAGTTT

>RXA00596-downstream  
TAAACAACATGACTGCTTTTGG

>RXA00607-upstream  
CACTGCCAGCAACGCCAACGGTTGAACCCGAACCAGAAGGCGATGAAGACTGGCCCGAAC  
CCATCAACCCCGCAGGCGATAACAAAGAGGAGGCAAACCG

>RXA00607  
ATGATTCTCGCACTGACAGTCGCGATACTTTTCGGTGGAGGTGTCTACCTCATTTCAGCAA  
CGCGGAATGGTGCATCGTCTTCGGCATGTCACTGATCGGCCACGCAGCGAACCTGACC  
ATCCTGTACGCCGGTGTGCCACGTGGCGCGGCGAAGCCTTCCCGACAGGACCCCGCTT  
ACCGACGCCGCCGATCCACTCCCCAGGCCTTCGTCTCACCGCCATCGTCATCGCGATG  
GCCACCACAACCATCATGTTGGCCTTGGCAGCACTGGGACGCAGCGACGACACCCGGTCC  
ATCGAACCAGATGACGATCAATCGCCTTTGACTACTAGCGCTCGTTCAGTCACCAACCCA  
ACAGATCAGGAGGATAAAGCT

>RXA00607-downstream  
TAAATGGCCATGGATGTTCTCCT

>RXA00623-upstream  
TTTAAGCTTCGTCGGCAACGATCACACCACGTAAATTTTCGACCATCAATGACGGTGGCC  
GTTTTTTGGCGAATCCCCAAAAGGTCTGAAGAGGAAGTTC

>RXA00623  
ATGGATTCAAACACAGAATCTTCAAGTGTTGAGGTCAAAAACGAACACATTAAAGTTCAA  
AAGCCGCCGAAGAAGGACCGCACTCACTGGCTCTACATTGCGGTCAATTATCGCATTGATT  
GGCGGTATTACCTTAGGCCTGATTTACCCGAGTTGGGCAAAGAATTCAAGATTTTGGGC  
ACCATGTTTGTGTCTTGATCAAGATGATTATCGCTCCAGTTATTTTCTGCACCATCGTC  
ATCGGAATCGGTTCAAGGCAGCGGCAACAGTCGACGCGCTGGTGGCATCGCCCTT  
GCGTACTTCATCACGATGTCCACATTTCGCACTCGCAGTTGGCCTGCTAGTCGGTAAC TTC  
ATCCAGCCAGGTAGCGGACTGAACATCTCAGTTGATGAAGAATCTTCATTTCGCATCCACA  
GAGAGCAGCCCTGAAGGACTCTTGGGATTTCATCCACTCGATCATCCCTGAAACGTTCTTC  
TCTGCATTTACTGATGGTTCGGTGCTGCAGGTACTGTTTCATCGCCATCCTCGTGGGCCTT  
GCAGCTCAGTCGATGGGTGAAAAGGGACAGCCCATCCTTGATTTTCGATATCCCATCTGCAG  
AAGCTCATCTTCAAGATTTTGAAGTGGATTCTGTGGCTCGCCCCAGTCGGTGCATTCGGT  
GCAATGGCCGGCGTTCGTTGGCGAAACAGGCTTTGATGCCGTTGTTTCAGCTCGGTATTTTG  
ATCCTCGCCTTTTACGTACCTGCGTGATCTTCATCTTTGGCGTGCTGGGCGCGTACTG  
AAGGTGTTTACCGGCGTGAATATCTTCAAGCTGGTCAAGTACCTTGCCAAGGAATTCCTG  
CTGATCTTTGCTACCTCATCTCTGAATCTGCCTTGCCAAACCTCATGCGCAAGATGGAA  
CACATCGGTGTGGCTAAACCAACCGTCGGAATCGTGGTCCCAACCGGCTATTTCCTTCAAC  
TTGGACGGCACCGCAATTTACCTCACCATGGCATCTATCTTCATTGCCGACGCGATGAAT  
ATGCCGATGAGCCTCGGCGAGCAGGTGGTCTGCTTGTCTTCATGATCATCGCATCCAAG  
GGCGCTGCTGGTGTCTCGGTTGCCGGTATTGCAACGTTGGCTGCCGGATTGTCTTCACAC  
CGCCAGAACTTCTGCACGGCGTTGACGTGATTGTGGGCATCGATAAATTCATGTCTGAA  
GCCCCGCGCACTAACCAACTTCGCCGGAACCTCCGTGGCAACACTGCTGGTCGGCAAGTGG  
ACTGGCACCGTGGACATGAACCAAGTCCATGACGTTTTGAATGGAAAATCTCCATTTGTG  
GAGTTAGAAGAAGACCAC

>RXA00623-downstream  
TAGTTTTCAACAGGACGACAACG

>RXA00660  
CCAGGCCATACCCCGGAACACTTATCGTTCCTGCTGAAGGACGGCGGTTTCGCACATGAG  
CCAGGATTCATGCTCACTGGCGATTTTCGTTTTTCGCGGGTGATCTTGGCCGACCAGATTTG  
CTCGATGAAGCAGCTGGGGGAGTGGACACTCGTTTTGAGGGGGCTCGCCAAATGTTCAAG  
AGCTTGAAGGAAAAATTCCTGACATTGCCTGATCACATCCAGATCTTCCCTGGTCATGGT  
TCCGGTTCCGCGTGTGGCAAAGCCTTGGGTTTCGTTTCCTTCAACAACACTTGGATATGAA  
CGTCAATTTGCGTGGTGGGGAAAGTATCTGGAGGCAGATGATGAACAAGGATTCATTGAT

GAGCTTCTGGAAGGCCAACCTGATGCACCTGCATACTTCGGCAGGATGAAGAGGCCAAAAT  
 AGGCAAGGGCCCGCAATTATGGGCGCTCGCGAGCTGTTGCCACAGCTGGAAGCTTCTGAT  
 CTGCACGACGTCATTGTTGTTGATACCCGCTCAGCCGATGAAGTTCACCAGGGCACTGTA  
 GCTGGTGCAGTGAATATTCCTGCGGGCAATTCGATGGCGAAATTTGGCTCGTGGACCGTT  
 GATCCCGAGAAGGATTCCCGAGCTTTGGTTCTGCTCGCGGCAAGCCAAATTGGTGCCATG  
 GAGATGTGGGACCACATGGTTTCGCGTGGGAATCGATAATGTTGCTGGTTTTATCACCAC  
 TTTGATGGGGTGGACCTAGTTGCACCGCAAACCTGTGTCCCGATCAGCTGGATGAATTG  
 GAATACGATCTACTTCTTGATGTCCGCAACCGCAGTGAAGTGAAGAAGGCTACATCCCA  
 GGAGCACTCCATATTAATGGTGCATCCGTGCTGTGGAATCTGGAGAACTGCCACGTGAC  
 GGAAAGATCGTGAGCTACTGCAAGAGTGGAACACGCAGCTCAATCGCCGCAAGCACCCCTG  
 CGTAATGCTGGTTTTGATGTGGTGGAACCTCAAGGATCCTATGACAACCTGGGTCCGGCAC  
 AAC

>RXA00681-upstream

AAGGGCAAGTTGTTCATTGTTGATCCAGATGCGCCACGCATCGAAGGACCCGGCGCGCAC  
 AGCCATGCGCACTCAGTAGCAGCACATGGGGTGGATACAC

>RXA00681

ATGCCCTAGTCCACGCACTGTTCTTATCACTGGTGCCGCTGGCGGTTTGGGTGCGGCATTC  
 GCTGAAGGTTTCGCAGCCCAAGGAGACCGTATCGCGGTGGCGGATATCAATCTGGATGGG  
 GCGCAAGAGACCGTTGACAAGCTGAAAGCATTGGGCGCAGATGCCGCAGCCTTTGAAGTT  
 GATGTCACGTCCTTTGGAGTCCACCGAGGCCCTAGCCGCCGGTGCCGCTGAGTTTGGCGGT  
 GGCCGAATTGATGTCCTTATTAATAACGCAGCGATATATGCGACAGTGACTCGTTCCACCG  
 TTTGAGGATATTGACCCTGCGGAGTGGGATTTGGTTCATGGGAGTCAATCTCAAAGGCCCG  
 TGGTTGGTGACGCGTTCTGTGAGTCCGTTTTTGTCCGATAATGCCCGTGTGGTCAATCTT  
 TCCAGCGCACTGTGTTTTAGGATCTGCACACTGGGCGCACTACGTGGCATCCAAAGGT  
 GGGGTCATTGCTTTAACCAGGGTGCTTGCTAAAGAGCTGGGTGGTCTGGGATCACGGTC  
 AATGCGGTTGCGCCTGGGTTTACGCTGACTGAAGCCAGCTTGGGACTCATGGATAGCGCG  
 GAAACGTACGGTGTGATCGCGGATCCATCAAGCGCGCAAGCCAAACGAAAGACATCGTC  
 GGCACCACCATGTTTTCTGTCATCCCCAGAAGCCGAATACATCACTGGGCAAACACTCATC  
 GTTGATGGTGGCCGACAGTTTCATC

>RXA00681-downstream

TAAGTACTAAAAGTTCTAAGGAG

>RXA00690-upstream

ATGGATCATTGGACTCACACTGGCTGTCAATTCCTTGGTTTCAGCGTCTGCTGTGGCGGC  
 GTGGCGGATTCGTCTGTTTCAGAGGTCCAGGGTTAAAGCTTC

>RXA00690

GTGAAATGGATTGAGCGATATGTGCTGTCCCGCGGATGGTTCATCCCTGGGCGTGGTGG  
 GTGTGGGCGTTGGGTATTGCTGGTTGTGCCAGCATGACCAACAATCCTTATATTTTGGCG  
 CTCACCTTTTGCCACGTTGTGTTTTGTGGTGTTTAACCGTCGTGGGTTCATCGCCGTGGTTCG  
 CGTGCTTTCCCGATCTATTTGATGATCGCGGGTTGGCTCGTGGTGTACCGGTTGGTCATG  
 CACATTGTGGTGGGAGCAAAAATTGGCACCATTGAACTGTTTCGGATCCCGCCGGTGCAG  
 TTGCCGGAATGGGCTGCGGGTATCCACGTGTTTGGCACGGTGTATCTCGAGGGTCTGATC  
 ATCGCGACGACGCAAGGCTTAACGCTTGAACGATGATCGTGGCGGTGGGTGCTGCGAAC  
 TCTTTGGCGGATCCCAAGAAGCTGCTCAAATCGTTGCCTGGCGCATTTGGGCGAAGTGGGA  
 ACTGCGGTGGTCATCGGTATTTCCATTGCACCTCAGATGGCTGAGTCGGCGTTCCGCATT  
 AATCGTGCACGAACCTTGCGTGGTGATGATGCCAAAGGTGTTTCGTGGTTTCGCGCGGATT  
 TTGATGCCCGTTTTCAGGACACTTTGGATAGGTCTTTGGCCCTGGCTAATTCATGGAT  
 GCCCGTGGTTATGGCAGGACAGGCTCATGTATCCAAATTCCAACAGCGTGTGACCTCTATT  
 TTTGGTGCATTTCGGAATACTCGGCGTGACCGTTGGTCTGTTTGTGGTCTTAGATGCATCA  
 TCACCGATGTTCTGTGCGGTTCCGGTGTATTACCGCGTGGGCTTCTTGATCATTTCG  
 TTGGTCTGTTGCTTCACATAGAAAACATCCACACTTTTGATCAGTTGCCTTGGGGTGCT  
 GCGGAATGGCTTGTGTGCATCACAGGTGTGATTCCGCTGCTCATGGCTGCGCTGACACGA  
 TACCTTGATCCAGGTTCCATGATCACACCTGGGTTTCCTTGCATATGCCAGACACCGTT  
 CCGTTGCTCGTTGTGGCAGGACTTGTGTGGCGACGATGCCAGGATTCTTGACGCCCCGC  
 TTGCCGAAGAACAAGTGAGGGTCAAGCGTCGAAAAGCAATAAATAGCCCAGAAAGGGCC  
 GAAGTT

>RXA00690-downstream  
TAATGAGTGCTCCTTTTAGCGCG

>RXA00733-upstream  
ACGGCGAGGTTGTCGGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACC  
GTGAAATTGTTGAATCCCAAGAGACTGCGCAGGCGCAATC

>RXA00733  
ATGAGTAATACTGCAGGCCCCCGCGGGCGTTCCCATCAGGCAGACGCCGCGCCGAATCAA  
AAGGCACAGAATTTTCGGACCATCTGCCAAAAGGCTTTTCGGAATTCTAGGCCATGACCGT  
AACACCTTAATTTTTGTTATCTTCCTAGCCGTCCTGAGCGTTGGACTTACCGTCTTGGGC  
CCATGGTTGCTGGGTAAAGCCACCAACGTGGTGTGTTGAAGGATTCTATCTAAGCGCATG  
CCGGCTGGTGCCTCAAAGGAAGATATCATCGCGCAGTTGCAGGCTGCAGGTAAACATAAT  
CAGGCTTCCATGATGGAAGACATGAACCTTGTTCCAGGCTCAGGCATTGATTTTGAAAAA  
TTAGCCATGATCCTCGGACTGGTGATCGGTGCTTATCTCATTTCGTAGC

>RXA00735  
GGTCCCACCGGTGCGGGCAAGACCACATTGGTGAATCTGATCATGCGTTTCTACGACATC  
AACAGCGGTTCCATCACTCTTGGTGAAACAGCACAAAGACGCCGTGGATATCCGCACCATG  
GCTAGAGAAGATCTGCGATCACGAACCGGCATGGTGTGTCAGGATACGTGGCTGTTTGCC  
GGAACCATCAGGGATAACATTCTTTACGGTAGACCTGAAGCAACTGAGGAAGAAATGCTT  
GCTGCGTCCAAGGCCGCTACGTGGATCGTTTTGTCCGTTCCCTGCCAGAAGGCTACGAC  
ACCGTACTTGATGATGAAGCCATGAACCTATCGGTGGGTGAACGCCAGCTGATCACCATC  
GCGCGTGCATTCTTGGCTAATCCCCGACTGCTGATTCTGGATGAAGCCACCTCATCGGTG  
GATACGCGTACCGAATTGTTGATTGATGATGATGATGATGATGATGATGATGATGATGATG  
GCCTTCGTCATCGCGCACCGGTTGTCCACGATTCTGATGCCAACCTGATTTTGATGATG  
AAAGACGGCGAGATCGTGAGCAGGGCAATCACCGTGAGTTGATGGCCCTGGAGGGCGCA  
TATTGGGAGTTGTATAACTCCCAATTCAACGCCCCCGCGAAAGAAGAATTACAGGCTGAC  
GGAGATCAC

>RXA00735-downstream  
TGATGATTTCTTCTTAGGCTTTC

>RXA00796-upstream  
CTGGAATCCCAAAGCGCTTGATGACGCGGAAAGTTAACATAGGCTAGGTACGTCAAGTT  
GTTGATACATCAACTTAATTAACCTTTAGAGGAGTACACC

>RXA00796  
ATGAGCAAGATCGCCATCATCACCGGTTCCACCCGTCCAGGCCGCGTCAACATTGACGTA  
GCCAACTGGGTTCTCGAGCGCGCACAAAGAGCGCAACGATGCACAGTACGAGCTCGTTGAT  
ATCGCCGATTTCAACTTCCCCGTCTCGACGAAGCAATGCCAGCCGGCTACGGCCAGTAT  
GCAAACGAGCACACCAAG

>RXA00801-upstream  
GGATAAGTTTGTCTGAGCGTATTGGTCTTGATGATGTTGAAGAGGCTTCAACACCAT  
GAAGGCTGGCGACGTGCTGCGTTCTGTGGTGGAGATCTAA

>RXA00801  
ATGGCTCACGACGGATTGCGCGTAGAAAACATTGTCACCTCAGGCATCTTTGCCCTTGAT  
GGTGGCGAATGGGAAGTCGACAACAACATCTGGGTTGTGGGAAATGATGATGAGGTTTTTC  
ATCATCGATGCGGCACACACTGCAGCACCCATCATCGAGGCTGTCCGTGGACGTGCTGTG  
AAGGGCATTGTTGTCACCCACGCACACAATGACCACATCACTGTCGCACCAGAGCTATCC  
AAGGAATTTGATGCACCAATCTTCGTGCACCCAGGTGACCAATGCTGTGGGAGGAAACC  
CACGGAACCTGACCCACGAGGATTTGGCAGATCAGCAGAAGTTCCAAATCGCTGGAAC  
GAACTGATCGTGCTTAATACCCCTGGACACTCACCTGGATCCAGCTGCTTCTACCTCCCT  
GAAGCAAACGAGCTCTTCTGAGACACTTTGTTCCAGGGTGGGCGGGAGCAACTGGC  
CGTAAGTACAGCTCCTTTGACACCATATTGAGTCCCTCAAGACCTCAATTTTGATCTA  
CCAGCGGAAACCACCGTGCACACTGGCCATGGTGATCACACCAGTGTGGGGGCTGAGGCT  
CCACACTTGGAGGAATGGATTAAACGCGGGCAC

>RXA00801-downstream

TAAGCCCCGAACGATTAGTAGGC

>RXA00802-upstream

GCCATGGTGTATCACACAGTGTGGGGGCTGAGGCTCCACACTTGGAGGAATGGATTAAAC  
GCGGGCACTAAGCCCCGAACGATTAGTAGGCTTGGGCACC

>RXA00802

ATGGATCTTAACTTGGTGGCCAAGTCATACTTGTGTTGGCGGTGCAGGAACATTGGT  
TCTGAAGTTGTAAACTCTTAACTGAAGAAGGCGCAACCGCGGTAGCGGCGTCGAGAAGC  
ACGCCCTTATCTATTGACGCTTCGGATGAAGCGTCCGTCCGTGCGGGCATTGATCAGGTG  
ATCGCAGAACATGGTCGCCTGGATGGGCTGGTTGTTCTTCTGCACCCGCTGCGCAAACG  
CTCAGCGCGGAGACAGCAGATGATCCGGACACTGTGTTGGCTGCTATTGAAGGCAAAGCC  
ATCACGTTTATGAAGGCTGCAACCGTGGCGCTCGAGAAGATGCGTGAGGCTGGACATGGG  
CGCATCGTTGCACCTTCCGGCATGAACCTATACAAAACATTGAGTACTACTGCGTCGGCG  
CGAAATGCTGCGTGAATGTCGTGGTGAAAAATTTGGCGGATCGTCACGCGGGCACCGGA  
ATTACAGTAAATGCGATTAGCCCGGGATTCTGTGGTAGCTGAGCCAGACGCTGAGGTAAAC  
CGCGCAAATGGTGACACCACGTGGAGGAGGTGCGGAGGCGATCGCGTTTTTGTGTCGC  
CGCGCACCGCATCAATTTCTGGAGAGATTATTTCTGGTGGGACATAAGGCGAAGGGCATCA  
TCCTTCCTTAGCTCGCGTGAGCTTCCCAAGCGTAAGCACCCCGTGTGAGGGCA

>RXA00802-downstream

TAACGGCCGTTCTGTAAAGATT

>RXA00819-upstream

TCTTCCGAACGGCCTGC

>RXA00819

ATGGTTGGTGGCTCCCCGGAGCAGGCGCAGCGATTGGATGCGCAGATCAAATCTGGTGAG  
GTCAAGGGCGTTTTTGCATGACGGAACCTGATCATGGCTCTGATATCGCAGGTGGTCTG  
GCAACCACGGCCACTAAGGACGCAGACACCGGCGAGTGGATTATCAATGGTGAAAAACGG  
TGGATCGGTGCTGCTTCCACTGCTGATTTGATCGCTACCTTCGCCAGGGATACAGCCGAT  
AACCAGGTGAAATGCTTCCCTCGTGGCACCTCAGGCAGAGGGCGTGTCCATGGAGATTAT  
GATCGCAAAGCCTCACTGCGCATCATGCAAAATGCACACATTACCTATAACAATGTCCGG  
GTGCTGTTGGGATGCGCGGCTGCACAACATCAATTTCTTTCAAGGATGTTTCGGAATGCCTG  
CGCCGTATGCGTTCGGATGTGGCGTGGATGGCGGTGCGTGCGCAGGCAGGTGCCTATGAA  
GCAGCCGTGAAGTATGTGCGCAGCAGGGAACAGTTTGGCCGTCCGATCGCGGGGTTCAG  
TTGATTCAGGAAAAGCTCGCGCTCATGCTGGGCAATCTCACGGCGTCGCTGGGCATGATG  
GTCAAACTCACCGATCAGCAGCAGGCGGGGAATTTCAAAGAGGAAAACTCCGCGCTGGCG  
AAAAATGTTTACCTCGCTCAAACCTTCGGGAGACCGCTAGTTGGGCGCGGGAAATCTGCGGA  
GGCAACGGCATCATTTTGGACAACGATGTTGCCCGGTTCCATGCCGATGCAGAAGCCGTC  
TATTCATATGAAGGCACCCACGAAATCAATGCACTCATCGTTGGNCGNNCCATTCTGGGN  
CNTCTNTTCTTTTTATATTATNACNCTTTTGGAGGAGATCTTCATGACTACTTCCACCAC  
CCCAAACCATCGTTTCTTTTGAAGACGCACCAACCCTCACCGGCCAGGACCTGGGCTTTT  
CGCAGTGGCGCACTGTCACCCAGGAGATGG

>RXA00819-downstream

TGAACACCTTCGCGGACGCAACT

>RXA00821-upstream

TTAAAAGCTTGCTTCTCGACGCAAAAACCCATCCGGCGCATCCCTTCAATGTTAGGGGTG  
CGCTGCTATTTTTCTCCCAGTTCTACGAAATGACTTATT

>RXA00821

GTGACTAAGCTTGAGCGCATGGAGCATCCTGCTTACAGCCAATTGCGGCCGGTTACCCCG  
TCCGCATCTGTTGTTTTGTGCCCTAATCCCGGTTACAGCTCGCTGGAAGGCACTAATTCT  
TGGGTTATCCGGGCACCAGAAGACCCCCGGAGCATTGTCATCGATCCAGGTCCTGAAGAT  
GAGGGCCACCTTAACGTCTTGCAATCCAAGGCTGAGGAGGTGGGTTTGATTCTTCTGACC  
CACCGTCACTATGATCATGCTGACGGCGCACAGCGTTTCCGTGAGCTGACCAATGCACCT  
GTGCGTGCGATGGACCCTTCGTACTGTGCTGGTGCGGAGGAGATTTCATGATGGTGAGATC  
ATCACGATCGACGGTGTACCCCCACAGATTGAGGTGGTGGCCACACCTGGTCATACCCGT  
GATTCTGTGTCTTATTTTCATCTGGAGTGGAGTCCCTCATGAGTCCACTTTGGAGGGCATC

GTTTCTGGCGACACCATTCGCGGGTCGTCACACCACGATGATTTTCAGAGACCGACGGCGAT  
 TTGGGTGAGTACCTGAATTCCTTTGGCCATTTTGGAGGAGCGCGGCAAGGATATTCCGCTG  
 CTTCCAGGACATGGTCCAGATGGACAGGACGTGTCCTCCTTCGCGCGTAAGTACATTGAG  
 CGTCGTGAGCTGCGTCTGAACCAGATCCGTGAGGTATGGGAGACCCGTGGCCGTGACGTG  
 TCCATGAAGGATCTCATCGACGCCATCTACGATGATGTTGATCCAGTTCTGCGTGGTGCA  
 GCCGAGCAGTCCACTCATGTGGCTATTTCGTTACCTGCAGGCTCAGGAAGCTTCCGCCTCA  
 AAC

>RXA00821-downstream  
 TAAACACTTTTAACTAAACAACA

>RXA00827-upstream  
 TCGGTGAATTAACAGACAACGGAATCAGCATTGTGTGTCAGTAACCCATGATCCTGATTTC  
 TCGCAGCGCTGGGCGATCACCACATTGAGGTGAGCGCGAA

>RXA00827  
 GTGAACCTGCTGATCAAAATTAATCCCGTCACCCGCATCATCGCGTTGATGGTACTGACC  
 ACGCCGTTGCTGCTGAGTTTGGATGTGATGTCGGCAGCGATCGCGCTGGTGGCAACCAT  
 ATTCTGGCACCATTGTCGGCGGTGACCTGGAAGATGCTGCTGAAACGTGGCTGGATGCTG  
 TTCCTCATGGCACCAGGTGGCTGCATTATCCATGGCGCTTTATGGCAGGCCGGATGGAAAA  
 GAGTACTTTAGCTTCCTGCTCATTACGTCAGTACTGATAATTCAGTGGCTTTGGCTGCTGCC  
 ATTGGGCTGCGTGTTCGCGGATGGTCTGCCCGTTGTGGTGCTGATTGCTCGCATTTGAT  
 CCCACCGACCTGGGCGATGGTTCGCGCAGCTGCTCAAAGTGCCTGAAAGGTTTGTCTATC  
 GGTGCTGTGGCAGGAAGCCGACTGATGACGCTTTTCGGAAGATTGGTACTCCATGTCC  
 AGGGCAAGGCGTGCCCGCGGAATTGCTGATCAGGGCAAGATCAAGCACTTTTTCACCATG  
 ACTTTTGGTTTGTGGTGCTCTCGCTTCGCCGTGGATCCAAGCTTGCAACGGCGATGGAA  
 GCACGCGGTTTTGGTTCGCACGACTGGCCGCACCTGGGCAAGGGAATCCACCGTCGGCGCG  
 CGCGATCTGGTGCTCATCTTGGTGCTGCTGCCATTTCCGCGATCGCTCTAACCGTGCTCC  
 ATTCAGACTGGTTTCTTTAAGTTCTTGGGCACA

>RXA00827-downstream  
 TGATCACAGTTTAAATTGATGGA

>RXA00842-upstream  
 CCTTGTCGCGGAGGTAAGCGAGGGTATTTCTGGATGTGGAACAACGCGGATTATGGAAAA  
 TCGTGACTTTCATAACGTTGAGCCTACTAAGGTTTGTTC

>RXA00842  
 ATGATTATTCAAATCCTAAGAGTGGCATTTGCCTTCGTCGGCATCATTGTTGGCGCCGGT  
 TTCGCATCAGGGCAAGAGGTGATGCAATATTTGTGGCCTTCGGCATAGACGGAATTTGG  
 GGAGTCATTGTTTCTGCAGTGATCATGTCGGTGATGGCGTTGATCATTTTGCAGCTCGGA  
 AGCTATTTCAATGCAGGTGAACACGGTGAAGTGTTCCGCCGAGTAAGTCACCCCGTTTTTC  
 TCCAAATTTTGGACATCGGCGTTGTGGTGACGTTGTTCTCCACCGGTTTTCGTCATGTTT  
 GCAGGCGCGGATCAAATCTGAATCAGCAGTGGGGGCTTCGCTCTGGATCGGTTCTGTG  
 ATCATGGTTCTTCTGGTGCTGGCTGCGGGCATGTTGGACGTGGATAAAGTAACCAAGTC  
 ATTGGTGCAATTACTCCGTTTCATCATCATTTTTCATCACTGCCGCTCGATCTACACGCTG  
 GTAGGTAATTTAGCTCAGTGAGCAGCTTGATTCTGCTGCTTTAGAAGTCGGCACGACG  
 TTGCCTCACTGGGCTGTTGCAGCGGTGAACATGTGGGATTCAACCTGATGGTTGCGGTG  
 TCCATGGCTGTGGTCATTGGTGGATCAATGTTTAACCCGCGGGTTCGAGGTTCGGGCGGT  
 TTGCTGGGCGGATTGATCCTGGGATTCTTGATCATCATCAGTGCGCTAACACTGTTCCGCC  
 ACCGTGGAAGAAGTTGGCCAAGATGATATGCCTATGCTGACGATCATCAACAATTTGAAC  
 CCGCTGGCTGGCCAAGTAATGGCAGTGGTTATCTACGGAATGATCTTCAACACGGCACTG  
 GGTATGTTCTACGCATTGGGCGGTGCTCTCACTGCCGAAAACCCACAGCGATTCCGTCGG  
 GTTATGTTGGTTCAGTGCTGATTGTTTGTGTTGAGCTTTGTGGGATTCAAGAAGTTG  
 GTGGGCTATGTGTACCCAGTCTTGGGATACATTGGCCTGCTGCTGATTGCAGTGATGATG  
 GTGGCGTGGGTGAGGGGACGCGTACGCATCTACAAGGAATCCGAACGCCGATGCGGATC  
 GCAGACTTGTGTCAGATCGGCCATGACGGAGCGTTGAGTGGAGCAGAGCTGGCGGTGCTC  
 AACCAGGAAATCCAAGATTCAAAGTTGGATGAGGAACAAATTAAAGCAGCGGTTAGGAAG

>RXA00842-downstream  
 TAGTTACTCTGCAGGGACGAGCT

>RXA00847-upstream

TCTGGCCCGCTGTGTCTCTGGACGCAGCGGGCCAGTAGTATTTGGGGGTGAGAATAAG  
GTTTGGAATTCTAAGTGTTCGCTGCACGGTTTCGTTG

>RXA00847

GTGGCATGTTCAGGCTAATCCGGGTCCTGCGCCCGTTGAGGAGCCAACTACAGCCACTGCG  
ACGACCACGGCAACTGAGACGACCACCGTAGAGACTGAAGCCCCCAAACAAGATCGGGAA  
ACCATCAGTATTGGTATCGATCCGATCCGCAACGGTTTCAATCCACATTTGTTGTCTGAT  
GATTCTCCACTGGTGCAGGATACTGCATCGTTGGTGTGCGGAGTGCTTTTGAGGGCAAT  
CAGCTGAACACTGACTTGTGGACAATGTTGAGCAGGTGGATGAAACCACGGTGAGGTAC  
ACGATTGCTCAGGAAGCGCAGTGGAGTGATGGCACTCCGATTACTGGGTCTGATTTTGAG  
TACTTGCGCAGGTCCATTGTGGCGGGGACAGGAACGCTGAACGATTCTGCATATTCGGCG  
ATTTAGAGATTAGGACCTCAGGCGGTGGAAAACTGTGACGTTATTTTGAACATCCT  
GTCGCTGATTGGCATTGCTGTTTAACAATTTGTTGCGGAGTCATTTGATCACTGGCAAT  
TCCACATTCCAGACAGCGTTTTATGATTCCATCCCGGCCCTCTGCGGGGCGCTACATGGTG  
CGTTCCATTGATCGTCAGCGCGGCGTGATTACGTTGTGCGCGCAATGATCGTTTCTGGGGT  
GCAAATCCGGCACACGTGGAAGTACTCCAATTCAACACCGTTGCCTCTGCATCCCGGGCG  
GGGGAGTACCTGCGCACCGGGCAGAGTTCGTTTATGAATCTGTCACCGCAGGAAACCCTG  
GTGGACACGTTGAATTTGGTGCCGGACACGGAAGTGCGGGTGTCTGACACGACGCGCACG  
CTGGAGCTGGTATTCAACGCCGAAGCGCTGGCACCGGCGCAGCGCGCCTACCTGACATCG  
CTTATCGAGTCCCTCCCTCACCGCCAAGTTAGCTGGCGGTGCGAGTGCAAACCTGGGTGTG  
CCCCAAACGGTGGAGGCGAGCGTCGATAAGCAAGAAATTCCTGCGTTGCGCCTGGCGGGCG  
GACCCCGCCGACGATGCTGGTTTGGCAGCTGCGCGGGGCATCGTCGATATGCTGGCTGCG  
GATGGAATCAAGGCTCAGGTCGTGACAACCGATTGAATTCGGCGATTGCGGGTAATTTT  
GATGCGATCGTGGCGTGGACCAGAACTGCCACGGATTCGATTGCGTTGGCGGACCGAGTG  
GGTTGTGGCGTGAACCTGGCAAAGTGGTGCGCTGAGGGAACCACGGAATATATCAACGGT  
GTTTGGCGGGTGAGATTGATTTTCGATCCTGCGTGGGAGCAGCTTTAACACCGAGAAT  
CACTTGCGGGTTCCGATCCTGCGGGAGACTCGGGTAGAAGCGAAAAATAACGGTATCCTC  
GGGGCTGCGGATGGCTGGCCTGGGGGAATTTCAAGTGCTGCAAGTTGAGGAAAAACGAT  
GTTGAAGAA

>RXA00847-downstream

TGATCTGTCTGGTGCTCGAGTTG

>RXA00851-upstream

TTGAGCGGGTCATTTGCATCAATGATCATAAAATCGCTGCTGATGGCCCTCCGCAAAAGT  
CCATTGACCTGTACGTATCGCTTATGGCGGAACCTGCGAA

>RXA00851

ATGAACAGTATTCCTTTAGGTTTTTACGTCGATAAGCAATCTGTTGTTTCATTCTTTTCCT  
GCTTTGTGGAAATTCCTACTTCTGCTGTTTTTTCATCATCGGCGGCTCCATCGCGGCTTCT  
ACCCCGGTTTCATGGGTTGATTTTGGTGGGGATTGCAAGTGGTGTTCACGTGCTGGCGAAG  
ATTCCGCTGAAGGTCGCGTGGGAGCAGTTGTGGCCAGTGCTGCCGATTTTGATCATGCTC  
GGTGCCTTTCAGTGGTGGCAGCGCGGCTTTGATTTGCGCGCAACCACAGTGCTCACGCTG  
TTTTCCGCGGTGATGGCCGCCATGTTGTTGACGTTGACCACGCGGTTGGAAGCGCTCATG  
AATGCAGTTGAGCGGATGTTGCAGCCTTTTGACGTTTTTGGCCTGCCAGTAGAGACGATC  
ACCTTGCTATTTCTCTCACGATTCCGCTCATTCCGCTGCAATTAGCCACGGTGAAGGAA  
GTCCTCGATGCCCGTAAAGCTCGTGGTGCCGGTTTTTCTATCGCCGCTTTGGCACGCCT  
GTGATCATCAGATCAATAAAGAGGGCCCGCAATATCGGCGATGCTCTTCTCGCACGTGGT  
GCCGGCGAT

>RXA00851-downstream

TAATTTCTTTCAACACATAGCAA

>RXA00852-upstream

AGATCACCGTCATGGTCATAATCGCCGCTGGAGTTCATGCAGCATTCCTGACATCCGTA  
AGAAATAGTTCCAACCCACTTTTCTCAGAATTGCAGTTC

>RXA00852

ATGCCCCGAGATCATTTTTGACAACACTGAAGTACGCTACGATGACTCGCTCATTTTTAGAG  
 CCCCTATCGTTAAACTGACAGAACAACGCATTGGCATCATCGGGGCTAACGGCGGTGGA  
 AAATCCACGCTCATCAGAATGATCAATGGTCTCGGCGAACCAACCACAGGGCGTGTCTA  
 GTTGATGGCCTTGACGTCTCGCATTCCGGACGGGAAGTTCGCAAGAAGGTTGGATTTGTC  
 TTCTCTGACGCTGAAAACCAGATCGTGATGCCAACTGTGCGTGAGGATATTGCCTTCTCG  
 CTTGCGCCGGCACAAAATGCCACGCGCTGAAAAGGCGCAACGTGTGACGAGATGATGGCG  
 CGATTCAACTTGAGCGAGCATGCAGATCAATCACCGCACACCCCTATCCGGTGGTCAAAAG  
 CAGTTGTTAGCGCTGGCTGCAGTACTGATTTTGGAGCCAGAAGTGATCATCGCTGATGAG  
 CCCACTACCCTGCTGGATCTGCGCAATAGGCTGATGATCAAAGACGTGTTCAATAAACTC  
 GAGCAGCAATTAATCGTTGTGAGCCATGATTTAGATTTCCCTCAGCGATTTTGAGCGGGTC  
 ATTTGCATCAATGATCATAAAATCGCTGCTGATGGCCCTCCGCAAAAGTCCATTGACCTG  
 TACGTATCGCTTATGGCGGAACCTGCGAAA

>RXA00852-downstream  
 TGAACAGTATTCCTTTAGGTTTT

>RXA00856-upstream  
 GTTTTTAGGAATAGAGTGGGCTCAAGCTTTGTGACAAGTTTTTTGGAGAAATCATTACTA  
 GTCGTAGTCTTCAATTTGGGTGCAGGTAGGGTGGAAACACC

>RXA00856  
 GTGAGTGATGTATCAGCAGGCGTAAATGGCGCACAAAGATCCAAGCAATCAAGCGGTCAAG  
 CCTTCCAACCTGGAACCTTCCGAACCTTCTTGACCAGCTTGCGTATCATTGTCATCCCTTTG  
 TTTGCGTGGCTTACGCTTAAAGGTGAGACGGAAAACAATGCTTTTGCCTGGTGGGCGTTG  
 GTTGTTTTCATTTTGCTCATGATCACCGACAAGCTTGACGGCGATATTGCGCGAGCACGT  
 GGCTTGGTCACTGACTTTGGCAAGATCGCGGATCCGATTGCCGATAAGGCGTTGATGACC  
 ACAGCATTTGTCTGTTTCAACATCATCGGCATTTTGCCCTGGTGGGTCACTGCGTTGATT  
 GTGCTTCGAGAGTTCCGGCATTACCATCTGGCGTTTCTTCCAACCTGCGCGCTGGAAATGTT  
 GTGCTTGCATCAAAGGGGGGGCAAGCTTAAGACTGCTCTGCAGACTGTTGCCGTTGCTG  
 TATCTGTGCCCTTTCCCAAGTTGGATGGATATTCCAAGCCAGATCGTCATGTATGCA

>RXA00870-upstream  
 CAAGACGGCGATGTCGCCGCCGCTGTTGATACCGCAGCGCGACTTGTTACACAGATATT  
 CAACAATTCACTTCGCAGAGCATTTAAGGAATTTACACAC

>RXA00870  
 ATGTCTGAACCACAAACCATCTCGCACTGGATTGACGGCGCGGATTTCCTCCATCCACTTCC  
 GGCAAGACCGCTCCTGTCTACAATCCTGCAACTGGCCAGGTACCGCCAATGTTGCGCTG  
 GCTAGCCAGGAAGAGATCGATGCCACCATCGCTTCTGCCACCAAGGCTGCTAAGACGTGG  
 GGCAACCTGTCTATCGCTAAGCGCCAAGCTGTGCTTTTCAACTCCGTGAGCTGCTGAAT  
 GCTCGCAAGGGTGAGCTGGCGGAGATCATCACTGCAGAGCACGGCAAGGTCTTGTCCGAT  
 GCCATGGGTGAAATCCTGCGCGGCCAGGAAGTCGTGGAGCTTGCTACCGGTTTCCCACAC  
 CTGCTTAAAGGTGCGTTCAACGAGAACGTCTCCACCGGCATTGATGTGTATTCCCTTGAAG  
 CAGCCACTGGGTGTTGTCGGTATCATCAGCCCGTTCAACTTCCCTGCGATGGTGGCGATG  
 TGGTTTTTTCCCAATCGCAATCGCTGCAGGCAACGCAGTTATTTTGAAGCCTTCAGAGAAG  
 GATCCTTCGGCAGCGCTGTGGATGGCTCAGATCTGGAAGGAAGCTGGTCTTCCAGACGGC  
 GTATTCAACGTGCTCCAGGGCGACAAGCTGGCTGTTGATGGTTTGCTGAACAGCCCTGAT  
 GTCTCTGCGATTTCCCTTCGTGGGTTCACCCCAATCGCAAAGTACATCTACGAGACTTCC  
 GCGAAGAACGGCAAGCGCGTCCAGGCGTTGGGCGGCGCGAAGAACCACATGCTGGTGCTG  
 CCAGATGCTGATCTGGATCTGGTTGCCGATCAGGCAATCAACGCAGGTTACGGCGCTGCC  
 GGTGAGCGTTGCATGGCTGTTTCTGTGGTCTTGGCTATTGAATCTGTTGCCGACGAGCTC  
 ATTGAGAAGATCAAGGAGCGCATCGACACCTCGCATCGGCAACGGTGCCGGCGACGAG  
 CAGGGCGAGCCGCACCTGGGCCCACATAACACCGACGTCCACCGCGACAAGGTCGCTTCT  
 TATGTGCACATCGCTGAGGCCGACGGCGCCAAGATCATCGTGACGGGCGTAAGTGCGCC  
 GTAGACGGGCACGAGGAGGGCTTCTTCTCGGCCCTACGCTTATCGACGACATCCCCTC  
 ACGTTCCGCGCCTACACCGAAGAAATCTTCGGCCCGGTCTCTCTGTCGTTTCGTGTCGCA  
 TCCTTCGACGAGGCAATTGAGCTGATCAACTCCGGTGAATTCGGCAACGGAACCGCAATC  
 TTCACCAACGATGGTGGAGCGGCACGCCGCTTCCAGCATGAGATCGAAGTGGGCATGATC  
 GGCATCAACGTACCAATCCCAGTGCCTGTTGCGTACCACTCCTTCGGTGGTTGGAAGAAC  
 TCCCTCTTCGGTGACGCCAAGGCATATGGCACTCAAGGTTTTGATTTCTTACCAGGGAA  
 AAGGCGATCACCGCGTTGGCTCGACCCAGCAACCCACGGTGGCATTAAACCTCGGTTTC

tream  
ACAGGACT

eam  
GCTGGGTGATCGGGGGCCGGTTGTTCCGGGTGTGATTGGTGACTG  
CAACAATGTGTCTAAGCTTAGGGGC

GAACTGGTTGTTTTAGCTGATTCCGAGGGCAATCCTATTGGTACT  
GTGCACACTAAGGACACGCCTCTGCATTTCCGCTTTTCCACCTAT  
GGGGAGCTGTTGGTGACGCGTCGTGCATTGTGCGAAGAAGACATGG  
AACTCTATGTGTGGGCACCCTGGTCCGGATGAGACAAACGCGGAT  
GGTGTGATGAGTTGGGGCTGGAGGTAGATTCTTTCTTGGATATT  
GATTACCAGTACCGTGCTGTGACGCGTCCGGCATTGTGGAGTGG  
CACCTCGTGCCTTTAGCGGTGGGGGAATTTGTGGAGCCACTGGAT  
TTCGAGTGGGCGGAACCGCAGAAGCTTTTCGACGCTGTTGATGCC  
TCTCCATGGCTAGTGGATCAGCTTAGCGCCCCTGAGCTGCGCCAA  
TTTGACGCAGAG

tream  
GAAGCCTT

eam  
TTCAGTTGTGGTGGCTCCGAATCTGATGAACAATGATCATTCCCTA  
TATCAAAGAGAGCCACCACCTACTA

CGAATTTTAAAAACCACGTCTGCGCTTTGGCCCTACTATCTCGGA  
ATTGTGATCGCGGCGTTGTGCTGCTGTGCGCGTTTATTCTCCGC  
ATTGTTTCTGCAGTAACCGGATCTAACACCGTCGATGCAGTTACT  
TTAGCTTTAGCCCTGTTTGTGCGCAAGCTTCCTCAATACGGTGATG  
TACATCGGTGATGTCATGGCATCTCGTATGCGCCAGATTCTGGCC  
AAGCTGTTGGCGCTGCCTCAGAAGTATTTTGATAATCAGGTCACC  
CGCCTTGATCGATCAATCAACGGCATCACGCAGTTTCATGCAGAGC  
TTCCCATGCTCATCACCATGGTGGCAGTGCTGATTATTTCCGCG  
CTGGCAATTCTGCTGGCCATGTTGTTCCCGATTTACATGTGGCTG  
AAACGCTGGCAGAAATATGAGGGCGAGAAAACCATGAAATCGAC  
TTCGCTGAGGTTGTGCGCCAGGTCAAGGTTGTTAAATCATTTCGTC  
CTGGCTGATTTCCGGTGGGCGTTACGGCAAAACAGTAGCGATTACC  
TGGTGGCACCGCATGGATACTCTCCGTGGCGCGGCACTAAATATC  
CACCTGCTGATTTTCTACCGCACCTTGCACGGCCATTTCACCATC  
CTCATCCAGCTTGTACCATGGCGCAGCAACCGGTGTACATGATG  
TCCGCGCAGCGCGCCATCGCCGGCTCCCGCGACTACTTCGAGGTC  
GAGCCCACCGCCAATAAGGAGCTTGTGACGCCACCCTCGCCTCA  
AGTGTGGGCACGCGCGCGCTGCGCGCTGGAGAACCAGCGATG  
ACCTTCGCCTACGAAGAAGGCAAGCCGTTATTTCCGACGTGTCC  
GGCGAGCGCATCGCGTTGGTCGGTGAATCCGGCGGCGGTAAATCC  
CTGTTAGGTCTGTACAAACCAACAGCGGCAGCCTTGCAGTATGT  
GATCTGACTTCCGAGGAACCTTCGCGCATCCGTGGGTGTGGTCTTC  
TTCTCTGGATCTATTGCAGAAAACATCGCCTACGGTCGCCCAGGT  
ATCATCGAAGTGGCTAAGAAAGCCAACGCACATGAGTTCATTTCC  
TATGAAACCGTCGTGCGTGAACGCGGACTCAAACCTTTCTGGTGGC  
TCTGTGGCACGGGCCATGCTTAAAGATGCCCCACTTCTTGTCTC  
GCACTGGATACCAAGTCTGAGCAGGCAGTCCAAGCCGGTTTGAA  
CGCACCACTTAATGATCGCCACCGCCTGTCCACCATCGCAGGC  
ACCATCCAAAACGGACGGGTTGAAGAGGTGGGATCTCTACCGAG  
GGTATCTATTCCGAAGTGTGCGCCTGACCAACTCCACAGCAGAA  
CTGCGCGCCTTTGGTTTCACTGGCGATGCACCAGCTGAAGAAGAG



>RXA00878-downstream  
TAGCCCCGCGAAAGAACAATCCC

>RXA00880-upstream  
TCCATGTGGTTAAAGATATGCCTAAAGATCTGACCAAAACGTGACTAAAGACGTGACGA  
CACAAGTACAGCCAAATTAAAGGAAAGGTTGAATTTGACC

>RXA00880  
ATGACTTCACCTAATACCCTGCAGGAATACACTGAACCTGCCAAGTACACCATCGGAGAA  
TCTGAAACCTGCCTGACCGCCCTTCTAGATCAGATTAAGACTCGACCTTACGGAGTTTTG  
TTCAGCAAGCCTGCCAACTATGAGTGGGTGAATGTAAGTGCCTAAAGAAATTTAGGACGAG  
GTTTTTGGCGTTGCAAAAGGAATTATTTAGTTCGGCGTAGAGCAGGGAGACCGTGTGCG  
CTGCTGTCCAATACTCGCTATGAGTGGGCTGTGCTTATTCGCTATCTGGGCCGCTGGC  
GCAGTGAGCGTGCCTATCTACAGCTCCTCTTCACTGTCCCAAATTGAGTGGATCATTGAG  
GATTCGGCGCTGTTTTGGCCATTACCGAAACCCCTGATCATACCGACTTGATGAAGAAC  
CTGGTCATCGGTGAAGACGGAACCTCCAGCGATTAAAGGTTTACCTTCCAAGCTGCGCCGC  
ATTCTAGAGATCAACTCTTCGGCGTTGGAGACCTTGAAGTTTGAAGGCCGCGAGCTTTCT  
GATGAGCTGGTGTGGGAACGCATTTCATGCAACCAAGGCCGCTGACCTGGCGTCTTTGGTG  
TACACCTCTGGCACAACCTGGTAGGCCGAAGGGCTGCGAGTTGTCCCACTACCACTGGTTG  
GCTGAGGTCCGAGCGCTGATCACAATGACATCGGAGCGATCGCGATGCCAGGTTCAAGG  
TTGCTCACCTTCCTTTGCGCACGTTCTTGCTCGCGCAGTGCCTTGGCCTTCGCT  
GTCACCGGTGCAACCCAGTCCCACTGGTCTGATTTAGCACCTTACTTTGGAAGTGCAG  
CGTTCCCGCCCGAACCTGATTTTGGGTGTTCCACGCGTGTGAAAAGGTCCGCAACGCC  
GCTGCTGCTAATGCTGCTGACGGTGGCGCAATCAAGCGCATCATGTTTGAGCGTGCCGAA  
AAGGCGGCCATTGAATACTCCATGGCTCTTGATACTGCAGAAGGCCCAAGCAAGTCCCAG  
GTTATGGCACATAAAGCGTTTGACAAGCTGGTGTACTCCAAGATCCGTGCAGCTGTCCGT  
GGCGATGTGCAGTACGCCATCACCGGTGGTTCAGCGATGGGGCAGGAGCTGCTGCACCTC  
TTCCGCGGTGTGGGCATGACCATCTACGAAGGTATGGTCTGACGGAATCTGCGGCTGCT  
GCAGCGGTGGACTTCACTGATCAAAAGATCGGCACCTGTGGGTAAAGCCGATGGGTGGCATG  
ACCATCAAGATCAATGAAGATGGCGAAATCATGCTAAAAGGCGAGATGTTGTTCCAGGGA  
TATTGGAACAACCCAGAAGCCACAGCAGAAGCCCTCCACGACGGTTGGTTCAACACCGGC  
GATCTGGGTGAGCTGTTGGAGTCTGGACACCTGGTGATCACCGGACGTAAGAAAGATCTG  
ATCGTGACCGCGGGCGGCAAGAACGTTTCCCCAGGACCCATGGAAGACATCATCCGCGCA  
CACCCACTGGTCAGCCAGGCCATGGTGGTGGGCGATGGTAAACCATTCGTTGGCCTGCTG  
GTGACCTTGGATCCAGATATGTTGAAGCGGTGGAAGCTGAACCACAACATTGCGGAATCC  
CGCACGTTTCTGAGATTGCTACTGATCCTGCACTGCGTGCGGAAATCCAGGATGCAGTC  
AACAACGCTAATGCCACGGTGTCTCAATCAGAGGCGATCAAGCGGTTCTACATCCTTGAT  
CGCGACCTGACCGAGGAAGCCGACGAGCTGACCCCAACGCTGAAGGTCAAGCGCAACGTT  
GTTGTTCCGCGTTACGCAGACGCCATCGACCACATCTACAACCGA

>RXA00880-downstream  
TGAGTAACACAGAGACCCAATTT

>RXA00899-upstream  
TTTGCTGCTCCCTACGTCCGACTCCCACTGTTCTGCTTATGGGATCGCCATACATCAA  
CCGGTGACGCCACCGCATCCAACAAGAAATCAACGACCTC

>RXA00899  
ATGGAAGACGTCCACGACGACGTCCCGACATCCCCACCGGAATGGATGTCTCCGCGGAA  
GTTGAATCTGTCATCAAACCTCAACCGCCGCTCACCCGCATGCCAGCAGTGACCGGCGGA  
AACAACGGCTTCTACTCCGACTACCGTGAATCCCTCAAACGGATGACCGCCGCAATCGAC  
GAAGCCGAAGAATACATCTACGTGAGATCTACATCATGGCCTGGGATTCCTACACCCAA  
CCATTCTTCGACGACTCGAACGAGCCACACCGCGGCTCAAAGTCCGACTCCTTTTC  
GACCACGTCCGCGAGCTGGAATATCCCGGCTACCAACCGCTCAAAGAAAGAACTCAACCGC  
ATGGGCTTCGCTGGTACCTCATGCTCCCCCTCCAACCTGGCGACGCGCTTCCGCGGA  
CCCGACCTGCGCAACACCGCAAAATGCTCATCATCGACGGCCACACCGCATTTCATGGGC  
TCCCAAAATCTCATCGCCCCGAGTTACCTACAAAAGAAAAACATCAAACCTCGGCCGCGAA  
TGGAAGACCTCATGGTCAACTCACCGGCCCCATCGTCTCCTCCATGGAAATGATCTTC  
GCCGCGACTGGTACGTCAATCCAACGAAGCCCTCGACATCCGCGACACGCGAGAAGCC  
CACGGCTACATCGGCAACACTCAAAAGACTCCGCCACCAACCTCGTGCAGCTCATCCCC

TCCGGCCCTGGTTACACCACAGAACCCAACTGCGCATGTTCAACTCCATCGTTCACCAC  
 GCCAAAGAACGACTCATCTTGTGCGAGCCCTACTTCATCCCCGACGAATCCCTCCTCGAA  
 GCCGTACCTCAGCCTGCTACCGCGGAGTAACCGTCGAACTATTCGTCTCTGAACAAGCC  
 GACCAATTCGCCATCGACCACGCCCAATCCTCTACTACCAGGCACTCCTTGAAGCCGGC  
 GTGAAAATCTACCAATTCCCCAAACCCGACGTCTCCACACCAAGTACATGATCGCCGAC  
 CCGGACGACACCACGGCAACGAAGCCCTCGGAGTCCTCGGATCCTCCAACCTCGACATC  
 CGCAGCTTTGGCCTCAACTACGAAATCTCCCTGATGATCGCCAAAGGCAACCTCATCCAC  
 GAACTCAACGCCCTCACCAGCCGTTACCGCACAGTAAGTTTCAAGCTCACCTTGGATAAG  
 TGGAACCAGCGCAGTTGGCGGGCGCCGTACGTGGACAATGTCATGCGTTTGACCTCGGCG  
 CTGCAG

>RXA00899-downstream  
 TAGTTTGGCGCGTTTGGAGTGCG

>RXA00902-upstream  
 TTGTTATTGGTTTGTTCCTCCCATGCAATGTACGATCGGTTCTAACGTCTACGGCAATT  
 GACACGTCAATTTAATTTCAGGAAAGGGGTGGGGAGAATTT

>RXA00902  
 ATGCTAGTGGTTTTGAATATGTTCAACATCCTCGACGAGCCCTCCCTCCGCCTATACCT  
 GAACGGAAAGGTCCTGCCGAGCATTCTGCCGGGAACTTTCCATCCCATTAAATCCAAAG  
 AATATTGCAGCGAGCCACGATCAGGTGCTTCTATCTGGTTGGGGCAAATTTGTGCGTTGG  
 CTCTTGGTATTGTTGTCCATTTTGGTCATCATCATTTGGCATCAACCTCATCTTGGACGGT  
 GTCTACGGATTTGGTACTTTTTCAACCACCCAGATGTACCAAGTTGCGAAAGATCCACTC  
 ATTGGTGTGCTGATCGGTATCTTGGCTACGGCCTTGGTGCAATCATCAACCACCACCACA  
 ACGTTGACGGTGACTGCAGTTGGTACGGGCATTGTGTCGGTGCCGTGTGGCGATTCCGATC  
 ATTCTTGGCGCAAATATCGGTACGACGATCACCGCGATGCTCGTTGCGTTTTCTTATGTG  
 GGTGAACGCAGGGAGTTTAAGCGAGCTTTTACGGTTGCCGCCATGCATGTGTGGTTTAAAC  
 GTGCTCGTCATTCTTGTCTATTTGTTGTGGAATTGCTCTTTCATCCATTCCGCACAATT  
 AGTGGTGCGATCGCAACGGAGATCACACTGACAACCTGGTGGCTCTTTCCTACCAGTGGT  
 GTGATGACCAAGATTTTGTATCCCCCAACCCAACTTCTGGGTATGAATGGTCTTATCGGT  
 TCGATCGGCAATCCTAGTATTTTCGGCGATTGTATGTCTTGTGGTGGGCACCATTCTTATT  
 CTGATTTTCGGTGCGTGCCATGAGTTCTCAGATCCGAACATTACGGCAGCGACCGTAACC  
 TCAATTATGGACAAGGTGATCAATCCAGAGAACAGCCCCAAGGCGACGATTCTTTCCAAT  
 TTCTGGAGCTTCATTCTTGGAGTTTTGTTACGCTCATGGTCACTGCCTCGTCAGTGACC  
 GTGGCTTCCATGCAGCCAGTGGCTGCCTCTGGTGTCGTTAAGCAAAGCCATTGCTGGGC  
 GTCATTTTGGGTGCCAACGTGGGCACCACGGTGACCGCAATGTTTGCTACTTTTCGCGATT  
 GTCAGCGATCAGGGTGAGTTCGCTATTTCAGGCTGCGTTGATCCACCTCATTGTGAACCTC  
 ACCGGCGCATTACTAGTGCTGTGTATTCCGCAGCTTGCCAATGTGATTATTCACTTGGCC  
 GAGAAAACCTGCGAACCTCACTGCCCCGAGTTAC

>RXA00931-upstream  
 CCGTAACCTAATCGTTGAAACATCACCTTATTGCTGGGCTTTGCACGCTACTCTTTGTGA  
 GTAACCTCACCGAAGTGCATAAATTAATTGGGAGTGATCA

>RXA00931  
 GTGAAAACCTATTGAAGATATTTTGACCTTGGAAAGAAATCGACCGCGATATTTACCGTGGT  
 CCCGTTATCGAATCTTATTTAGCCAGGACTTTCGGTGGCCAGGTCGCTGCCCAAGCTTTA  
 GTAGCAGCAACGCATACTGTTGATAAAGCCTTTACTGTGCATTCTTTCATGGCTACTTT  
 ATAGCTCCTGGTGATCCAACAGCACCCGCAATTTATTTAGTGGATCGAGTTTCGCGACGGA  
 AAAAGCTACGTCACCCGCTCGGTGCGTGGCATCCAAGACGGCGAAGTAATCTTCAGCATG  
 CAGGCCAGCTTTTCATCGTGGGGATGAAGGCATTGAGCACATGGACAAGATGCGTAAAGTT  
 CCAGCTCCTGATGAGATCAAGGGAACAGTAGAACGTATGCCGATCTCAAGTAGGCGAGTG  
 CTTGATGAATGGGCGGAATGGGATATCCGCGTTATTCGCGAGGATCAATTAGAAGCTCAGC  
 GATTTACCGCTACTGAGCAAGCTGTGTGGATTCCGGTGACCGCTGATCTTCCGGATAAT  
 CCCACCTTCCACAGTGCTCACTGACTTATCTGTCCGATATGACTTTGCTGCATAGTGCC  
 CTGGTGCCACACCCAGGTGAGAAAATGCAGATGGCCTCACTTGATCACGCTGTGTGGTTT  
 CTGCGTCCCTTCCGCGTCGATGAATGGTTGCTTTATGATCAGCGCTCTCCATCGGCCTCA  
 AGTGGGCGAGCCTTGACTCACGGGCGGCTTTTCAACCAGCAGGGAGATTTGGTGCCTATT  
 GTCAATCAAGAGGGAATGACCCGCACACTCCACGAGGGTGCGCAATCAATTCCGATGCGC  
 AAAGAC

>RXA00931-downstream  
TAAAATGCAGCGAACTTGAAGAT

>RXA00941-upstream  
AGCCGGGTGGCCGTTTGGCTGTACGGGTTTGGCTTATCGACGCCACTTCTGATTTTAA  
AGGCAAATATTTTGTGTACAGCGAGTAATCTTTTCGGGC

>RXA00941  
ATGAACCTAACCCGGAATGACAGGCTCGATCGACTGCCCCGTAACCTCCAAACATAAAAAAG  
ATTCTTGGCGGCTCAGGTATCGGCTGGGCATTGGATGCCATGGATGTCGGACTGATCTCT  
TTCGTATGCGTTCGTTGGCCACTCATTGGGGCCTATCCCCTACTGAACTTCCCTGCTC  
GGATCCATCGGTTTCGTTGGCATGGCCATCGGCGCTTCGCTGGGCGGTTTGGCTGGCGGAC  
AAGTTGGGGCGTCGACAAGTTTTTGGCTTGTCTTTGCTAGTTTATGGCGTTGCCACTGGC  
GCGTCGGCGCTTTCAGTGTGCTGGCAATGTTGATGGCGCTGCGCTTCGTCTGTTGGACTT  
GGCCTGGGCGCTGAACTCCCCGTTGCATCCACTCTGATTTCCGAGTTTTCTCCACGAAAA  
GTTCTGGCCGCATGGTCGTTATCCTGGAGGCGTTTTGGGCGCTGGGCTGGATCATGGCT  
GCAATCGTCGGAACCTTTGTCGTGGCAGGATCCGATAATGGTTGGCGTTGGGCGTTAGCT  
CTTGGCTGTGTCCCTGCAATTTACGCGGTGTATGTCCGTCTCGGACTTCCAGAATCAGTA  
CGTTTCTGGAGAAGAAAGGCCGGCAGCAGCAAGCAGCAAGCCATCGTTGTTTCTTCGAA  
GAAGCTGCCGCTGCCGAAGGTAAAGCTGCCGATGCCACCACCGCTGTGGTTCATGACAAC  
GCTGCCGAGGTTCCGTATCCATCTGGTCAGCTGCTTTGCGCAAGCGCACCGTCGCGCTG  
TGGATCGTGTGGTTCTGCATCAACTTGTCTACTACGGAGCCTTCATTTGGATTCCATCG  
CTGCTGGTTGCCGACGGTTTACCCTCGTGAAGTCTTTCCAATTCATCTGATCATCACC  
TTGGCTCAGCTTCCAGGCTATGCGGTTGCAGCGTGGTTGATTGAAAAGTGGGGCCGTCGC  
AGCACATTGGCCACGTTCTGGTTGGTTCTGCTATCTCTGCAGCGCTCTACGGCTTGGCA  
AATGTGGAGTGGCAGATCCTGGTCGCAGGTTGTTTACTATCCTTCTTCAACCTGGGCGCA  
TGGGGCGCACTGTATGCCATTGGGCGGAGCTTTATCCCACTAATGTCCGTGGAAGTGA  
ACGGGTGCTGCCGCGGATTTCGGGCGCATTGCTTCCATCATCGCTCCGCTCATTGTTCCG  
CCAGTGATTGCTTTTGGTGGACCAATTGCTTGTTCGCTCTCTTTGCCACCGCGTTTGGC  
ATCGCAGCGATTGCGGCGTTTACGCTGCCTGAGCAGAAGGGTAAGTCTCTCGCTGAT

>RXA00941-downstream  
TAGTGAGATCCTTCCACCAGTTT

>RXA00962  
GATAAGGCCATCAAGGCGGATCACGACATTAGAGAAGGCCACGATGAGCCAGCAGGTTTC  
AAGGATCTGCTTGTGATCGCTACCGCTGGATCTCCATTTGGTTTCGCGCTCGCCACATTT  
GTCACCCCTGCTCGCGTGGTACGGAAGTGGGCACATGGTTGCCTCGCCTCATGGAACTGCA  
GGTTATGAGTTTCGGCCATGCATTGATGTTACCCCTGGCTCTGAACCTCGGTGCAGTGATC  
GGATCCGTGGTTACTGCGTGGGCGGCGATCGCTTCGGGCCAATCCGTTCCGGTGTCTATC  
GCTGCAGGTATCGCCGGTATTGCACTGCTCCTGCTGCTCACTTACCCGCTGTACCCGCG  
GTTTATGTCACTTCTCATTTTGGCTGGCGTGGGCACCCACGGCACTCAGATCCTCATCATT  
GCAGCTGTGCCAACTTCTACCCAAGCAACCTGCGTGGCACAGCACTGGGCTGGGCGCTA  
GGTGTAGGTGCTATTGGTGTGTTGTGGCCCCGAGCTCGCTGGCCTGCTGCTGGCATGG  
AACTTGGGCGTGAACCTCAACTTCATCATGTTTCGGCACCGCTGCGCTGCTCTCTGCGCTG  
GCTCTCAGCGTGTGCTGCGCCTGCAGAAAACCTACAGCGTCACCCACAAAGTCGAAATC  
CAAGGC

>RXA00962-downstream  
TAACCCCTTTTTCAACTCACAG

>RXA01060-upstream  
TTCCATTTACACATCTGTTGACTCGCGCCCGAATGATGTCGCATCAACATGAGAAGCTA  
CTTCATACTTTTACTGATTGATAAGAATGGACAAAGACA

>RXA01060  
ATGAACCGCACACTCCGAACACTTGGCTGGCTTGCTGCCGTAATTCAAGAAGATCCGGAG  
CCCTGGTTTACCACTGATCCCGACACCGATTATGTCCCTTATGTAAATAGTTTCTCATTT  
GAATCCCTTTCCCTCGTTCCAGATGCTCTGATGCTGCTCAAACGTTCTCTTACCTTGCG  
ATGGAGCAACAGGACCTCCCAGTGAAGGATCTACAAGAAGCACTGAGGCACGTACTAGTT

TTCAAATTCCACTTCAGGGAAGAATGGGAGCTGGAATTAGCATGGGACTCCGAGCGGACC  
AAGTCTGCGGTGAGAATTATTGAGAGCACAAAAGAATCTCTTGCCGATCAATACAGAGAT  
TACAAATACGCATTCTTGCTGAGCTAATTTTCCAGGAATCACGCGGGATCTTTGACTTT  
GAGCTGGAGGGATACACCCCTCAAAGTAGGACAAAGCACGCTTTCCATTCTTTGGGACATG  
ATCGCCAATGGTTATGTCCCTGCAAGTCTTCGGAATTTTGGAGAATTAATGGACCGTGAC  
ACCGGAGATCTTGATGCAGATCCCATTCTGAGACCTCGAGAACTCAAATTTGAGATCCAT  
AATTGTCCAGATCTTAATCCTTGATAATGCGGGAACTTTTGATTTTCATGATGGAAATC  
GCAACTGAAACAGGATGGTTCCATGCTCTCAACCCCGCATATAATTCCGTCTACACCTAC  
GATCTTATTTCTCGCATGCCAGATTTCTTGTGAAGGGAGCTTTTCGTCCGCATTCAGTG  
AAACGATCTTGGGAAAAAATTCAAAAGATAGCTAAAGCTGTTGAGTCTTATGCATCTCAC  
GATTACTGCATGTCAACGCTGACACATGACTACAGGGCAATCGAGTTATCCCTGACGCTT  
ACAAAACTGAGGAACCAAGCACA

>RXA01060-downstream  
TAAGAAAACCTCGCCTGCCACT

>RXA01067-upstream  
GGCTTTAAGGCCGAGGTGCCTGGCTGAACTGCAGCCCCTCCAGACCCTGAGATCAGGCTA  
AATGGCAAACACAAATAGTTTGCATGGCAGAATAGCTTAG

>RXA01067  
GTGAGTGAATTCCAAGTACCCGAAATCCCTGCCCAATTCCTACCCAAGCATATTGCGCTT  
GTCATGGATGGAAATGGACGCTGGGCTACCGAGCGTGGCATGAAGCGCACCGAAGGCCAT  
AAGCGTGGCGAGGCAGTCTTGCTTGTGTTGATGCATGCATTGAACTTGGTGTTCCG  
TACCTTTCTGCTTATGCCTTCTCTACTGAAAAGTGGCGTCGTTCCACCGATGAGGTCGGT  
TTCCTCATGGGATTCACCCGAGATGTGCTGCGACGACAACGCGATGACCTACATGAAAAG  
GGCGTTTCGTGTGCGTTGGGTTGGCCGTCTCCCGCCTGTGGCGTTTCGGTTATCCGTGAG  
CTGGAAACTGCGGAAGAGCTAACCAGAGACAACACCAACCATGACCTTGGCCATGTGTGTG  
AACTATGGTGGACGCGCCGAAATCATCGACGCGACCCGCGACATCGCCCGCCTTGCAGCT  
GAAGGCAAATGCGCCCGGAACAAATCACTGAGAAGACCTTCCCGAACTTCCTCGACGAA  
CCTGACATGCCAGACGTCGACCTGTTTCTGCGCCCATCCGGTGAGAAGCGCACGTCAAAC  
TTCCTGCTGTGGCAGTCTGCCTACGCGGAAATGGTCTACCAAGACAAGCTGTTCCCTGAT  
TTCACGCAGCAAGATCTGTACGACGCGGTCTGGAATACGCCAAGCGGGATCGCAGATT  
GGAAGCGCA

>RXA01067-downstream  
TAATGCCCCACCAACCAGCCGACG

>RXA01114  
CGCCTTGACAGAAGCACGCGAAACCGCTGGCGGACGCAACCACCCGATCCCTGGTGGCATG  
ATCGAGACCGCTGAGAACCTGCGTCGCGAATACGGCATCTCCCGAGAGGAGCAGGACAAG  
ATCTCCGACGCTCCAGCAGCGTTGGGGCAAGGCTGCTGATGCGGGGCTTTTCGACGAC  
GAGATCGTGCCAGTCAACGTCCTGCCAAGAAGCGCGGCCAGGAGCCAACCATCGTTTCT  
CGAGACGAGCATGGTCGACCAGGAACAACCGTCGAAAAGCTTGCTGCTTTGCGCCCCATC  
ATGGGCCCGCCAGGATGCGGAAGCAACCGTCACCGCTGGCAACGCGTCCGGCCAAAATGAT  
GGCGCTGCTGCCGTATCGTGACCACTCGCGCCAAGGCCGAGGAGAAGGGCCTGCGCCCA  
GTCATGCGTTTGGCTGGCTGGTCTGTGGCTGCTGTTCCCCAGAGACCATGGGTATTGGA  
CCTGTTCTGCCACCAAGAAGGTCTTGATCGTTTGGGCCCTTACCCTGGAGGACATCGGC  
GCGATCGAACTCAACGAAGCTTTTCGAGCTCAGGCACTGTCTGTGCTGAAGGAATGGAAC  
ATTTCTTGGGAAGATGAGCGCGTCAACCCACTGGGTTCGGTATTTCCATGGGACACCCA  
GTCGGTGCCACCGGTGCTCGCATGGCAGTAACCTTGGCTCACCAGCATGCAGCGTGAAAAC  
ACTCAGTACGGAAGTGGCCACCATGTGCATCGGTGGCGGCCAGGGTCTTGCAGCTGTCTTT  
GAAAAGGAGAAC

>RXA01114-downstream  
TAAAAATGGCTATTTTGCACAGC

>RXA01136-upstream  
CCCTCGCAACACCGACGCTAGCCTCTTGGAATGGCGCGCATCGTGCGTGAGCTTTCCCG  
CTAGGACCTGTCTACTGCCTTCACTTTGTGCGAACACCGC

>RXA01136

ATGACCTTGGATTACTTCAAGGCATCCGGCACTGACTATGCTTTGGGATTGGCTGCAGAG  
TCGGAAGGGGACGACGCACTGGTATCACCGGCATGGCGAGTGCATTCAAGGAGTTTGCT  
GGTTGTGGTGAGATCGACCTTGAAGCAACCAGGGTAGAAGGTGGCCTCAAAGTTAGTGGA  
AAGCTTCGTTGGGCTTCCAACCTTGTCGAAGATCCAGTGATTGTGCCTGCTGCAAAGACC  
GCAGAGGGCTTACAACCTACTGTTTCGCATTGGGCGCAGAAACCGAAGGTGTCACCCTCGGT  
TCTTCACTTGCTCTACTCGGTTTGAACGCAACTGCTTGCCTTGGGTGAGCTTTGAGGAT  
GTCTTCATTCTTGGGGCTCAGATTCTAAGCCACGATTTCCTTACCTTGTGGCATCGGTGC  
GCCCCAACCTTCG

>RXA01136-downstream

TGATCCTACGGATCTCCGAATAC

>RXA01138-upstream

CTTATTCAAGTTTTTTGGAAAGATAATTAAGTATGACTTTAAAAACAGTAAACGGAACGCA  
GCTGCGAGACACTGTCGGATCGTTCCCTTCAGGTGTCACG

>RXA01138

GTGGTCACCACTACCGATGGGGAAGTGGACCACGGGTTGACTGTGAGTGCCTTCGTGTCC  
TTGTTCGTTGGAGCCTGCCATGGTGTGGTGAGTATCGATAAGAAATCAAGCGTTGTGCCG  
TTTTTGGAGCAGGGTTCACCACTTGCTGTGTCTGTGTTATCGGAAGAGCAGAGCGATTG  
GCCATCACATTTGGCCGTCATCTGGAAACAAATTCGACGGCGTTTCCATTAAAGCGTTCA  
ACAAACAGGGCAGCGGTCTTGAAGGTGCGTCAGCATGGTTGAGTGGCGCTGTGGTGGAT  
AAATACCCAGGTGGAGATCACTTTATTATCACCATTGCCGTGGAAGAGTGTGCTCACGAC  
GAGGAGCAAAGCCACTTCTTTACCACCGTGGCAGGCTTTTTTTCAGTGGCAAGAAGAT

>RXA01138-downstream

TAATTCTCCACCCCTTCATTTTC

>RXA01172-upstream

TAAATTTTTCTAGACTACCCAGATTAAGTGAGATTCTTTTCGTGTCTTCGACAACCTTCGAC  
AACTTCGGCCACCCGACAAGAGCCGTTGAGCCCCGACGGGT

>RXA01172

GTGCTTGCCCTCGTTTAGGTTTCGCGTTTAGTAGCCCCGCGGAGGTTTCGCACCGAGGTTTTA  
GCTGGCCTCGTGGTGGCGCTCGCGCTGATTCCGGAGTCGATTGCGTTTCCGTATTAGCT  
GGCGTGGATCCTAAGATGGGTCTTTTTGCGTTCGTGCACCATGGCAATGACCATTGCGCTT  
ACAGGTGGACGCCCTGCGATGATTTCCGCGGCGACAGGCGCTGTGGCGCTGGTGATTGCA  
CCGGTGGTTCCGGATCATGGCGTGGAAATATTTCTGGCCACGGTAATTTTGGCGGGCATT  
ATTTCAGATTGCGTTGTCGTTGCTGGGTGTAGCCAAGCTGATGCGGTTTATTCCGCGTTCC  
GTTATGCTCGGATTTGTTAATGCGCTGGCGTGCTTGGTGTTTTTTGCGCAGCTGCCGCAC  
CTGATCGATGTTCCGTGGATGGTGTATCCGCTGTTTCGCGCTGGGTATTGGCATCATGCTG  
TTTTTGGCCGAAGCTGACCTCGGTGATTCCGGCTCCGCTGATTGTTATCGTGGCCTTGACT  
GCGATCGTGTGGGTTTTTCGGAATCAACATTCCAAACGTCCTGACCAGGGCGAACTCCCC  
TCTTCCCTACCAGAATTCCTCATTCCCCAACGTTCCGCTTACTCTTGAGACTCTAAAAATT  
ATTGGGCCGATGCGCTTGGAAATGTCGCTTGTGGGTGATGGAATCGCTGCTGACCGCC  
AAGCTGGTCGATGATATTACGGAGGTTCACTCCAATAAATCCCGCGAAGCTGCAGGTGAG  
GGCATCGCAAACATTATCACCAGCTTTTTTGGGCGGCATGGGTGGCTGCGCGATGATCGGC  
CAGACCATGATCAACGTGAAAACTCAGGAGCCCGCACTCGCCTATCCACCTTCTTGGCC  
GGCGGCTTCTGCTGCTCCTGGTGGTTTTTGTGGGCGATGTCGTGGGCAAAATCCCCATG  
GCGGCGCTCGTGGCAGTCATGATTATCGTCTCCATCGACACCGCCGACTGGCATTTCGCTG  
AACCCGCGCACCCCTCAAATTCATGCCGCTGAGTGAAACGATCGTCATGTTTATAACGATC  
ATCGCGACCCCTCGTCACCGGAAACCTGGCGATCGGCGTCATCCTCGGAGTGCTCACCGCC  
ATGGTCATGTTTGTCTCGCCGCTGGCCACCTCGTGTCTGTGGAGCGCACCCGACAAC  
AACATCAGCACCTATACCGTCAAGGGCCAGCTATTTTGGGCGTCTCGAACGATATGGTG  
TACTCCTTCGACTACTCCGACGAGGCCGAGCAGATCATCATGATCTCACCGCCGAGAA  
ATCTGGGACGCTCCACGGTAGCCACGCTGGACAGCATCATCCACAAATACGCCGCGCGC  
GGCAAGAGCGTGGAGATCATCGGGCTCGACGGCCCCAGCCGCGATAGGCTTGAGCGCCTA  
TCAGGCAAGCTGGGC

>RXA01172-downstream

TAAAAATTTGCTTATCGACGCGC

>RXA01191

GTGAGTTTGGATGCGAACACGATTGAAACGGCGGGGCGCGGCGACGTGATTTCGCGTATC  
GCGGATGATTTCGCGGGAGGTGTCCACTGCGGCGAGCACCGTGGTGCCGCTGATGGTGCAG  
GCGGGCTTTACCGTGGTGATTTCGCGTGTGGCATGGCGGCGGTGATTGGCGCCTCGGC  
CTTGTCGGTTTGGTTCGCGATCCCGCTGTATTGGACCACGTTGCGCGTCTATTTACCCCGC  
TCAGGTCCGCTTTATACGCGTGAGCGCGAGGCCTTTGGGGTGCGCACGCAGCGGCTTGTC  
GGCGCAGTCGAAGGCGCGGAAACCTTGCGCGCTTTCCGCGCAGAAAGATACAGAATTAAAG  
CGTATCGACGCAGCCTCCGGCGAAGCCCGCGACATTTCCATTTCTGTTTTTCAGGTTCCCTC  
ACATGGGCAATTTCCCGCAACAACCGCGCGGAATGCATCACCCCTCGTGCTCATCTTGGGC  
ACCGGCTTTTACCTGGTCAACATCGATCTGGTCACCGTCGGCGCAGTCTCAACCGCCGCA  
CTGATCTTCCACCGACTCTTCGGTCCAATCGGCACGCTCGTGCGCATGTTCTCCGACATC  
CAATCCGCCAGCGCATCGCTGATCCGCATGGTGGGCGTTATTAACGCGGCATCGAACCAG  
GTCAGCGGCACCTCGCCGGCGTCTGCCAGCACCGCTTTAACGCTTTTCGACGTCTCCAC  
CACTATCACACTGCACCCGTCATCAAGAATGCATCCGTGCAGCTGGAACCAGGGGAACAC  
ATCGCCATTGTGGGTGCGACCGGCGCTGGTAAAAGCACGCTCGCCCTCATTCGCGCAGGC  
CTGCTCAGCCCAACTTCCGGGCGAGTGGCTCTCGGCGGATCGAGTTTTTCTAACGTCGAA  
CCGGAAGCATTTGCGCCAGAAGATCGCGATGGTCAGCCAAGAAATCCACTGCTTCCGAGGA  
TCTGTTTTAGATAATCTTCGTATCGCACGCCCCGAAGCCACCGATGCGGACATCCACGCC  
GTTCTCGCCGATATTGGTGATTCTCGTGGTGGAGCGCTTACCGCAAGGCATAGACACCATC  
GTGGGTGATGGCGCTTTCCGTTTAACTCTGTGGAAAACAGATCATGGCGCTTGCTCGC  
GTACATTTGGCCGACCTAGCAATCGTCATCTTGTATGAAGCAACGGCTGAATCAGGCTCT  
GATCATGCAAAACAGCTTGAAGATGCAGCCCTTAAAGTCACTGAAAACAGATCAGCCATC  
ATCGTGGCTCACCGCTCAACCAAGCGAAAACCGCCGATCGCATCATCGTCATGGACTCC  
GGAGAAATCATAGAATCTGGAACCATGAAGAGCTTCGAGCGATCGGCGGTTCGATATGAA  
CAACTGTGGACTGCGTGGTCTGCGCGC

>RXA01191-downstream

TAATTAGCCACCCAAGACCACGC

>RXA01205

GTATCGGCCTATCCGCCGGCCATCATCGCAGCGGCTCTCGTAGGAATTTGCGCGGGAGTT  
TTGCCCCATAATTTTGAACCCCTCGCGAATATTTATGGGCGATTCCGGCTCCATGCTCATC  
GGCCTGCTGTTGGCTGCAGCATCGACCTCAGCGTCAGGAAAAATCAACATGAGCCTGTAT  
GGCGCAGCTGATTTTATCGCATTGATCTCACCCATCATCGTTGTTCTCGCCGCCGTCGCC  
ATCCCACTGCTCGACCTCGTGATGGCAGTGGTTAGGCGCGTGGGCAGGGGAGCATCACCC  
TTTTCCCGGACAAAATGCATCTGCACCACCGACTGCTGTCCATCGGACACACCCATAGG  
CGCGTGGTCTAGTGCTCTACACCTGGGCGAGCGCCGTGGCATTTCGGCGCAGTGAGCTTC  
TCCGTGCTTCCGCCACTGTTTGCCACCGGATCGAGCATCTGTGGCATCTCATCGCCGTC  
GCTGTACAGCCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAAACTTGAT

>RXA01205-downstream

TAAGTGATTGTCACTTTGGATTG

>RXA01212

GGCCTGAATTTCCATGTACAGCGCGGTGAAGTATTTGGTCTGCTCGGCACCAACGGGGCC  
GGCAAAACCTCCACCTTGGAAGTCATCGAAGGACTTTCCGCACCCAGCTCCGGCACCGTG  
CGCATCTCCGGGCTTGACCCCGTTGCCGACCGCGCGATCCTGCGCCCCGAGCTCGGCATC  
ATGCTGCAATCAGGCGGCCTGCCATCACAGCTCACCGTCGCCGAAACCATGGACATGTGG  
CACGGCACCTGCACGTATCCGCGCGCCATTAAAGATGTGCTTGCCGACGTGCACCTCCTA  
CACCGGAAAACGTCAAGGTCGGCGCGCTTTCCGGAGGCGAACAACGACGCCCTTGATTTG  
GCCTGCGCACTGCTTGCGGACCCCTCAATTTTGTCTCCTCGACGAACCCACCACCGGCCCTC  
GACCCAGAATCTAGGCGCCACACCTGGCAACTCCTGCTGGACCTGAAACAGCGCGGCGTC  
ACCATGATGCTGACCACCCACTACCTGGAGGAAGCCGAATTCCTCTGCGACCGGATTGCC  
ATCATGAACGCCGGTGAGATCGCAGTGGAAGGCACCTTGATGAACCTGGTGGCCCGCGAG  
AAGTCGATCATCAGTTTCGTGCTGCGTGGCGGGCAGGTGGAGTTGCCGGTCTTGAGTGGG  
GCTGAAATCATCCGCGACAACAACACGTCCGCATCGCCACCACCACCTGCAGCAGCAC  
ACCTTAGAAATACTTACCTGGGCTGCAGAGACCGGGATCGCGCTGGAAGGCTTCGCTGCA  
AAACCCGCCACCTTGAATCCGTATTCATGGAC

>RXA01219-upstream  
 CACCATTTGGGAAACCGATTCCCCAGTTGATCCGGACCCATACTTGTCTTCTATGACTG  
 GGCCAAGACCACCGCTGCGACTTCCTAAGAGATAAAAAATC

>RXA01219  
 ATGGACATTTTACTCAATCAGCTCGTAGCCGGGCTTTCAGTTGGATCGGTCCTTCTATTG  
 GTCGCAGTGGGATTGTCACTGACCTTTGGACAGATGGGCGTTATTAATATGGCGCACGGA  
 GAGTTCATCATGGTCGGCGCATACACCGCATATGTGGTGCAGCTGGTCGTGCGTTCTGCC  
 GGTTTATCCCTACTGATCAGCATTCCGCTGGCCTTTATTATCGGTGGGCTTTTCGGAGTT  
 CTCCTCGAACAATTCTGCTGAAGTATCTTTATCACAGGCCACTAGACACGCTGCTGGCC  
 ACATTCGGTGTGCGTTTGATCCTTCAGCAGCTGGCCCGAAACATTTTCGGAGCTCCCGCA  
 GTGGATGTCAGGGCACCGGAATTTCTCCGCGGAAACGTCGAAGTTCTAGGCGTCTTGGTG  
 CCGACCGCGCGACTATTTCATCCTGGCGCTGGCCATCGCATCAGTGACTGCACTAGCTGTG  
 TTCTTAAATCGCACTGCCTGGGGCCGACGCATCCGCGCCGTGGTTCTGAACCGCGACCTC  
 GCGGAAACCGCAGGTATTGATACCCGAGCTACTGACCGAATGACGTTCTTTGTGGGCTCC  
 GGTCTTGCCGGAATCGCCGGGGTAGCTATCACATTGATTGGCGCGACCGGCCCCACCATC  
 GGTGAGAACTACATCGTGGATGCCTTCCTTGTGTTGCCGCCGGTGGCATCGGCCGGGTG  
 AAGGGCGCTGTGATCATGGCTTTCTGTGCTGGGAATTACTCAAGCATTCGTGGAATATACG  
 ACAGGTGCGAGCATCGCGAAGTTCATCGTACTCATCGCTGTTGTTGCCTTCCTGCAGTTT  
 AGGCCTCAAGGACTCTTCCAAACCCAACTAGGAGCCTCGTA

>RXA01219-downstream  
 TGAGCACTCAACTCAAGCTGAAG

>RXA01220-upstream  
 CAGGTGCGAGCATCGCGAAGTTCATCGTACTCATCGCTGTTGTTGCCTTCCTGCAGTTTA  
 GGCTCAAGGACTCTTCCAAACCCAACTAGGAGCCTCGT

>RXA01220  
 ATGAGCACTCAACTCAAGCTGAAGAAGCCCGCAAAGAAGAAAACCTACGCCGAAACTTAGC  
 GTCGTAAATGCTCCCACGCTGCGCACTGCGGCGTTGGGCCTGGCCGCGCTCGCTGCGGTA  
 TTGCTGTGCGCCCCGCTCTTTTATCCACATTCCAGCTGACGTTGATGTCGCGCTTGGTG  
 TGTTATGCGATCGTCGAGTCGGCATCGGGCTGGCGTGGGGCAGAGGCGGCATGCTCACG  
 CTGGGGCAAGGCGTGTCTTTGGAATCGGCGCGTACATCATGGCCATGCACATGCTGTAC  
 AGCGATTGCGAGATTTTGGGACCACAGTTCCGCAATGGTGGTCCATTTTGGCAACCCG  
 GCAGTCGCACTCATCGCAGTTGTGGCGCTTCCCGGCATCGTGGCTTTTGTGCTCGGCTTC  
 TCCATTTCAAACGACGCATCAAAGGCGCCTACTTTGCCATCGTGAACCAAGCGCTCGCC  
 GCAGCTGTTGTGGTGTGCTGGTTCGACAAACAAGATTCCCTTGGAGGTTCCAATGGTCTT  
 TCCGGATTTCGATCGTTCATGGGTTTGGCGCTACGACCCCATCAACCGCATCATGTTT  
 TACTTCACCGCAGTGGGAGTTCTCTTGGCTTTGGTGGCTATCTCATATTGGCTCATGCGC  
 AGCCGCTATGGAGAATGCTCGTGGCCACCAGAGATGCAGAAGAACGCGTCCGATTCCCTC  
 GGATATGATCCCGCATGATCAAAACCGCCGCATATGTCATTGCTGCGATGATTGCCGGA  
 ATCGCCGAGCGCTGTTCTGTGCCGATCGTGGGCATCATTTACCCCGCAGAAATCGGCGTG  
 GTGCCATCAATCGTGTTCGTGATCGCCGTCGCCGCTGGTGGCAGGGCATCCCTATTCCGT  
 CCCGTAGTTGGCGCGCTGGTGTGCTGGGCTGGGTGGAATCCACACTTGCTCAAACCTTTCCC  
 AGCATGTGGTCCATTTCCAGGGTGCATCCTGGTTCTCGTGATCGTGTGCTGCCGGC  
 GGAATTGCTTCAATTAACTTTCCGCGCTCAAAAATAAGGCCAGGAAGGCCACCTCA

>RXA01220-downstream  
 TGAGCCTTAAATCACCAACCTC

>RXA01221-upstream  
 TCCAGGGTGCGATCCTGGTTCTCGTGATCGTGTGCTGCCGGGCGGAATTGCTTCAATTA  
 AACTTTCCGCGCTCAAAAATAAGGCCAGGAAGGCCACCTC

>RXA01221  
 ATGAGCCTTAAATCACCAACCTCAAAGTCGCTTTCCGGGTCGTTTCATCGCCGTGAATGAG  
 ATTAGTTTTAGGTGCTGCCGGTCACTTCCCTCATCGGTGCCAACGGTGCAGGT  
 AAAACCACTGCATTGACGCGATCAGCGGATTGGCGCCGGGGCAGGGATCAGTGCAGTTG

GATGGCACTGAGATTCTGGGAACCCCTGTGCACCGCATTGCTCGGATGGGTGTGGGGCGA  
 ACGTTTCAGACCGCCAGCGTGTGGAAGAATTGTCTGTGTTGCAGAATCTGGATATTGCG  
 TCGGGGATTCATCGTCCGTTGCGGGCGCTTCTCGGGGTGCGTCATCGGATTGATCCCCGA  
 ATTGAACACGCCCTGGAGGTCACGGGTCTTGCTGATCTGGTGAATGCTCAGGCGGGAACC  
 TTGTCGCATGGGCAGAAACAGTGGCTGGAAATTGCAATGTTGCTGGTGCAGGATGCGCAG  
 GTGCTCATGTGGATGAGCCGGTGGCGGGCATGAGTGAGGAGGAGCGTGTGCAACGGGT  
 GAGCTTTTGCAGAGGGTTGCGCGGGGACGGGTGGTGTGGTGGTGGAGCACGATATGGAG  
 TTCATGCGTCGTTTTGCCACTCGCGTCACTGTGATGAATCGCGGCACGATCTTGTGTGAG  
 GGGTCGGTCGATGAGATTCAGGCGAATCCGGATGTGCAGTCCATTTATTTAGGTACGGCA  
 GGAAG

>RXA01221-downstream  
 TGAGTTAGTCATGTTGGAAATCA

>RXA01222-upstream  
 AATCGCGGCACGATCTTGTGTGAGGGGTGGTTCGATGAGATTCAGGCGAATCCGGATGTG  
 CAGTCCATTTATTTAGGTACGGCAGGGAAGTGAGTTAGTC

>RXA01222  
 ATGTTGGAAATCACTAATTTGTGTGCAGGTTATGGCCGCACGCAGGTACTTCATTCTCTT  
 TCAATCTCCACGAGCAGCAACGGCATCCTGTCGATCCTCGGCCACAATGGCGCTGGTAAA  
 TCCACCTTGCTGCGAACC GCGGTGGGGTTGATTAAGCCGACTTCCGGAGAGGTCAAACCT  
 TTCGGCCAGGATGTCACCTCGTTGTCCACGCATGAGCGAGTAAAGCGCGGAATGGCTTAT  
 GTGCCGAGGGCCAGCAGTCTTTTACGCAGCTTAGTTGCATGGAAAATTTGCAGGTGGTA  
 GCGGATCTGCAGGGACGTGTGGGCAAGGCACGCATCGCGGAGGCGCTTGATCGCTTTCCG  
 GCGCTGACCCAGGTGCTGGACCGCCAAGCCGGCCTGTTGTGCGGGTGGTCAGCGTCAGCAG  
 CTTGCCATCGCCCGCGCGCTGATCACGGCGCCAAAGCTTTTGTCTCTCGACGAACCCACC  
 GAGGGTATTACAGCCTTCGGTGGTTGCTGAAATTCAGCAGACCATCATCGATTTGGCTAAG  
 GACGGCATGAGCATTGTCTGGTGGAGCAAAACATTGGTTTTGCATTGGATGCTGCAACA  
 AGCTACGCCATTGTGGCGCGTGGTCAGGTCTGGAATCGGGACAAGGCGCTGAAACCACC  
 GCAGAGAAGCAGACTAAAGTGCGGGAATCTCTAGCAATC

>RXA01222-downstream  
 TAGCGGCTGTGGATAGCGTTTTG

>RXA01235-upstream  
 TTCTGAAGCTGTGCCGGCCGCTGCTTAAGTTTTCTGTCTGAAGAGAATTTTCTCAACCC  
 CTGGGTGGCTACCGCGTTGTGCGTAGTCATTTTGGGGTTT

>RXA01235  
 GTGGTGCTGTTTTAGGTTTATAGCGGTGTTATTGATTTAAGCCCCACAGCAGTGATTAGA  
 CATTTGAGTGGGCAGGACACGCTCACCCCTCGAGATCAGGCCATCTTCTTTGATATCCGG  
 CTGCCTCGAATTATCGCTGGTGTCAATTGTCGGAGCAACGCTGGCTATTTCTGGTGCTGCT  
 TACCAAGCGGTATTTAGAAACCCGCTGGCTGATCCTTATTTGTTGGGTGTGTCCGAGGT  
 TCTGGCCTTGGTGTACGGCAGTGATTGTTGGCGGTACCGTGCTGGGATTTTCTGCACCG  
 AGCATCGGCGTGATTGGTGCAGCATTTGTAGGTGGTGTGCGCAGTACTTGCCACGCTG  
 ATGGTGAGTCGGGGAGTAGGACAGGGATCATCAACCACCGTGGTTATTTTGGCGGGCGTG  
 GCGGTTGCTGCTTTTGCCAGTTCCATCCAGACCTATATTAGCAACGACACATCGATACG  
 GTGGCGCGCTATATGTGTGGATGTTGGGCAACCTCAATGTACCAACTGGATGTGATC  
 TTCATCGTGGCTGTGGTGGCGGACTATGCGCGGCCGTGATCATGTCTGCGCCAGGTTG  
 TTAGACGTGATGGCTGTTGGTGATGTGGAAGCCCGCACATTGGGCGTCGATCCAGGCCTC  
 GTACGCATTGGCATTGTCACTGGCAACCCTTGGTACAGCTGCAGTGGTATCCATTTCC  
 GGTCTCATCGGGTTTGTGGGCATCATTGTTCCGCACGCCCTGCGCCTAATTGTTGGCCCG  
 GGGCATCGGATTTTACTGCCACTGTCTTTCGTATGGGGTGCCATTTTCTCGTGTGGCA  
 GATACCGCAGGGCGAACATTGATGGCTCCTCAGGAACCTCCCGTGGGTGTGGTGACAGCT  
 GCACTCGGCGCACCGTTCTTCTTATTTATTTTGGCGAGAACCAGCAGACAACGAGTTCCA  
 AAAAGGAGTGCT

>RXA01235-downstream  
 TAAGTGGCGATCATTGAATGCGA



>RXA01260-upstream  
CTAAACGTGGGCTGCATTTCCTTCCAAAGTCTCTGATCAAAAACGCTGAAGTTGCCCATAC  
CTTTACCCATGAGAAGAAGACCTTCGGCATCAATGGCGAA

>RXA01260  
GTGACCTTCAACTATGAGGATGCTCACAAGCGTTCCCGTGGCGTTTCCGACAAGATCGTT  
GGAGGCGTTCACTTCTGATGAAGAAGAACAAGATCATCGAAATTCATGGTCTTGAAAC  
TTCAAGGATGCTAAGACTCTTGAGGTACCGACGGTAAGGATGCTGGCAAGACCATCAC  
TTTGATGACTGCATCATCGCAACCGTTCCGGTAGTCAACACCCTCCGTGGCGTTGACTTC  
TCAGAGAACGTTGTGTCTTTTGAAGAGCAGATTCTTAACCCCTGTTGCGCCAAAGAAGATG  
GTCATTGTTGGTGCAGGCGCAATTGGAATGGAATTCGCCTACGTTCTTGGTAACACGGT  
GTAGATGTAACCGTCATCGAGTTCATGGATCGTGTGCTTCCAAATGAAGATGCTGAAGTC  
TCCAAGGTTATTGCAAAGGCTACAAGAAGATGGGCGTTAAGCTTCTTCCTGGCCATGCA  
ACCACTGCTGTTTCGGGACAACGGTGACTTTGTGCGAGGTTGATTACCAGAAGAAGGGCTCT  
GACAAGACAGAGACTCTTACTGTTGATCGAGTCATGGTTTCCGTTGGTTTCCGTCCACGC  
GTTGAGGGATTTGGTCTTGAAACACTGGCGTTAAGCTCACCGAGCGTGGCGCAATCGAG  
ATCGATGATTACATGCGTACCAACGTCGATGGCATTACGCCATCGGTGACGTGACCGCC  
AAGCTTCAGCTTGCTCACGTCGAGAAGCACAGGGCATGTTGCCGAGAGACTATTGCT  
GGTGCAAACTCAGACTCTTGGTGATTACATGATGATGCCACGTGCAACCTTCTGCAAC  
CCACAGGTTTCTTCCTTTGGTTACACCGAAGAGCAGGCCAAGGAGAAGTGGCCAGATCGT  
GAGATCAAGTTGCTTCCCTTCCATTCTCTGCAAACGGTAAAGCAGTTGGCCTGGCAGAA  
ACTGATGGTTTCGCAAAGATCGTTGCTGATGCAGAATTTCGGTGAGCTGCTCGGTGCACAC  
CTGGTTGGAGCAAATGCATCAGAGCTCATCAATGAATTGGTGCTTGCCTCAGAACTGGGAT  
CTCACCCTGAAGAGATCTCTCGTAGCGTCCATATTACCCAACGCTATCTGAGGCAGTT  
AAGGAAGCTGCACACGGTATCTCTGGACACATGATCAACTTC

>RXA01260-downstream  
TAGAATCCACCTCGTTGGCCCTG

>RXA01261-upstream  
GTGGGTGTTTTTCATTTTCTTCCACTCTAAAATTAAGTATGGAAAACCAACCGCACCCGG  
ATGCACGACAATGACCCACTAAACACGTATCCTTGAATGC

>RXA01261  
GTGACTGAACATTATGACGTAGTAGTACTCGGAGCCGGCCCCGGTGGCTATGTCTCCGCC  
ATCCGTGCAGCGCAGCTTGGCAAGAAGGTTGCTGTAATTGAGAAGCAGTACTGGGGTGGT  
GTTTGCTTAAACGTGGGCTGCATTCTTCCAAAGTCTCTGATCAAAAACGC

>RXA01261-downstream  
TGAAGTTGCCCATACCTTTACCC

>RXA01269-upstream  
GATTATCTCTGCGCCGATTACAGCTGGCAATAGCAGCAGTTGTATTGAGAGCTCATGGTCG  
TCCGATTCTATTTCGTCAACCACGACCTGGGAAAGACGGT

>RXA01269  
GTGGTATTTGAGATGATTAAGTTTCGAACCATGCTTGAACCAGATGAAAAACATGTAAC  
GATGAACAGCGTCTAACTAAAGTTGGAAAGCTTCTGCGGGAAACGAGTTTAGATGAGTTA  
CCTACACTCTGGAATGTATTTAAAGGTGATATGAGCCTTGTAGGGCTCGACCTTTGCTT  
GTTAGCTATCTGGAACATTACTCTTCTGAACAAGCTCGACGCCATGAAGTTCTGCTCGGG  
ATTACTGGTTTGGCTCAGGTGAATGGCCGTAATCAAACACTTGGGATGAACGACTTAAG  
TTGGATGTCGAATATGTGGATCGCTGTAGTTTGAACACTAGATTCAAAAATATTAATCGCC  
ACTGTAAAAACAGTTCTTTCTAAAAAAGGCATTAGTAATGAAGGTCATGTCACGATGCCA  
TCCTTCATTGAAGAAAGAAAA

>RXA01269-downstream  
TAGCAGGTAAAAATTTACTTTT

>RXA01291-upstream  
AACCCGCAGCGGGTGGAGCGGGGCTGAGGGAGACGTCGAGAAGCGTCCCTTTTCGGTTGTC

TGGATTTCTCGCGGTAAAGTTTCCTGTGAAGGAGGCGAGT

>RXA01291

GTGGCTGATCAGCAAGATTTTTTGGGCCGTTTTTGATGCGATGAGCTCAAAGGCGACGGCC  
ACGGTAATCGCCATTATTCCTCCAGTTTTACTCTGGCATCGAAGCTGTTGTCGCCGAAA  
ATTCGTGCGGATATTGAGGCATTGTACGCAATGGTGCGAGTGGCCGATGAGGTTGTGGAC  
GGCGCTGCTGCTGCCGCGGGGTGTGCGCCGACGCCGTTGCGGAGATTTTGGACAATTAC  
GAACGCCAGGTTCTGCTCAGTTTGTCCGTTCCTTTTCATACCGATCCAGTGATCCATGCG  
TTTGGCAATACCGCCCGCAAATGTGGTTTTGAGCAGGCTCACATCGTGGCGTTTTTTGAT  
TCCATGCGCCGCGATCTCTCCCAAACCTCCTATGATCCGACTCAGTTGGATGAGTACATT  
TACGGCTCCGCTGAGGTCATCGGGTTGATGTGTTTTGAAAATTTTCTCCAAGATTCCACT  
GCCAGCCCGCAGGATCGGGCCACGATGGAACACGGCGCCAGGCGTTTGGGTGCGGCATTT  
CAAAAGGTAAATTTCTGCGAGATCTAGCTGAAGACCGCGAAGGCCTAGGCCGTTCTTAT  
TTGCCGGTATTCACCGAAGAAATGCGCGATGAGATCGTTACTGATATCCGAGAGGATTTG  
GATGCCGCGCGGCTGAGCATTCGCGTGTGCCATTTGGCGCGCGAACC GGTTGTGCGCGCC  
GCGACCGATCTCTACGGTTGCCTCGTGGACAACCTGGAATCCGCGTCCCTCGAAGACTTA  
AAAAACGGGCGGGATTTTGTGCCGTCTTTAAAAAAGCCAGCCTGGCAACCAAAGCAATGT  
GGAAAGAAGTGTTCAAAAATGACAAAAGCAGTGGTCATCGGCGGGGGACTAGCAGGACT  
AGCCACCACCGCACTGCTCTTACGCGAAGGATA

>RXA01291-downstream

TGAAGTCCACCTCGTCGAACAAA

>RXA01292-upstream

TCCGCGTCCCTCGAAGACTTAAAAACGGGCGGGATTTTGTGCCGTCTTTAAAAAAGCCA  
GCCTGGCAACCAAAGCAATGTGGAAAGAAGTGTTCAAAA

>RXA01292

ATGACAAAAGCAGTGGTCATCGGCGGGGGACTAGCAGGACTAGCCACCACCGCACTGCTC  
TTACGCGAAGGATATGAAGTCCACCTCGTCGAACAAAACGAGCACCTCGGCGGGCGCGCC  
GGGACCTTCGAACCTCGACGGCTTCCGCTGGGACACCGGCCCCAGCTGGTACCTCATGCC  
GACGCCATGTCCCACTTCTTTAAGCTCTGCGGCACCTCCATCGACGACCACCTCGACCTC  
GTGCCACTTGAACCCGCCCTACCGCTCATCGACGACCACGGCGAATTCATCGACGTCACC  
TCCGACATCGATGCGATGGCCGAGCTTTTCGAATCCCGCGAACCCGGCGCCGGCGCCAAA  
CTGCGCACCTATATCGACTCCGCCACACAGGTCTACAACCTGGCCATCGACGGCTTCCTC  
TACACCAACTTCACCAACTTCATCCCATACTTAAGCCCCGGCATGCTGCGCCTTTTACCC  
AACTTCTAGCAAGCCTGTGACCTCGCTAAAAGTCAAGGTCAACACCCAATTCGCGAT  
ACAAAACCTGCGCCAAATCTTAAGCTACCCCGCAGTTTTCTCTCCTCAGACCCCTTCGCAC  
ACCCCGGCGCTCTATCACCTCATGAGCCACACCGACCTCGTCCAAGGCGTCTCCTATCCC  
CGAGGCGGCTTCACCGCCTTCATCAAGGCACTAATTTGCTTATCGACGACGCCGTCTC  
CACCTCGGCACCCCCGTCAGCGCAATCACCACCAAGGCCGAAACGCCACAGGCGTCCAA  
GTCGGCTCAGAGTTCATCGAAGCCGATATCGTGATCAGCTGCGCTGATCAGCACCACACC  
GAAACCAACTCCTACCTGCTTCTGTTGTGCGCGAAGCCGGAGACGAGCTGGAAGAACAAA  
CAACCCGGCCTCAGTACTGTGCTGGTTTTGGCAGGCGTGAAGGGGGAGCACACCCGTGCTT  
TTTCTCCTCGACTGGGACGAAGATTTCCGCAAAGTTTTCGACGGCTCCACCCAGAATTCC  
CGGCTTCAGAATCCATCTAGATCTCCAAGACCTCCGCAACAGATTCCGATGCCGACCCG  
AAGGCCACGAGAACCTCTTCATCCTGGTCCCAGTACCCGCCGATGTCTCCATTGGTCACG  
GGTCCGCTTACGGAGAAGAATCTGACATGGTGGGCCGGATCGCAA

>RXA01292-downstream

TAGCAGCAGTGGCTCAAATTGGG

>RXA01293-upstream

CGATGCCGACCCGAAGGCCACGAGAACCTCTTCATCCTGGTCCCAGTACCCGCCGATGT  
CTCCATTGGTCACGGGTCCGCTTACGGAGAAGAATCTGAC

>RXA01293

ATGGTGGGCGGATCGCAATAGCAGCAGTGGCTCAAATTGGGCGATGGGCTGGCATTGAT  
GGTTTGGAAAGCCGCATTGTTGTGACGCGACCATCGGCCCTGCCGACTTCGCAGACCGA  
TACAACTCCTGGAGCGGCGGGTCCATTGGCCCCCTCACACACCTGGCACAATCGGCGTTC  
TTTAGGGGTTCTAACAAATCCCGCAAAGTAGATGGCCTGTATGACGCAGGTGACACCACA

GTTCCAGGGGTGGGCGTATCTATGTGTTTGTATCTCTGCAGAAAACGTGCTCAAGCGTCTC  
CGCGGGGACAACAGTGTGGATCGGACT

>RXA01293-downstream  
TAACGGGACTTTTTTCTTTTGCT

>RXA01339-upstream  
GAGAAGGCGGAACCGAAGGAATCGAAGAATATCTCTCCGTGCGTTACCTCGCTTTGCCGT  
GACACATGAGCTGTCCGGTGAATAACCCGAAGGAAAAAAC

>RXA01339  
ATGACTACCGAATCAATAGTTGCGCACAATGCTGCAGGTACAGCACCTCAGAATGTGTCC  
TCTGCTAAGAAGAAGTACCTCAGCGTTGCCCAAGGCGTTGCCCTTATCTACGGAACCAAC  
ATCGGCGCCGGTGTGCTCAGCCTCCCATACGCTGCCCGCAACGGTGGTTTCCCTCGCCCTG  
GTTGTTGCCCTGCTCATTGCGGGAACACTGACCACCATCTCCATGCTCTACATCGCCGAA  
GTATCCCTGCGCACCAAGAAGCCACTGCAGCTTTCCGGCCCTGGCAGAAAAATACCTGGGG  
CAGTGGGGCCGCTGGCTGGTGTTCATTGCCATTGTGGTCAACAGCGTGGGTGCACTGATT  
GCCTACGCATCAGGATCCGGCATTGATAGGCAACCTCACCGGCCCTGCCACCAATCGTG  
GGCACCCCTTGGATTCTTTGTTTTAGGCACCTTGATCATGTGGAAGGCCTGCACACGGCA  
AGCTTCGTGGAGGCATTGATCACCCTGGCATGGCAACGATCATCATCGTGCTGTGTGGA  
TGGACAGTGCTTGGCCCTGGAATTTCCGCAGACAACCTGATCGTGTTCACCCATTCTTC  
ATCGTTCCGATCATGAACCTCGCGGTCTTTACCTTCCCTTGCCCAATATGTGGTTCCAGAA  
ATCGCACGAGGAGTTAACCTGCCACCCCGAAGGCAGTGCCACGCGCGATCATCATCGGC  
ATGGTCGCAACTGGTGTACCCTGGCAGCTGTACCATTGCGGGCACTAGGGCTTCTGGGC  
ACAGGCGTCAGTGAAGTTGTCACCATCTCCTGGGGCGAAGCACTCGCCCCAGTGGCCTAT  
TACATGGCCAATGCCTTCGCACTATTGGCCATGTTCACTTCATTTCATCGCCATTGGATT  
ACCGCGATGCGCAACGTACTAGATATTGGCCACTGGCCACAACACGGATGGCAGCGATCC  
GTTGCTGTGCGACTAACTGTTCTTCCACCACTGGCAATTTCACTTGCGGGATTAGGCGGA  
TTCGTGGCAGCACTGAGCTACGCCGGAGGATTGCGCGAGCAATCATGTCCATCATCCCC  
GTGCTGTGTGCTGCGCAACTCCCGCAAGAGTGGCGACCAAGAACCAGTGTGGAAGCCACC  
TGGCAAGCGCACCCCATCTTCCAGATCCTGTTGATTGTGGTGTACTCCCTGGCGTTTGTG  
TACTCGGTTCTCGCGATCGTCGGATTAATGCCTGCGGGTTGGGCA

>RXA01339-downstream  
TAGTCACTTCCCTGTTGTGGCTGC

>RXA01382  
TCCACCTCCACCGCAGCTGGCACCGGAACCTGCAAATGAAGAAGGCACCATCACCGCAGCC  
ATCTCCTACGAACCTGGGAACCAACGGCTACGACCCAATGACCACCACCTCGGCTCTCACT  
GTGGCAGCCAACCTGGCACACCCTTGAAGGCCCTACCGAAATCGACCCAGCCACCGGCGAG  
GTCTACGCAGCACTCGCCAGCGCACTGCCTTCAGCCGATGCGACCTCCCTAGACATCAAG  
CTTCGCGACGGCGCCACCTTCCACAACGGCGACGCAGTCACCGCAGACGACGTAGTCTTC  
TCTTTTGAGCGAGTCCCTCGATCCAGCCAACAACCTCCCTTTACGCATCCTTCATCCCATT  
ATCAAGTCAGTCACCAAGAAGGATGACACCACCGTCACCATCGACCTCGACTACGCAACC  
GGCATCATCAGCAACGCCCTCGCAGTAGTAAAGATCGTGCCAAAGTCCGTGCGTGAAGCA  
GACGCATCCGGATTGACGCAACCCAATCGGCTCCGGCCCATACAAGATGACCGACAAC  
GGTGCATCCAAGGTGGTCAAGTTCGAGCGCAACGACGACTACAACGGCCCCACGCCAGCA  
CGTGCCGCCAAGATGGAATGGCAGATCATCCCCGACGCTCCACCCGACCAACTCCCTT  
CAGTCCGGCAGCACCATGGCCATCGACTCCGTTCATACCTGTGATCCACAGCTTGAA  
GCCACCAGCACCGTAGAATCCGTCCAAGGATTCGGCCTCCTGTTGCGCATGTTAGCTGC  
TCCGAAGGCAACCCCTTCAACGACGTCCGCAACCGCCAGGCATTCCTCTACGCACTGGAC  
ATGGACAAGATCGTTAAGACCGGCATGTCCGACCAGGCAACCCAGCCACCTCCTTCGTG  
CAGAAGGAACACCCCACTACAACCAGGCATCCACGGTCTACTCCCTCGACGCCGACAAA  
GCCAAGGCGCTGTTGCTGAAACCGGCCTTACCAGCCTCAACCTCCTGTGCACCGACCAC  
GACTGGGTCAAGAACTGCACCCCACTGATCCAGGAATCCCTC

>RXA01399  
ATTCTCAGCCCCGCAACCGCACTTGTCTGGCGATTGGATTGATTGCTGCTGCAATTATC  
CCTCCCCCTGCTTGCTGCTCGCGGAGTTAAACAGCCGAAGCCCGGCGCTGAATCCAGC  
GAAGCCTACTTGAGTTCCTTGATCAGGTGCTGTCCAACAGGCGGCGCTTCGTGTTGCT  
GGTGAAATGCCGGCGCTCTGTCCAAGGCGGATGTGGCTGCGCGTTCTATTCTTCTCA

CTGGAGGCAGGCGCGAAAGACACTGCCATTGGCGCAGCGAGTTCCCTGTGGATTACGGT  
TTCACGTGTCATTGGTGTGCTCATGGTTTCCGCGTCACTGTATGCAGATGGAAGCCATTCA  
CCGCAGTGGTTTGGTGTGTTGGTGTGCTTCTCACTCGCAGCTTTCGAGGCTGTCTCTGTT  
CTCCCGATGTGCGATTGCTCGTACCCGCGCCGCGAGATGCCACCAGGAGGCTTGCGGAA  
ATCTCGGCGCTGCCAGAATCTGTCTCTCTTGAGCTTCGCACGGCCCTTGACCAGCCCGTA  
TTACGCGCCGAGAATCTAGTTTATGGATGGGACAGCGACCTAGGCACGAGCAACCTGGAT  
CTCACCTTTGGTTCACGACATGAAATCATCGCACCCCTCTGGAACCTGGCAAAACGACCCTG  
CTGCTCACACTTGGCGGGCTGTTGGAACCTCGTGGAGGCCAAGTGCTTATCGACGGCACC  
AATCCTTCCGAGTTGAAAAACGCCGTGCTGTTTCAGTCCAGAAAGATGCCACATTTTTGCC  
ACCACTGTCCGAGATAACTTAGCACTCGGAGCACCCGGAAGCAACCGACGCGGAAATGACA  
TCGATCCTGGAACATGTTGGTTTGTCTAGAGTGGGTTCAGGTTTACCCGATGGTCTTGGC  
ACTGTCCTTGATTCAAGTGCCGATAGTCTCTCGGGAGGTCAGCGCCGCGCCTGCTCCTT  
GCCCCGCTACTACTAAGTGATGCACCAATTCTGCTTTTGGATGAACCCACCGAGCACCTC  
GACACTGCAGGCTCCTCTGAAATCTTGTCTATGCTGGCCTCCGATGAACTCCCTGGTAAA  
AGAGCTAGGAGAACCGTAGTGATTGTGAGGCATGTGAGG

>RXA01399-downstream  
TAATTTTGCCCCGCTGTCTTCTG

>RXA01419-upstream  
GCGCCCACTCATCGGCGAGCTTCAGGAGATGAGGTTGATGCTCCATTGATAATTTCTTTT  
GCTAATAGTCAAATGATCATTGAGTGTTAGTGTTTTCTC

>RXA01419  
ATGCTTCTTTCCGCCCCGACACACACGAGTTTCCAAGAACTTGGACTCAATGCTAGTCGG  
CGCAAAGCAATCAACTGGACACTGGCACTCACTGTGGTGCTAATTGCCCTCCATGTTTGT  
GGCGTGCTCATCGGTGCATCCGGGACCTCAGTGTTTCCACGTGGACCGTAATTAGCCAC  
CATCTTTTGGCACTGAGCTAGGTGGCTCCGACACTGCCGACGCCATCATTGGGTACATC  
CGCACCCACGCGTCTTGCTCGCT

>RXA01420-upstream  
CGAAGTTCACGACTACAGGCATTACCTGGGTGCTGATTTTGGCGGAGTAAAGCTGTGGCT  
GCGGAATGCGCTGCTCATCCACACGTGGAATCCTGATTGG

>RXA01420  
GTGACGCTGGGTGGATTGAATGTACCATCGTGGTTCGCTGGGCGCGGAAATGCTGTTCTAC  
CTGACGTTCCCGCTGTTTATTCCGTTAGTGCGCAAAGTGAAGGGCGTGGGCAACTGGTGG  
GCATTTGGCATCACCTTTGCCGTGAGCCTGGCGCTGATTACAGTGATTCACTTTTATGCG  
GACGGACCAAAGGGGATTGAGAACTTCTTTGTCTCCTCGCCTGTGGGACACCAATGTGTCA  
CCGGTCGCGGAAGTTCACGCCGATCCAGTGTTGGTTTATGCAGGAAGAAATCCCGTGCTG  
GAATCTTACTGGCTGTCTTACTACTTCCCCGTGACCAGACTCATCGAGTTCTACCTCGGT  
GTGTTTGGCGCGAAGCTGGTTGCTGAAGGCATGTTAAAAACACCAACATCACCATCCCG  
CTGATCGCACTGGCTGTTTCTTTTGTGCTACTTGGTTTGTGCCACTGGCATTCAAGATG  
TCTGTTCATCATGTCCCTGCCAATGGCTTTTGTGTGGCAACGCTTGCGGTGAGAGACATT  
GAAGGCAAGAGTGGGGAAATCGCCTCGCCTCGCGCAGTTTTGTTGGGTAATATTTCTTT  
GCCTTCTACATGGTGCAATTCCCCGTGATGGTGTGTCAGCGCTATTTCAATTGCTGGC  
AAAGAATACGGCTTCTTGGCTGGGCATTCTATGCAGTGGTGTGTTTCATCGTGTGGTC  
ATTCTCGCGTGGGTGCTGTTACCTTCGTTGATGATCCTT

>RXA01420-downstream  
TAATAAGGCCACGGAA

>RXA01467-upstream  
GCGTCATCTTTAGCCTTGCTTTATGAGCTTTTCCCCGCAATGAGCCGCGTTGTGTATCCA  
TAAGTCTTAGCCTACAAGCGCTTTGAGGTAGTTTGGGATC

>RXA01467  
ATGGATTTCAACGACAAAGCCGCTTCAGAAAACGCTGTAAAGACTGGCGCAGAAGGCCCC  
AACGTTTTTCGCGAGCGTGGCCAAGATTTGCAGGATGTTGGCGGAATTTAGCCGAAGAC  
GTCACTCCGGAATCTCGTTTACTGAGGATTTGGCAGTGAGCTCACTCAATTACATCGAG  
TTGATTGTCAATGCGGAGGACGCATTTGGTGTTTCGATTGAGGACGCCGATGCCAAGGAT

TTGACCACCGTGCAGGATTTGATTGACTTTATTAACACCAATAAGGCTGAT

>RXA01467-downstream  
TAGCGGGAAAATTTGCGCCCAAAA

>RXA01538-upstream  
TCTAAACTCACTCTCAACTCACCAAGATTGTTCAACAATCTGCGATTGGTGTGCAATCTA  
CCCCAATCATTTTGAAAGCCCCACGAAAGGAGCGCGACA

>RXA01538  
ATGGCCGACAACAAAAATGCCGATGACAGCCAGCTAGTCTCAGCCAGCACTGGAACCCCT  
GGGCCTGGCGACATTGCAAAAGCCAATGCGCCATCCCTCAAGCAAGCTGCAGTAACCGCC  
TCTGGCCGAAGCGCTCTGATGGGTGCCATCTTCCTCATGGCAACTTCTGCCATCGGCCCA  
GGGTTCCTCACCCAAACCGCTGTCTTACCAACCAGCTCGGCGCAGCTTTCGCATTTGCG  
ATCCTGGTGTGATCCTCATTGACATCGCGGTGCAGCTGAATGTGTGGCGCATCATCGGC  
GTCTCTGAAATGCGCGCCCAAGAAGCTCGGCAACACGGTTATCCCAGGTTTTGGTTGGGTG  
CTGGCCGTACTGGTCTGTATTGGCGGCGTA

>RXA01576-upstream  
ATCGGTGATCTTTTCGCGATTGATACGTGCGCGATTGCGTGCCCGCCAGCTGCTCAAGATC  
AATGGATTTTCATGACAATCAAGTTATCATCACTGGGGTCG

>RXA01576  
GTGGCACCTAACAGGAAAATCAGCCATCATGCACTAGGCTCTATTCCTATCATGGATGCA  
TCAAAAAACAGCGACTTTAAAGACACCTGGCTAGTCGTACCTTGTTATAACGAGGCAACA  
GTTATCCGGGAAGTTTTAGAGAACGCACTCAAAACATTCCCTAATATTGTTGCGGTCAAC  
GATGGTCCCCGGACAACCTCCGCGGAAGAAATCCATGCGGCCGGCGCACACCTGGTCAAC  
CACCCCGTGAACCTCGGACAAGGTGCCGCGATCCAAACCGGCATCGAATACGCCCCGAAG  
CAACCCGTGCAAAATACTTTGTAACCTTTGACGCGCGACGGCCAAACCAAGTGAAGAC  
GTTATCCGCATGGTGGAGCGACTGCGTGCCGAGGACGTGGACATTATCGTCGGCACGCGT  
TTTGACGCCCACGCCAAGCCGATGACCAGGTGCCACTAATCAAGCGCCTTGCTGCTGCGC  
ACCGTGGTCCGTGCTGTCACCGAAAACCCGCGCACTTGGGCTCACCGACGCCACAACGGC  
CTGCGCGTATTCAACCAAAAAGTGGCGCAGGAAATGAACATCCGCATGAACGGCATGTGCG  
CATGCATCCGAAATCGTCGACCAATCGATGAACGCGGTGGCGCATTTCAGAAGAACC  
GTAGACATCCTCTACACCGAATACTCCATGAGCAAGGGGCAATCCCTGCTCAACGGCGTA  
AACATCCTGGCCGACGGCTTCCTAGCGAGGAGACTCCCA

>RXA01576-downstream  
TGACGCAGACCACCACCAAATC

>RXA01580-upstream  
CGGTAAACGCCTCATTAAGTCCAATGCCATGCTCATAACACTAACAGTTAACCGTGCGG  
TCAACTTTGCTCCCTATCCTTAAAAAGCCACAGAAAAGG

>RXA01580  
ATGTATAAGAATATGCACATTGTTGCCCATCGCGGTGCGGAAGATCTGCACCTCGAAAAC  
ACCATGACCGCTTTCCAGGCTGCCGCGCCCGCTGACGCTTTTGAGCTGGATATCCACGCC  
ACCGCTGACAATCAGGTCGTCTGTTATCCACGACCGCACCGCAGCGCTGTTGCCGCGCCA  
GATTCCCTGCACCGCGACACCCCGGTTGCGCGCTTAAGCGCCGCGCAAATCAAGGAGATA  
ACGCTTATCGACGGATCCCCCGTACCAACCTGGAGGAAGTTCTACTCCAGACGAGCCTG  
CCGATCCAAGTGGAATCAAATCTGCCGGTGCACTTCCAGCAGCCGAGCATTATTGCAG  
AAATACCCAGAGCACCTGGAGCGCCTGCTGTTTCATCAGTTTCATCGATGCAGCACTGGTG  
GAAATCGTGGATCGACTGCCAGAAGCTCGCGTGGGAATCTTGCGCGATGCGTCCATGGAT  
GATCTGCGCATTTCTTGATTACATCCCGCTAAAAAATGTGGGCGCGATCTTGCCCTCGTGG  
AAAGCACTAAACGTGGCGTCAATTGCTGATCTACATACCAAGGGAATCAAGGTTGGCTGC  
TGGACAATTCGGGATGAAAATGCGTTTGGGATCGCACAAAGCTGGCGTTGATTACCCC  
ACTGTTAGCGATCCCTCTCGTTTCTCGCGCCCTCCCTGCTG

>RXA01584-upstream  
CCACCCCTTCCCCGCTACGCGCCATACCGGCTTGGGCGGGCATCGGATCACTA

>RXA01584

GTGGTGTTTTTGGGCGCACTTCTCGGCGCCGTAATCATGGGCGGGTTTTATCCAGCATTC  
ATTCAAGCCGGATCCACAGTGTTCGGCGGCGGCCACGTGGTTTTGCCACTGCTGGAAAAG  
CTCGTTGTTGCGCCCGGTTTTATTAAAGAAACCGACTTCCTATCCGGCTACTCCGCAGCG  
CAGGCAGTGCCCTGGCCCCATGTTTCAGCTTCGCCAGCTACCTCGGCGCAATCTACGGTGGC  
ATCGGTGGTGCAGTGTCTGGCCAGCCTGGCGATCTTCTTCCCGCCGCACTCTTGAGCATC  
AGCGGAATGTACTTTTGGGGACGCTGGCGAAAAGCACCAGCGCATCCAAGCAGCAGTCACC  
GGCATCAACGCCGGTGTGGTGGGGCTTTTGGGCGCAGCGCTCTACGATCCCGTATTACACC  
CACGGCATCACCAGCGTTTCCGCATTAGCTATCGCAACGGTGTGTTGGCTGGGGCTAGCC  
CACTGGAAAATTCCGCCGTGGGCCATCGCCGCGGGTGCAGGCTGGGTCTTG  
CTT

>RXA01584-downstream

TAGAAAACGCTCAGACCCAAACC

>RXA01591

GCCTCACTTAACTGGTCAGTCATCGTTCCAGCCCTAGTCATTGTCCTAGCGACAGTGGTG  
TGGGTATCGGATTCAAAGATAGCTTTACCACCTTTGCTAGTTCTGCGTTGTCAGCAGTA  
GTTGACAATCTCGGCTGGGCCTTCATTTTTGTTTGGCACAGTCTTGTATTTTTTATCGTT  
GTTATCGCCGCTAGTAAATTCGGCACGATTTCGCTTAGGCCGCATTGATGAAGCACCAGAG  
TTTCGCACGGTGTTCATGGATTTCATGATGTTTGTCTGCAGGTATGGGTATTGGTTTGATG  
TTCTACGGAACCAAGAACCTTTAACCTTCTACCGCAATGGTGACCTGGACATGATGAA  
CACAATGTTGGCGTTGCTATGTCCACGACAATGTTCCACTGGACCTTGCATCCATGGGCT  
ATCTACGCAATTGTGGGCCTAGCCATTGCCTATTTCGACCTTCCGAGTGGGCGCTAAACAG  
CTTCTAAGCTCTGCATTTCGTGCCACTCATTGGTGAAAAAGGTGCAGAAGGATGGTTGGGC  
AAGCTCATCGACATCCTGGCGATTATCGCCACCGTATTCGGCACGGCATGTTCCCTTGGC  
CTTGGTGCCCTGCAGATTGGTGCAGGCCTGTCCGCAGCAAAACATCATTTGAAGATCCAAGC  
GATTGGACCATCGTTGGCATTGTTTCTGTTTTGACCCTGGCATTTATCTTCTCCGCTATT  
TCTGGTGTGGGCAAGGGAATCCAGTACCTCTCCAACGCCAACATGGTTCTGGCAGCTCTG  
CTCGCGATTTTCGTGTTTCGTTGTTCGGACCAACCGTGTGCGATTTTGAACCTGCTGCCAGGT  
TCTATTGTGAACTACCTGTCCAACCTTCTTTCAAATGGTAGGCCGCACTGCCATGAGTGCC  
GACGGCACACCAGGTGAGTGGCTTGGTGGCTGCACCATCTTCTAC

>RXA01604

GACACACCCTTCGCCGATGTTGAGATAGCTCCAGACAGCGGACTCACTTTGCTGAGCACC  
GGGCGCGAATCCCAATCCAGTTCCTTTTCTTTGGTACTTTCCGGCCGCATGCGCGCCTCC  
ACCGGAACCATCGAATTAAACGGCGAACCCATCAAGGCAACCAAGCTGGCCAAGCATGTG  
GCTTTGGCGGGCATCCCTGAAATCGATTCACTCGAGCGACTTGTCACTGTGCGCACCCTT  
GTCCGTGAACAACCTCGCCTGGTCAAGCCCTTGGTACCTGATGGTGCCCAGGGATATTAGT  
GATTGCGGACGGTGGGTTGACGTCGAAAAGCATCTTGGCCTGAACCTGAACCTAAAACC  
TTAATCGGCGACCTCAGCGTGCTCGAGCGTTTTAAGCTGCGCATCGCGCTGGCGCTGCTG  
GCGCGGCCAGAGGCGCAACTGTTGGTTCGTGGATGATCCCGATCAAGTGCGCAGCATGGAA  
TTGCGTGCGGAGGTGTTGCACGCATTGAAAGGCGTTGCAGAGGATCTCCCTGTGGTTCGTG  
GTATCCACCAACCCAGATTTTGATTCTTGGCCGATACCGCTTTGACCATTACGGGGGCT  
GGAAC

>RXA01604-downstream

TAATGGCATTTTTACACTTTGGC

>RXA01614-upstream

TGCAATTTCGCAAACATGAGTAGTATCGCGGAAGTTTACCACGTGAACATTTTCAGTCGAC  
TCGCGCACACCACCAACAATCGACCTATCGTTATACGT

>RXA01614

ATGAATCAGATGCAGCAGTGGAAACCAGACTTCCTGGGAGAGGGCTACCAAACCTCACC  
ATCGAGCTCGGCGACGACCCGGATAATGAAACAGATGTTGTGACAACGGTTGTGCGCTAC  
AACCAGACAATCAGCGGACGAGTCTTTTGTGCCCCGCCAGCGTTGCTGTGGGTTTAC  
GGCATGACGGACTACTTCTTCCACACTGAATTCGCGGAGTTTTTCCACAATGCCGGTTTT  
GCTGTGTACGGCATTGATCTTAGAAAATGTGGACGCTCCTACCGTCCAGGACAGCAGTGG  
CACTACACCTCTGATCTTGCCATTACTTCCCTGACTTAACAGCTGCTGCCGAGGTCTATC  
TCTTCCACCCACCTGAGCTAGTCCCGTCGCCCATTCCACTGGTGGACTCATCGTTCTC

CTGTGGATGTCCCAGATGCGCACAAGCAATCCAGCTGCCATTGAGAAGATTCCAGCGCTG  
 GTCCCTCAACAGTCCGTGGCTGGACATGATGTATCCACCACTGTTTCATCAAGCTGATCACC  
 CCTATGGTGAGGGTGTTGGGCAAACGCTCCCCACAACCATCATCCCAGGCGGAGGTTTG  
 GGAGCATACGGAAAAATCGATCCATAAGAAGCTTTTACGGCGAATGGGACTTTGACACCACC  
 ATCAAGCCTGTAGAAGGACATAAAAAGAGCATCGGATGGCTTCGGGCAGTCATGGCTGGC  
 CAAGCAGAAATCCATCACGACCACGTGAATGTGGAGTGGACGTGCTCACGCTGTGTTCA  
 AATAAGTCTCGTTGAAGTCTGAATACACAGAGGACACCAACACTTCAGACGCGGTTTTG  
 GATGTGAAACACATTCAAAAGTGGGCTCCTCATTTGAGCTCGCCATCGTCCAGGGTTGAT  
 GTTGAGATCATCGACAACGCTCGCCACGATATTTTCTCTCAAGGAAACCCGCCAGAGAT  
 CACGCTCTGAAGTACTCAACAACCTGGCTGCAATCGAAGCTTCCAGCCTCAAACCATCT  
 CAA

>RXA01614-downstream  
 TAACACCGCGAATTATAGACTGA

>RXA01629-upstream  
 CAGGAAGAAGTTAACACCGCCCAGGGGTGCGTTGGATGATGATCATCTACAAAACAAACAT  
 TCCGTTATGCACTCATAAGATATGACGAGAGGTTTTACTC

>RXA01629  
 GTGAGCCCGATTTCGCTCAAAAAAGAAAATCAAGAACGAACCAAGACTAACAGTCGATGAC  
 GTCACCGTTGTTCCCCCAAAGAAGATCCGTCCGGCCATTAAAGGCACTGTGGTGGGTAAC  
 TTCATGGAGTGGTACGACTTCGGAATTTATGGTTATTTGACGGTCACGATGACCGCAGTA  
 TTTACCCAAGGCCTGCCGCAAGAATGGCAGTTGTTGGCCGTGATGTTTGGTTTCGCGGTG  
 TCTTATTTAGTTCGCCCCGCTTGGTGGCCTGGTTCTGGGTCCGCTTGGCGATAAGGTTGGC  
 CGCCAGAAGGTTTTGTACGTAACCATGGCCATGATGGCCGTGTCTACGGCGCTGATTGGC  
 TTGCTGCCGACGGCGGCGTCGATAGGCGCTTGGGCTTTGGTGCTTTTGTACCTGTTGAAG  
 ATGGTGACGGGATTTTCGACTGGTGGTGAATATGCTGGTGCGACCACCTATGTTGCTGAG  
 TTTGCGCCGGATCGTCGACGAGGTTTCTTCGGAGCTTTCCTAGATATGGGTTTCCTACCTG  
 GGCTTTGCCGCGGTGCTTCGGTTCGTGGCGATTACTACCTGGGTGACCACTCACTTCTAT  
 GGCACAACCTGCCATGGAGGATTTCGGTTGGCGTATTCCCTTCCTGACTGCGATCCCGCTG  
 GGCATCATTGCGGTGTACCTGCGTACTCGTATCCCTGAGACCCCTGCGTTTGAGAACAAAC  
 CAAGACGAGCCAAATGCAGTTGTTGAAAAGGACACTGAAGATCCTTATGCACGCTGGGC  
 CTGGCTGGTGTATCCGCCACCACTGGCGTCCACTGCTGATTGGTATTGCGATTGTGGCA  
 GCGACCAACACCGCCGGTTACGCGCTAACCAGTTACATGCCTGTGTATCTAGAGGAGCAG  
 ATCGGTCTGCACTCCGCATCCGCTGCCGCTGTGACCGTGCCGATTCTGGTTGTTATGTCC  
 CTGCTGCTGCCATTTGTTGGTATGTGGAGTGACCGGTGGGCCGCAAGCCTGTCTACGCG  
 ACTGCTGTTGCGGCAACGCTGATCTTGATGGTTTCTGCCTTCTTGATCATGAACACCGGA  
 ACCATCGGCGCGGTACTGATTGCATGTCCATGGTTGCTATTCCAACCGGTTTGTATGTG  
 GCACTGTCCGCATCTGCCCTGCCAGCGCTGTTCCCAACCGCGTCACGATTCTCTGGAATG  
 GGTATTTCTTACAACATTTCCGTGTCGTTGTTTCGGTGGTACAACCCCGCTGATCACCCAG  
 TTCCTGCTGCAGAAGACTGGCCTGGATATCGTTCCAGCGCTCTACATCATGTTCTTCTCT  
 GCAATCGCAGGTGTGGCGCTGCTGTTTCATGACCGAGTCTTCACAGAAGCCACTGCTTGGC  
 TCATTCCCAACCGTGGAACCAAGTCTGAGGCCGTGGAGATCGTGAAGAACCAGGACGAG  
 GATCCAAATATTGATCTTTCCCATATGCCGTTTCTGATGAGGAAAACGTAGGTGCTGAA  
 AAGCAAAACGCA

>RXA01629-downstream  
 TAACCGTAAAGCCCGCTGCAAGG

>RXA01644-upstream  
 GTAGGTAGAGGCTTGTGGTCACTACTTGTGGCCACATTTTAAAAAAATGCACAAGAAGAG  
 AAAGCAAAGCATTATGAGTAACGCCGTAGCGCAGGACCTC

>RXA01644  
 ATGACCATCGCCGACATCGTCGAGGCCACGACCACTGCACCCATCCCATTCCACATCACT  
 GCCTTCGATGGAAGCTTCACTGGCCCTGAAGATGCTCCCTACCAGCTGTTTGTGGCCAAAC  
 ACGGATGCAGTATCCTACATCGCAACAGCGCCAGGAGATTTGGGTTTGGCACGTGCCTAC  
 CTCATGGGAGACCTCATCGTGGAAAGGTGAGCATCCCGCCATCCTTATGGGATCTTTGAT  
 GCGTTGAAGGAGTTCTACCGCTGCTTCAAACGCCAGATGCATCCACCACCTTGCAGATC  
 ATGTGGACTCTGCGGAAAATGAATGCCTTAAATTCAGGAAATTCACCAATGGAACAA

GCCCCTGCATGGCGTAAAGCACTGATCAACGGGCTAGCATCCAGGCACTCGAAATCCCGC  
 GACAAGAAAGCCATTAGCTACCACTACGACGTGGGCAATGAGTTCTACTCCCTGTTTTTA  
 GATGATTCCATGACCTATACCTGCGGTATTATCCAACGCCAGAATCAAGTTTGGAAGAA  
 GCGCAAGAAAACAAATACCGCCTCATCTTTGAAAAACTGCGTCTGAAAGAAGGCGATCGC  
 CTCTAGACGTGGGATGCGGTTGGGGAGGCATGGTCCGCTACGCCGCCAAACACGGTGTG  
 AAAGCCATCGGAGTTACGCTGTCTGAACAGCAATATGAGTGGGGTCAAGCAGAGATCAAA  
 CGCCAAGGTTTGGAAGACCTCGCGGAAATTTCGCTTCATGGATTACCGCGATGTTCCAGAA  
 ACTGGATTTCGATGCGATCTCAGCAATCGGCATCATTGAACACATCGGTGTGAACAACATAT  
 CCCGACTACTTTGAATTGCTCAGCAGCAAACTCAAAAACAGGCGGACTGATGCTCAACCAC  
 AGCATCACCTACCCAGACAACCGCCCCCGCCACGCAGGTGCATTTATTGATCGCTACATT  
 TTCCCGACGGTGAACCTCACTGGCTCTGGCACCCCTGATCAAGCACATGCAGGACAACGGT  
 TTGGAAGTGCTGCACGAAGAAAACCTCCGCTTTGATTACCAACGCACCCCTGCACGCGTGG  
 TGCGAAAACCTCAAAGAAAATTGGGAGGAAGCAGTTGAACTCGCCGGTGAACCCACTGCA  
 CGACTCTTTGGCCTGTACATGGCAGGTTTCGGAATGGGGATTGCCCCAACATCGTCCAG  
 CTGCACCAAGTACTGGGTGTGAAACTCGATGAGCAGGGAAGTCGCGGAGAAGTTCCTGAA  
 AGAATGTGGTGGACTATC

>RXA01644-downstream  
 TAAAGAAACAATGTTTCTTTTAA

>RXA01667-upstream  
 TCTCGGCGTTGATGATCATCCGCAATATCATGCCGCCGAAGATTCCGCTTTTCCAGACT  
 TTGCTCATTCCTTCCTCTATTACTGCTCGCCATCATCGGC

>RXA01667  
 ATGATTTTGGGGCCTAAGGTGTTGGGTCTGATTGGTTGGTCCGATCATCTTTCCACTTAC  
 ACTACGGTGCTCATTGCGATTGTGTTTGCTTCGATGCCGTATTCGATGAAGTTTGACCGT  
 GCGTGCGTACTGGCATGAAGACGATGTGGGCGTATTCGACTGCGATGTTTGTGGGGCAG  
 TGGGGTCTGTTTCAATTTTGTGCTGGGTCTGTTTTTGTTCACACCGGTGTGGGGTACCGATGAG  
 TGGTTCGGCATGATGTTGCCGTTGGTTTTGTTGGTGGTTTTGGTACTGCTGCTGCGGTG  
 GGTACTGCGTTGGAGTCTTCGGGTGCGGAGGCTGCGATGTCTTTGGGCTTTACCTCTGCG  
 ACGGTGGGTACTTTTGTGCTGCGATTGTTGGTGGAATTATTTTCAACCGTGGGGTATTAAG  
 AAGGGCAAGACTGCGGCGATGCCGTGCGCAGTTGCCGTGGGATTTGCGTTCGGGTATATATC  
 GATAAGCTGAGTGATCGTCCGTGATTGGTAAGGCGAGTACGAATCCGTCTGCGATTGAG  
 CCTTTGGCGCTGCATATGGCATTATTTTGTGACTGTTGCGGTTGCGTATTCCATTAAT  
 CAGTGGTTGGGTAGCATGTTCCCAACCGTGCAGATTCCGTTGTTTGCATGTCATTTGTG  
 GTCGGCATGTGGGCATGGGAATTATGCGTTTGTGAAGAAGCCTGAGTATTTGGATCGC  
 GACACCGTGAATCCGTGTGCGGCGCGGCGACGGATTACCTCATTGCGTTTGGTATTGCC  
 TCGATTGCTCCTGCTGCGATTGCTGATTACTGGGTTCCCTCTGTGGTGTGTTGTTTTG  
 GGCACCATCAACTGTTGTTTCTTCTTTTTCTGGGTGCGCCTCGTTTCTTTGGCGAGAAG  
 TGGCTGGAGCGCGCATCTTCGGTTGGGGTGGGCTACTGCCGCGGTTGCTACCGGTATC  
 GCGTTGCTGAAGATCGTGGATCCGAAGTTGAAGTCGGGAGCGCTTAATGAGTACGGCGTG  
 GCTTATATCGGTTTTTGTCTCATTGAAATCGGCATGACCATCATCGCGCCGATCGCGTG  
 CTCGAGGCTTTACCATGGGGTGGGTTGGGCGTCGTTGATTGTTGCGATCGTGATTTTT  
 GGCTCGCGTGGGGTCTGAAGTGGTTGCCGAGCGCGGACATGTCCGCGCGAGGGTAAG  
 CCGCAA

>RXA01667-downstream  
 TAAAGGTGGAAGCGCCGGGTCT

>RXA01722-upstream  
 CTCATTCCCCCTCGCTAAAAGCTGCATAAAGTTTTCGACGTTTTCAAAGTTGATTGCTTGCA  
 CTGTCGTTGCGTGTCGATGCCCCGGCTATTGTTGATTGC

>RXA01722  
 ATGCTCAGCACGATGCAGGACGTCCCACTGTCAATTAACCAGAATCCTCGAGTACGGGTCC  
 ACTGTTACGGTGATACTTTGATCACCACGTGGGGCGGTGCCGATGGCATTGAACAAGCA  
 CAGCAAACTTTTAGTGCTGTGGGGGCTAGAGCTGCGGCTTTGGCTCATGCGCTGCATGAT  
 TCTTTAGGTATTACTGGGGATCAGCGAGTGGCGTGCATGCTCTATAACTGCGCGGAACAC  
 ATGGAACTATGTTTGCAGTCGCATGCATGGGTGCCGTGTTTAAATCCGCTGAACAAGCAG  
 TTGATGAATGATCAGATTGTGTTCAATCACTCTGAAGCTGAAGTGGTTATCGCT



GATCCGCGCATGGCTGAACAATTGGGTGAGATCTTAAAAGAAACACCAAAGTTCGTGCC  
GTGGTGTATTATTGGACCGAATGATTTCTCTAGCGCGGCGGCCACATGCCGGAGGGAATG  
AAGCTGTATTCTATGAAGCGCTCCTTGACGCGCGTCCACTGTTTACAACCTGGCCCGAG  
CAGGATGAACGCACTGCTGCTGCAATTTGCTATTCCACCGGTACATCGGGACCGCCGAAG  
GGTGTGGTGTATTCCACCGCTCGCTTTATTTACAGTCGTTGAGCTTGCGCACCACGGAT  
TCCCTCGCAGTGGAAACACGGCGAAACGTTCTGTGCTGTGTGCCGATTTACCACGTCCTC  
AGCTGGGGCGGTGCCGATCGCAGCGTTTATGTCCGGCACTCCCTGGTGCTTCCTGGACCG  
GATCTTTCTGCGCCGACATTGGCAAAGATCATTTCACCACGCTGCCTCGCGTGGCGCAT  
GGCGTGCCTACTCTCTGGATTGAGCTGATGGTTCCTACCTGAAAAATCCCCAGAGCGT  
ATGTCTCTGCGTGAGCTATACGTGGGCGGTTCTGCGGTGCCTCCAATCGTGATCACCATG  
TGGGAGCAGCGCTATGGCGTGGATGTTGTCCACGTGTGGGGTATGACGGAAACCTCCACC  
GTGGGTACTGTGTCTCGCCACCATCAGGTGTTTCTGGTGAAAGCCGGTGGAATTATCGA  
GTCTCCCAGGGCCGATTCCCCGCCTCCCTGCAGTACCGCATTTGTCAACGACGGCCAGGTC  
ATGGCGTCCACCGACCGCAACGAGGGCGAGATTGAGTCCGCGGTCCGTGGGTGACTGCA  
AGTTACTTCCACCCCGATGTGGAAAAAGAGGTGGCACCAGCTCAACATTCCGCGACCAT  
GACGTTGAAGAGGAAAACGATGAGCTCTTACCGCCGACGGTGGCTGCGCACCAGGGGAC  
GTTGGATCTGTACCAGCGATGGATTCTCACCATCCAAGACCGCGCCCGCGATGTCATC  
CGTTCTGGCGGCGAGTGGATTTACTCCGCTCAGCTGGAAAACCTCATCGTGGCTACSGAA  
GAGGTTGTGAATGCGCCGTCATTGGCTTCCCCGATGACAAGTGGGTGGAACGTCCCTC  
GCAGTCACCATGCTCTACCCCGGCATTGAACGCACCCGGGAAACCGCCGAGCGCCTCCGC  
GATCAACTTCGCGACCGCCTACCCAACCTGGATGCTGCCAGAATATTGGACATTTGTTGAT  
GAGGTGGATAAAACCTCCGTGGTAAATATGACAAGAAGGACCTCCGCAACCACCTGCGC  
AACGGCGATTTCTGAAGTAATTAAGCTTAAAGGGCCAGGTGARAAA

>RXA01722-downstream  
TAACTTCCCTATTTATTCCGGCT

>RXA01727-upstream  
AGCTTTTGGTGGTTTACCACCTGCGCTCGTCTTAATTTTGGCTGTTCCAGAGAGACCCT  
TGAGGAGGGGCTGCGCCGATCGCCAGCGTGTGTAAATA

>RXA01727  
ATGAGTAAAAAGTCTGTCTGATTACTTCTTTGATGCTGTTTTCCATGTTCTTCGGAGCT  
GGAAACCTCATCTTCCCGCCGATGCTTGGATTGTGCGCAGGAACCAACTATCTACCAGCT  
ATCTTAGGATTTCTAGCAACGAGTGTCTGCTCCCGGTGCTGGCGATTATCGCGGTGGTG  
TTGTGCGGGAGAAAATGTCAAGGACATGGCTTCTCGTGGCGGTAAGATCTTTGGCCTGGTG  
TTTCTATTTGCTGCCTATTTGTCTATCGGCGCGTTTTACGCGCTGCCGAGGACTGGGGCG  
GTGAGCTATTTCGACGGCGGTTGGCGTCGATAATGCGCTTTATTCGGGCTTGTTTAACTTT  
GTGTTTTTTGCGGTGGCACTGGCGTTGTGCTGGAATCCGAATGGCATTGCAGACAAGTTG  
GGTAAGTGGCTCACGCCAGCGTTGCTCACGTTGATTGTGGTGCTGGTGGTGTGTGCGTA  
GCCAAGTTGGATGGCAGCCAGGTGAGCCAAGTAGTGCGTATGCGCAGCAGCCTGCGGGG  
GCGGGTTTGCTTGGGGCTACATGACGATGGATGCGATTGCTGCGTTGGCGTTTGGCATC  
GTGGTGATTTCTGCGTTCAAGTACCAAAAGGTTAACAAGGTCCGCACGGCAACTGTCTGTG  
TCGGCGTTTCAATGCGCGAATTTTGTGGCGCTGGTTTATCTTGGTTTGGGCTCAATCGGT  
CAAGTAGTAAACGGTGAGTTCGCTGATGGCACCGCAATTTTGAACACGCTGCACTGTCC  
ACGATGGGTGAGGTGGTGCATCATGTTCTGGCTATTTTGATCCTTGATGTATGACC  
ACCGCAGTTGGTCTGATCAGTGCGACGCTGAGTTTTTCAATTGCTGCTGCCAGGTGTC  
AAGTACCACGCTCTGGGCCACTGTTTTGCGCTGATTTCCCTTGGCGTTGCCACCATGGGT  
TTGGATACGGTGTGGCCGTTGCGGCTCCAGTGATTAGTTTCAATTTACCCATCGGCCATC  
ACCTTGGTGTCTTGTGCTCATCGAGCCCTGCTGTCCGTCTCAAGTGGACCTACCTA  
TTCGGCATTTGGAAGTGCAGTTGTGTGGGCGCTGTTTATGTCTATCCCTGCGCTGAATCCA  
TTCATCGAATGGGCGCCGCTGCACAGCATGTCTTTGGGTGGGTTGTCCAGTTCTCGTG  
GCCTCTGCCATCGTTTGGCTATTGATTGGAACAAGAAAGGTGCCAGTCTGTTGCAAAG  
AAGGAATCCATTTCCGTC

>RXA01727-downstream  
TAATCGCTAATTGCGAGGAGTCT

>RXA01737-upstream  
CTTTGAGCCGAACGATCTGCCGACTCAAGAAGAACTAGCCCGGCTGCTCAGTCAGGAATG

ATGCGCCTAAGATCAAACAAGAATGAAAGGACGGTGAACA

>RXA01737

ATGGGCCGAATGAAAAACGATGGTGAACCTCGCGGATCTGCCGGATCATGCACTTTTGAGC  
ATTATTCGAATCCCGCAGGCGGCGAAAAGAAGCCCCCTGGGCGCTGATCTTAACGCGCATC  
GGATACGCGATGGTGTCTGGTTATCGTCACCATGGTTGTCTATTTTGACCGCAACGGA  
TACTCCGAAGACCTCACGTTTCATCGACGCGTTGTACTATTCCACAGTCTCGTTGACCACC  
GTGGGCTACGGCGATATCACCCCGGTGACGCAATCGGCACGCCTGATCAACATCATCGTC  
CTCACCCAGCAGCATCGGCTTCTGATCCTCCTGGTCCGCACACCTTGTGAGTGCTC  
ACCGAAGAATCGCGCCGGGCCCCCTGCAAATCCAACGTTGGAGAAAACGCATGCGCAACCAC  
ACCGTCTGTGTCGGATACGGAACCAAAGGTGCTCCGCGGTGCTGCACTGCTTGGCGAC  
GGCGTCCCCGCCAACCAGATCGTTGTTATCGACACCGATCAAGTCTCCCTCGACGCCGCC  
AACAACAGCGGACTCGTCACCGTCAAAGGCTCCGCCACCAAAGCAGATGTGTTGCGTCTA  
GCTGGCGTGTACGAGCGCGCGCCGTGCTCGTGGCACCAGAACCTGGACGATACTGCAGTT  
CTGGTGACTCTATCGGTGCGAGAAATCGCGCCGAGGCAATGATTGTGGCCAGTGTCCGA  
GAATCTGAAAACCAACACCTCCTCGAACAATCCGGTGCGGACTCGGTTGTGATCTCCTCA  
GAAACCGCTGGCCGAATGCTCGGTCTGGCAACAGTTACCCCATCGGTTGTGGAGATGATG  
GAAGACCTCCTCTACCCGACGAAGGATTCTCCGTGCGCAACGACTAGTCGGTGAGGAT  
GAAATCGGCTCCAACCCACGACACCTCGCTGACATCGTCTCGGTGTTGTTTCGATCCGGT  
GAGCTCTACCGCATCGACTCCCCAGAAGCAGAACTGTAGAGCCCGCGATCGTCTCCTT  
TACGTTCCCGAGTATTTAGCGAGGAGGTAAATGACAAA

>RXA01737-downstream

TGAGAATTCTTCCCATCGGCCCC

>RXA01755-upstream

TCGTTGGCTTACATGGTCATTGATGACCGGGCTGAATATGTGAGAAAATCCATCCCTTCT  
TTAAGCAAGGGAGTGAATTACAGAAAAGGATTGTTTCAGCA

>RXA01755

ATGAGCACACCTGACATTAAAGAAGGCTCGGCAGAATCACCGGGCGAAGTAATGGTCGTT  
GGAGACAGGCGAGAGTGGCGTCGACAAGCAACCGGCATCATTGCCGGCCTCGTCTTAGCC  
GCCCTGGTCTATCTTCTTCCCCTCGAACTCCGTGGAAACCGTCATGCAATCCAGTGGC  
GTCGATCCAGAACTGAATACACCAACAACGCGATGCGTCTTACTGCTGCAGTCACAATC  
TTGATGGCAGTGTGGTGGATGACAGAAGCAATCCCACTAGCAGCAACCGCACTTATCCCG  
TTGGTTGCATTCCCTGCTTTCCAGGTTGTGGACTTTGGGAAGGCAGCA

>RXA01762-upstream

TGGAGTGATGAATTTTCTTATAGAACGTTTTTTAAACGATTGACTTTTTTAAACGTTTACG  
CTTTTAATGACTTCAAACGTGATCTAAAGCACAAAGGAGA

>RXA01762

ATGAAAGTGAAACCTCGGAATAGGAAGCTACCCACGACGCGAGGGCAACTGTTCCGACCAGAG  
TCCACTGCAATCGAATTCGAAGGCACAGCATCACCTACGGAGAATTCAGCAAACGAGTC  
AATCGGCTTGACATGCTCTTCTAGACCTCGGCGTTGCGCACCAAGATCGAGTAGCTTAT  
GTCGGATTCAACCACCTGCCCTGCTAGAAGTGTCTTTTCAACGAACCTCATTGGGGCA  
ACACCCGTGCTTGTTAACCTCGCCTATCGGCAAAACGAAATCGATTACATCATCCAAGAC  
AGCGGTGCGAGCATCGTGTTTTACGGAATCGACCTCATCGAGCACGCCACTTACCTCCAA  
GAACTCCATCCAGAGATCATCATGGTGGCCGTTGAAGGCGATGAGGGTCCAGGTTTTCGT  
CGAAAAGCGCTTATTGAAGCGGCGAGCGACGCCGACATCGACCTAGAAGTCAGCGATGAT  
GACCTGGTGTGCTCATGTACACCTCCGGAACCACTGGCCGCCCAAAGGGCGCCATGTTA  
TCCCACCGAAACCTCTTCTTTAACTACTTCAATGCCCTGCTCAGCCAGGAAATTGAACAA  
GGCGCGGTACTTTTATCCACTGCGCCGTTATTCCACATCGCGGGCCTCAACATGACCACC  
ATCCCCTGATGATGAAGGGCGAAAGGTGATCATCCACCGCAATTCGGGCGAGAGCAC  
GTCTTCGACGAAATCGAACGCTCCAAGGTATCCGAATCCTTCATGGTGCCAGCGATGATC  
GACATGTTGTCCAACCAACCATCATTTTGGCGAACGCGACCTTTCTTCCCTTCGCGCCATC  
ATGGTGGGCGGCTCTCCCTTAGCGAACGTGCGCTGCGAATCTGGCAAGGACGCGACGTA  
AAAATTGTCCAAGGCTTCGGCATGACAGAAACCGCACCGGGCGCCTGTATCCTCGAGGCA  
ACAGACACAAGCACACACCTTGAACCGCAGGTGAGCCCACTTCTTACCGACATCAAA  
CTAGTGGAACCGGAAACCGGCAAGAAGTCCCCACCGGAGAGGGCCGCGAAGTTCTCATC  
CGCGGACCACATGTGATGACCGGATACTGGAACCGACCAGAAGACACCGCCAGCGCACTA

CAAAATGGCTGGTACCACTCCGGAGATATCGCCATCAAAGATGAAGACGGCTACTACACC  
ATCAAAGACCGCATCAAAGACATGTACATCTCCGGCGGCGAAAACATTTACCCCGCAGAA  
GTC

>RXA01762-downstream  
TAAGTACCC

>RXA01764-upstream  
TTTTCAAAATTAATAGTTGACATTTTCAACGTTATGAGTTTTCATTGGTATCACGCCCCG  
ACGAAGTGTCTGGGATCACAAACCTTCAAAGGAGTTTGAA

>RXA01764  
ATGTCTCTCAATGGAAAAGTCGCCATCGTTACCGGATCTGGTGCAGGACTTGGTCGTTCC  
TTCGCTCAGGAGCTTGCCCGTCAGGGTGCATCTGTCATCGTCAATGACGTAAACCAGGCA  
GCCGCAGATGAGACTGTCGCAGCAATCACCGAAGCCGGCGGCAAAGCCGCCGCCGTTATC  
GCCCCCGTTGGACCCTCTGAAAGCGCCGCATTGCTGGTGCAGGAGCCGTCGACAAGTTC  
GGTTCTTTGGACATTCTTGTACAAACCGCGGCATCCTTCGTGATAGGTCCCTGCTGAAG  
ATGACGGACGATGATTTTCGATGCAGTCATTAACGTGCACCTCAAGGGCACTTTCACCTGT  
GTTTCGCGAGGCATTTGGATACTTCAAGGAGAATGGAATCGCGGGGCGCATCGTCACGATT  
GGTTCTCCACCGGGCAGCGCGGCAACTTCGGACAGAGCAATTACGCTGCAGCTAAGGCG  
GGCATTGTGGGTATGGTTTCGCACGTGGGCGCTGGAGATGAAGCGCGCAGGTGTACCAT  
AACCGCATCATTTCCGGAAGCAGCCACCGATATGACCAAGACGGTGCCATATTTCCAGAAG  
GCTGTAGAGGCCGATGAGCGTGGCGAGGCCATGCCAGCATTTCTTCCGCGAGACCCTAGGT  
TTTGGCACTCCTCAGGATGTTGCGGGACTTGTGGCCTTCTTCTCTGATGAGGCAGCG  
AATATTTCTGGACAGGCCATCGGTGCAGGCGGCGACCGCATGCAGGTGTGGAAGCACCCA  
GAGCCAGCAGTTACTGAATTTAACCCAGGTGGCTGGACCTATGAAGCACTGCAGGAACGT  
GGCAAGAACATTATTGAGGGCAACCTGCAGTCCGTCGGTGTCTGTTTCCCTGAACCTGCCG  
GCAGAGCTTCAGCCACAAATCCCAGTCAAGGCA

>RXA01764-downstream  
TAACACCGCACACCAAGAATTTT

>RXA01766-upstream  
GATGAGGTTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCT  
AGCACTGAGCGCGGATCTCAAGCAGAAAAGGTTCGTGCAAC

>RXA01766  
ATGCGTGATCCCATTCAGGTGCTGTTATTCCTTCTGATCTTTTTGGTTTCGCAGAAGTT  
CTCACCGAAGCCGAACGCGCAGTTCTTCTGGAAACCCGAGGGTGCTTGAGGAAGAGGTG  
AAGCCTTATATTAATGAGGCCCTGGGATAAGGCAGTCTTCCCCGATGAGATCGTGCAGCCC  
CTCCAAGATCTGCAATTGCTTGATCCGCTGCACTTCGGGAAGCAGGGGAGTCGGTTTCA  
GACATTTTCACTGGTTTCCGCAATTTTGAACCTCGCGCGCTGTGACATCAAT

>RXA01801-upstream  
TTTGGATTCCCTTTCCGATTATGTCTTGATCGCCCATCTGTGCATCCGGGTTGTCTAA  
CACCCGCGAAGATTTCTGTGATGTGCCACACTGGTTCTC

>RXA01801  
ATGTCTAACGTAGTGAACACTTTTGTCCAGAATTCACCGGTATGGTGGAGCTTAATCGT  
CCCAAAGCGCTCAATTCTCTTAATCAGGAAATGATCGATCTCGTTCAGGAAGCTCTAAC  
ACTTGGGCTGATGATGATCAGGTGCAGCAGGTCTCATTTACTCATCCTCGGAGCGTGCA  
TTTTGTGCCGGCGGTGATGTGCGCGCGGTCCGTGAGAGCGTGTTGGAGGGCGATGTTGCG  
GCCGGCGATAAGTATTTTCATCGATGAGTTTCGCGATGAACAACACGTTGGGAACCTATCCG  
AAGCCGGTCATTTCTGTGATCAACGGCGTCGCGATGGGTGGCGGAATGGGAATTTCCATG  
CATGGATCGCACCGGATCGTCACGGAAGAACGTTTCGCGTCGATGCCTGAGATGGCGATC  
GGCTATGTTCCCGATGTGGGCTTTACTTATTTTCGGTCAGCGTGCATCGTTCGCTGGCCATC  
GCCACATTTTGGCGGTGACCGGGTGGCGCATGAGCCCTGCCGATATGCTGTGGGCTGGC  
GTCGCAACGCATTTTGTGAGGATGCGCAGGGGTTTCATTGATGCGGTCTTGAACGAGTCG  
CTTGATGGCGCGCTGGAGAAATTTCTCCACGCAACCTACGGGCGAGCAGCGAGCTGGCCGGC  
GTCGCCAGCCAGATTGAGGAGACCTTTGGGCACAGCTCTTGGGCGCTTATCGACGCCTCC  
CTCCGGTCTCACCCGATGCTGAATTTGTTGCCAAGGTGGATGGGCTGATGGCGTCGGCA

GCACCGGCATCGGTGGTGGCTACCGTGAAGCTGATGCATCAAAACAGTGAGGCGACCACT  
 CTGCGTGAAGGCTTGGACAATGAATTGGCGATGTCTCTTTATATGATCCGCCAGCCTGAT  
 TTTGCTGAAGGTGTGCGTGCAGTGTGGTTGATAAAGACCGCAATGCAGCCTTCTCCCCA  
 GCCAACTACGAAGATGTTGATGAGTCACATTTTGTGACCTTGTTCAGCGCAGTTCA

>RXA01801-downstream  
 TAAAACCGCCAAACTTTTGATAG

>RXA01823-upstream  
 GCAACACGTTGATACTGAGCTGCACACGCCCCGTTGGCCTGGTGACCAGTTTGCTGGGCGG  
 GGTGTATTTGATGTGGCTTTTGAGCCGAAAGGAGGCATAA

>RXA01823  
 ATGCTGCAAGCGCATGATCTCACGCTGAGTTACGGCGGGCGAAATATTGTAGAAGGGCTC  
 AGTCTGGACCTTCCGAAAGAGGCCTCAGCATCATCATTGGCCCCAACGGATGCGGGAAA  
 TCAACCGTTTGAAGCGTTGGGCAGACTGCTGAAACCACAATTGGGGAAGATCACGCTA  
 GGTGGGCGAGATATTTCCAGCATGGGCACCAAGCATGTGGCGAAACACATCGGGGTGCTT  
 CCGCAACCCCCATATGCGCCCGATGGGGTGAGCGTCACGGAGCTGGTCAGCCGCGGGCGG  
 TATCCGCACCAACATCTGCTGTGCAATGGTCGAAAGACGATGAAGCCATTGTGGCGCGC  
 TCGCTGGCGGAAGTCGGCATGCACACCCATGCTGAGCATTTAGTGTGCGAACTTTCAGGC  
 GGGCAGCGCCAACGGGCGTGGATCGCCATGGCGCTCGCTCAGGAAACAGACATTTTGCTT  
 CTCGACGAGCCACACGTTTCTCGACGTAGCCACCAAATATCCGTCCTCGATTTATGC  
 TCCGACCTGCACCAACGTGGTCGCACCCTGGCCATTGTTCTACACGATCTGAACATGGCT  
 GCACGGTATGCCACCCACATCATCGCCATGCGGGACGGCACCATCATCGACCAAGGAAAA  
 CCCGAAGAAATACTCACTAAAGCGCTGCTCAAAGAAGTTTTTGACCTCGACGCACTCATC  
 CTCAAAGACCCCAACAACGGCCGACCACTCATCGTGCCACAGACAGGAGAACTCA

>RXA01823-downstream  
 TGAAAGAAACCGACAACCTACTG

>RXA01833-upstream  
 AAATATACCCCCAGGGTATCTTGACAGATTAAAGCTCGATGTTTTAGGCTCTACATATA  
 CCCCCACGGGTATCCCCTCAACTTTGATCTAAGGTGTCAC

>RXA01833  
 ATGCTTTTTGAACGCATCTACGAAGAAGGCCTCGCCCCAAGCCAGCTATTTTCATTGGCTGC  
 CAACGCGAAGGCAAAGCGATTGTTGTTGATGCTCGCCGAGATATCCAGACCTATCTGGAC  
 CTTGCAGCAAAAAACAACATGGTCAATTAGCGCCGTAAACCGAAACCCATATTCATGCCGAT  
 TATCTCTCCGGTACTCGCGAAGTTGCAGCTGCCACCGCGCCGAGATTTTCTCTCTGGC  
 GAAGGCGGAGCTGATTGGCAATATGGCTTTACAGGCACCACCTTGATGCACAATTCCACC  
 ATCAAGCTGGAAAAATATCACCATCACAGCCAAGCACACTCCCGGACACACTCCAGAGCAC  
 CTGTCAATTTTTGATTACTGATGGTGCGGTCTCAAAGGATCCCGGTTTTATGCTCAGCGGT  
 GACTTCGTCTTCGTAGGTGACGTGGGACGTCCAGATTTACTTGATGAGGCAGCTGGCGGC  
 GTGGACACCCGCTTCGCCGAGCACAGCAACTCTTCATAGCCTAAAAGAGCAGTTTCTT  
 GCACTCCCCGACCACATTCAGGTTTATCCAGGTCATGGTGCTGGCAGCCCTTGTGGCAAG  
 GCATTGGGCGCGATCCCTAGCACCAACCGTGCGATATGAAAAGGCTAATGCGTGGTGGGCT  
 CCATATCTGCGCAGTGATGATGAAGCCGGCTTTGTGGAAGAGCTTCTCGACGGCCAGCCA  
 GATGCCCCACGCTTACTTTGCTCGCATGAAAAAGCAGAACAAGCAGGGACCTGCAGTACTT  
 AGTACATTATCCCCGCTTGTGAAGCTAGAAGCCGAGGAAGTCGTCGAAAAGCTTGGTTCT  
 GAAGCAGTATTTGTGGATACCCGCGAGCAAAACCAAGTCCATCTCGGAACCGTTGTTGGG  
 GCATTGAATATTCCGCGCGGCGCCAAGGCGTCCAATTTTTCGCGCGTGGGTTATTGATCCT  
 CAAAAGGATGCTCAGGACCTTATTGTTTTGGCTCCGGACGCCAATACCGCTGCGGATTTTC  
 CGCGACGCTTTGCTGCGGGTTGGCATCGACACTGTGCGTTATTTACCAACAGTATCGAT  
 GGATTGCCTACCTTTGTGCCAGAATCATCTCCCCGCTGAGCTAGCTGAGACCAACTAT  
 GACGCACTGATTGATATCCGTGCAAAGTCCGAATTTGCGCGTGGCAGCATTCCCGGCGC  
 CAGCAGCTTTCTGGAGGTTTCGGCCATGTGGCGCCTCAATGAGCTGCCTGCGGGTGGCACT  
 TTGGTAACCTTCTGCCAATCAGGAGCGCGAAATACCGTGGTAGCCAATGCTTTGCGACGC  
 GCCGGATTACCGTTATCGAGCTCGAGGGCAGCTACGCCGCGTGGGAAAAATCAGCTGCC  
 AATCCTAAAAACTTGCAGACTGCCGTC

>RXA01833-downstream

TAGTTTTAGATCCGGCGCTGTAT

>RXA01853-upstream

GAATGTCCAACGTCAAAAAAATTCTTTTCTATCTTAACCGTATCTTCACACCTTGAGGGA  
ATGATGGGGGAGCGCCGCTTACGCACTACACTGTTTATTC

>RXA01853

ATGGAGATCCTCGGATTGCGGGCTGGTCCGTATAAAACAAATTGCTATGTGGTGCGCGGG  
GAGAATGAGGTCGCGATCATTGATCCTGGCATGCATGCCCACGATGATTTGGTGGAATAC  
ATCACCACGAATAATTTGAGCGTGGACAAGATTGTGCTCACCACGGACACATTGATCAC  
ACCCGTGATGCTGGTGTGTGGCAAAGCGTTTCAATGCGCCGGTCTATATCCATCCTGAT  
GATGCGTTTTTTCCTTGAGGTCTACAAGGGATCTGGAACAAAGACGGCCATGCTTTTCGAC  
GCCGACAACATGGTGTCCCCTGATCCTGAGTCACTGCGTGATCTGGTTGATGGTGAGACA  
ATCACTTTGGCTGGCGAAGAATTACGTTGAAGCATGCACCAGGGCATTACCTGGTTGT  
ACGCTGATCGTCGGCAAGGAATACTGCTTTAGCGGTGATGTGTTGTTCAAGGGCTCTATT  
GGTCGCACTGATTTTGAAGTGGTCTGATGCAGATGCCATGAATGAGTCACTACGCACGGCA  
GTGCTCCCACTT

>RXA01853-downstream

TGATGATGCATTGCAGATTCTTC

>RXA01881-upstream

ACCGGCCCTGCGGCTCAACCGCCGACCAGCGCGGCGCACACATTTTGAAGTGTTCATAA  
TAAAGACAACTTAAGTATCGGAGTCGAAGAAAAACCACA

>RXA01881

ATGGCCAATCTGATTAATCTCGAGAACGTCTCCAAAACCTGGGGATTAAAAACGCTTCTC  
GACGGTGTCTCCTTAGGTGTTCAAACCGGCGACCGCATTGGCGTCGTCGGCCTCAATGGT  
GGCGGAAAAACCACTGCTGGAAGTACTTACTGGCATCGAAAAGCCGGATCAGGGCCGT  
GTGTCTCACAACTCTGACCTGCGCATGGCTGTGGTGACGCAGCGTGCTGAAGTCAATGAT  
GACGACACCGTCGCTGACGTGGTGTGCTGGACCTTTGGGTTTGAAGTTTTCGAATGGGCA  
TCAAACGCCACGGTGCGGACGTCTCGGTGGCTTGGGCATTGTGATCTTGGCCTTGAC  
ACCAAGGTGGGGCAACCTTTCCGGTGGGCGAAGCGCCGACGCACCAACCTGGCCGCCG  
CGCTGGTTTCGCGACCTTGACC

>RXA01881-downstream

TGATCGTGCTCGACGAGCCACC

>RXA01894-upstream

AGAATTTTTTCGAAAATGCTGGCACCATCAACAGTGACATTGTTAGAACTTCAAGGAGA  
ACCCATGAATGAACCGGAGCAACATCACCGGTCCATGAGG

>RXA01894

ATGCCCAAACCCAAAAATAATGCGGGTCGAGATCTCAAAGCTGCCATTGCTGTGGGGATC  
GGACTGGGGGTCTGGTTCTTTTGGGGATTGTCTTAAGCCCATGGGGTTGGTACATCCTC  
GTTGCAGGTTTTATGGCTGCAGCAACATGGGAAGTTGGTAGCAGACTTAAAGAAGGCGGC  
TATCATTTGCCACTGCCGATTATGATCATCGGCGGTCAGGCAATCATCTGGCTGTATGG  
CCATTTGGCAGCATGGGCATTTTGGCGTCTTTTGTGGCCACTGTGTTGGTGTGATGTAT  
TTCCGAATTTTCTACAATGGCACGGAAAAAGAAGCCGCAACTATTTGAGGGACACCTCT  
GTGGGCATCTTCGTGCTCACCTGGATTCCATTGTTTCGGAAGCTTCGCTGCGATGCTGTG  
CTGATGCAAAACAATTCCATCCCGGGTACATATTTCAATTTGACGTTTCATGCTGTGTG  
ATCGCATCGGATGTGGGCGGGTATATCGCGGGTGTGTTCTTTGGATCGCACCCAATGGCG  
CCGTTGGTGAGTCCGAAGAAGTCTTGGGAAGGCTTTGCCGGCTCCATTGTCTTAGGATCG  
GTCACTGGTGCATCACTGTTCACTTCTGCTCGATCACCCTGGTGGATGGGTGTGATC  
TTGGGTTGTGCCCTAGTTGTGTGCGCCACGTTGGGTGACTTGGTTGAGTCGCAGTTCAA  
CGGATTTGGGCATCAAGGATATGTCGAACCTTCTTCCAGGCCACGGCGGATTGATGGAC  
CGTTTGGATGGCATGCTCCCGCCGCGATGGTGACGTGGTTGATCCTGAGTGTGATCAGC  
AGCTCGTATCCGTCG

>RXA01894-downstream

TAAAGCTTGGGCCAGCTTTAAGT

>RXA01897-upstream

CTATTTAGATCGTTCCGGAACCGATCCACGCGCCGATATCCACTCCCTGGATGAACTCTT  
TCACTAGGCTGGCCCTTATTGTTTCCGGAAGGGGTGCT

>RXA01897

ATGAAAATTGGTGTCATCCTGGGCAGTATCCGCGAAGGCCGCTTCGGCCAAGGCGTTGCC  
GATTGGGTTCATGGAACAAATCGGGGCTTATGACGCACCCGATGTGGAATTTGAACTCATC  
GACCTCAAAGCTTTCAACGTGCCCTGTTGGAATCCGCGACAGTTCCAGGTTCCGCGGAT  
AAACAGTACGACGACCCGCGCTAACTGCCTGGTCACAGGCCATTGATGCCTGCGATGCC  
TTCCTTTTCATCACCCCGGAATACAACCACGGTGTGCCCGGCGCTTCAAAAATGCGTAT  
GACATCCTGGGCAATGAATGGCTGAACAAAACCGTCGGTTTCATTTCTACGGTGCAGTC  
GAAGGGATCCGTGTTGTGCAACAGTGGCGTCAGATCGTCGCCACCTTCAACATGTACGAT  
ATCCGCGAGCCAGCTATCCTTTTCCACCTTACCAGAGAACAACAACGGCACTTTTGGCGCC  
AATGATCGACGCCCCGGTGAACATAATCCGCTCCTTGATAGCCTCCTAACGGCTGTCCGC  
GAT

>RXA01897-downstream

TAAGGCTCTGAAATACTAATGAG

>RXA01946

ATCCGCAAGTACTCCAGGCTCGAGGAACAATTCCAGTCGCTCGGCGGCTACGAAGCTGAC  
GCCGAAGCAGCCAGATCTGCGACAACCTCGGCCGAGGCACGCATCCTCGACCAGCAG  
CTTAAACCCCTGTCCGGCGGCCAGCGCCGCGCTCGAGTTGGCGCAGATCCTCTTCGCC  
GCCACCAACGGCTCCGGCAAATCAAAAACCACATTGCTTCTCGACGAGCCACCAACCAC  
TTGGACGCAGACTCGATCACCTGGCTCCGTGACTTCTGGCGAAGCACGAAGGTGGACTG  
ATCATGATTTTCGCACGACGTGCAACTGCTTGGCGCCGTATGTAACAAGATTTGGTACCTC  
GACGCAGTACGACGGAAGCCGATGTCTACAACATGGGCTTTAGCAAATACGTTCGATGCA  
CGTGCACTCGATGAAGCACGCCGACGCCGTGAGCGCGCAAACGCCGAAAAGAAGGCCGGA  
GCCCTCAAGGACCAAGGCTGCACGCCTCGGCGCGAAAGCAACCAAGGCTGCCGACGCTAAG  
CAGATGATCGCCCGTCCGGAACGAATGATCGACAACCTCGACGAAATCCGCGTAGCTGAC  
CGCGCCGCCAACATCGTTTTTCCAGAACACGACCCCTGTGGAAAACCCCACTCAACGCC  
AAGGGCCTGACCAAGATGTACGGCTCCCTCGAAGTCTTCGCCGGCGTCGACCTAGCCATC  
GACAAAGGCTCCCGCGTAGTCGTCTCGGATTCAACGGTGCAGGTAAAACCACCCTGCTC  
AAACTCCTCGCCGGTGTGGAACGCACCGACGCGAAGGCGGCATCGTCACCGGATACGGC  
CTCAAAATCGGCTACTTCGCCCAGGAACACGACACCATCGACCCCGACAAATCCGTCTGG  
CAAAACACCATCGAAGCCTGCGCCGACGCCGACCAACAAAGCCTCCGCAGCCTCCTCGGA  
TCCTTCATGTTCTCCGGGAACAACTCGACCAACCAGCAGGAACACTCTCCGGCGGTGAA  
AAAACCCGCTCGCACTGGCCACCCTCGTGCTCCTCCCGCGCAAACGTCTCTGCTTCGAC  
GAGCCACCAACAACCTTGACCCGATCTCCCGCGAACAGGTCTCGACGCACTGCGCACC  
TACACCGGCGCAGTCGTCTGTTACCCACGACCCGGGTGCAGTCAAGGCCCTTGAGCCA  
GAACGCGTCATCGTGCTTCTGATGGCACCGAGGATCTTTGGAATGATCAGTACATGGAA  
ATCGTGGAATTGGCG

>RXA01946-downstream

TAGGTTCTAAGGCTGTTTATGCT

>RXA01980-upstream

AGGATCGTACCAAATAAGGCAATAAACTCTTTTTACTTTTCTCAACTTCCTGAAAAGTC  
GCCGCCCTAGAATTCACTAAGTTTCCGATATCTTTAACC

>RXA01980

ATGCAGATCATTGATCTCTCTCATGCGTTCGCGCCCGGACAACCCCACTACCCTGGGGAT  
CCAGATCAAGAAATTAAGACGGTCTCCACGATTGAAAACGATGGCTTTTTAATGCATCAA  
TACAGACTTGTGGTCCCTGGGGAACGCATGTAGATGCACCTGCACATTTTCGATCCACAA  
GGTCGGACGCTTGATCAGATCCCTGTGGAGGAAACGCATTTACCCCTTATTGCCTGAGG  
TTTTCTCGCCCCGATCTATGTACTGCTGCTGATATAGAAGCGTTTGAACATACACACGGG  
AAAATCGAACCAGGATCCTTCGTGCACTCCACACTGGATGGGAATGGGGTAAACAAGGG  
ATCGCACCCGGCTGGTCTATCGAGGCTTTAGAAATCCTCCATGCCCGTGGAGTCATTGCC  
ATTGGCCACGATCTTCCCGATACAGATCCTTCACTGGAGGCACAGCGCTGGTGGCTGTGC  
CGTGACCATTGGCAGATTGAAAACCTACCAATTTGGACAAGGTTCTTGCAACGGGTGCG

ATGATTGCTTGTCTTGGCCAGTTCCAAAAGATGGTGCTAGTTTCCCAGTGCGTCCAATT  
GCTCTCGTCCCAGAGCACCTATCCCCTACTCGC

>RXA01980-downstream  
TAAAGCGAACGGCAGCACCTTCT

>RXA01983-upstream  
ATATCGCTGCCATGGCAGCCTTGCTGGGCAACCTCAAGCACACTGACCTAGAAGAGCTCC  
CCACCGATTACCAGGGGTGTCTCCCATGTCCGCTGCGTT

>RXA01983  
ATGGAAGGCTACGGACCTACCCAGATCGAAAAGCTCTTACCTGCATACACACAGGTCAAC  
ACAGCCGGGAATAATCCAGCGACGACGCTGAGCAAGATCTCCTCGGCGGAGCTGCAACC  
TCGCCGGAAAACCTACGACCACGCTGACGACGCTGACGCGGAGTCCGGTGCATCAG  
AATGCGGCACAGGCACCGCCCTTCTGATCATGCACGGCACTGGTGACCGGATGGTCCCT  
CCGGAGCAATCGGCTGCGCTGCACACCCATCTTGTGCAGGCTGGTCCGGCAGTCCACCCG  
GTACTCATTGAGGGCTTTGGCCACGGTTTCTCAATCCCGGGGAAGTCGCGGAGCTGGGG  
CCAAACGTTGACTAGACAATGGTGGGCTCGAGCGGGAGCCTCAGACAAATTTACGCGCG  
CAGCAGAGTCCGGGAAACCCCTTTGAACTACAGGGACTTGCCGCCGACCATGAGATGATC  
AAGCGCTTTTACCCCTGCACCTTCGC

>RXA01983-downstream  
TAAGACTCTACCTTACCCAACT

>RXA02020-upstream  
TTGGTCAATCAAGCGTGAATCCGGCTTCCATGAGCCAGTTGCCCGCCTCAAAGCTTGACC  
CATTTTCATAACAGTGCCATGTGGGTTTACGGTTGATAC

>RXA02020  
ATGGCTAAATCTAATGAAGGGCTGGGAACCGGACTTCGGACCCGCCACCTCACAATGATG  
GGACTCGGCTCCGCAATTGGTGCCGACTGTTCTCGGCACCGGCGTTGGTATCCGCGCA  
GCCGGCCCCGAGTGCTCCTGGCGTACATCATCGCCGGAGCCATCGTTGTGCTTGTTATG  
CAAATGCTCGGCGAGATGGCTGCTGCCCCGTCCCGCCTCCGGATCGTTTTCACGTTACGGC  
GAGGATGCTTTCGGCCACTGGGCTGGTTTCTCCCTCGGTTGGTTGACTGGTTCATGCTG  
ATTATGGTGATGGGCGCCGAAATGACTGGCGCTGCTGCCATCATGGGTGCATGGTTCCGGC  
GTCGAACCGTGGATTCCCTTCGCTTGTCTGCGTGGTCTTCTTCGCTGTGGTGAACCTCGTC  
GCGGTTTCGCGGTTTCGGTGAATTCGAGTACTGGTTCGCATTCAATTAAGGTCGCGGTGATC  
ATCGCTTTCCTCATCATTTGGTATTGCTCTTATTTTCGGATGGCTTCCCGGATCCACCTTT  
GTTGGAACCTCAAACCTTCATCGGTGATCAGGATTTCATGCCCAATGGTATTTCTGGTGT  
GCTGCTGGTTTGTCTCGCGGTGGCTTTTGCCTTTGGTGGCATTGAAATTGTCACCATTCGA  
GCTGCAGAGTCCGATAAGCCACGTGAAGCTATTTCCCTGGCGGTGCGTGCCGTGATTTGG  
CGTATTTACAGTCTTTTACTTGGGCTCTGTTTTGGTCATCACTTTCTCATGCCTTATGAG  
TCGATCAATGGTGCCGACACCGCTGCGGAATCCCCCTTACCCAAATCCTGGCGATGGCA  
AACATCCCTGGCACGGTTGGTTTCATGGAAGCGATCATCGTTCTAGCACTGCTTTCCGCT  
TTCAACGCCCAAATCTATGCCACTTCTCGTTTGGTATTTTCCATGGCGAATCGACAAGAC  
GCTCCGCGAGTTTTCAGTAAGCTCAGCACCAGCCACGTCCCCACCAATGCG

>RXA02029-upstream  
CGCAGTACACTACTTTTAGCAGTTAACCCGCCGAACCTTCTTGATTAAGTATTCATTGA  
GCGTTCTTGGCATAAATCCCACTGGAGGTGCATCAAACGT

>RXA02029  
ATGGCAGAGGCACGTTTGGCCATCTTGAACCCATTGATGTGGAAGAGTGGCCTGGGGTG  
GCGTCAGTGCCCAACCTAGCGTTTGCTGGTGACGCGCACGGCAAGCAGAATATCGATTT  
GCCAAGGCCTGCAGCAACGCGAGGTTTAGTTCTGCTAGGAAATGACCCGATCTCATTATT  
GATCATGAGGAATTATTTCTACGTTTGGCCGCATCGGGCTGGCTGGGGCTCGCTGAGAGC  
TACATGGCAGGCGAGTGGCGCAGCGAGAGGCTTGCCGACGTCTTGACCGCTTTGTTGGGA  
ACTGGGTTTAAACCCCGCGGCAAACCTATCTGGATCGTTTACCCTGCCAGGGCAAGCTGTG  
GATGCCGGAGGCGCACTACCCAAATGAACCTCATTCGTTTAAAGTTCAGGTGATGGCATGAGC  
GCATTTGGTGGAGTTTTTGCCTCCGGTGTTCGAACCACTTTACGTACCGCAGTGAAAAGC  
CATGTGCCGGGAGCTGGTTCGAATAGGGAGCCCGCATCTCACTTTGTGGATATCAACCAAG

ATCTCGGAGCCTGTGGCCGTGGAGCGTGAAGACCTCGGCGAGGCTCAGCGCCGAGCAGCG  
TCCTTTTTTGCTTGACGGCGCCAAAGTTAAAGCCGGAAGCCATGTGTTGGAGTTTCCCAGC  
AGTGGTGGAGCTTTAGCTATTTTGGCTGCTCGACGCCAGGGAAGTGTGACGCTTTAACG  
GCTGATCCCGCGCAAGTTTCAAGCCTGGAGGAGACGTTTGTGCTCGCCGGTGTGGAGGAG  
GATATTCACATCGAGGTCATTCCCCAGGCGATTCCCTCGCCACGCGAATGGGGTGGCGCC  
TACGATTCGATAGTCGCCATGGAGAAGCTAGAAGTGGTGGGCAAGCACGGTTCCAAGCGG  
TTTATTAAAGCTATCGACAGAATGCTCACCACCGGCGGCAACGTAGCCATGCAATCCTTG  
GTAGCTACTGACCAATGGAGTCCTGTGTGTTCTGAAGCGATTTCTTTGCTCAAGGCCTAT  
ATTTGGCCTGCGCTGCATTACCCAAGTGTGATGAAGTTCATCAGCTTGTGATAGGGAT  
TCTTCTCTGCGCGTGGTGAAGGAAACACACTTTCGCGGCCATTACCTAAAAAGCGTGCAG  
TTGCAACGTGAAGTGTGTTGAAGGCCAGATACGCGAAGCGGCGGAGATGGCTTTGATGCC  
GTCTACCGCGCATGTGGGTGTATCACTACGCGCTTATTGAAGCCCTGTTACGCTTGGGA  
TGTCTCAATGCAGTGCAATTTGCGTTGACGACAAGAAACAGAAGGGGGCGTCA

>RXA02029-downstream  
TAAGCAAAAATCTTTTAGACCTC

>RXA02030-upstream  
GCGCCTAACATCTCATTTGTATGGGATTGACTCTAATAATCTCCTGTGGAAACATCGCAAG  
GGTAATTATTGGAATCTATTATTGTGTGAGGCGATAACTC

>RXA02030  
GTGACCACAACTGATCACTCCACGGAGTTGAATCCTTCTGATCCAGGTGGGCAGACGGCA  
ACCCTAGTGATTGACAAGAAAACCTAAACGTGCGGTTGCAGCAGCCTCCACCATCGGCACA  
ACCATCGAGTTCTACGATTTTTATGCGTACGCTGCGGCAGCTGTCGTTGTTTTCCCAAGT  
CTGTTTTTCCCTGCCAATGACAACCCAACCGTGAACCTGTTGGCATCGTTTGCCACCTTT  
GGTCTTGCGTTGTTGCTCGTCCACTCGGTTCAATCATTTTCGGGCACTTCGGTGACCGT  
GTGGGACGCAAAGCTACCTTGATCGGTTCACTGCTGACCATGGGCATTGCCACCATCTTG  
ATCGGCCCTGCTGCCTACTTATGGTCAGGTCGGAATCATTGCACCGGCGCTGTTGGCGCTC  
ATGCGTTTTCTGCCAGGGCCTGGGCTTGGCGGTGAATGGTCTGGCGCTGCGTTGCTGGCT  
GGTGAAAACGCGGAAAACACTCACCGCGCTCGTGCTGCAATGTGGCCACAGCTGGGTGCA  
CCGTTTGTTTCTTCTTGGCCAATGGTTTTATGCTCATTTCTGGTGGTGTGCTTGCCCAT  
CAGGACGGCGATCTTCACGGCGCGTTTCATGACCTGGGGTTGGCGTCTGCCATTCTGTCT  
TCGGCGATCATGATCGCAGTTGGCCTGTGGGTGCGTTTCTCACTGGAGGAACTCCAGTG  
TTCAAGCAGGCTGTTGATCAGGGCAAGAAGGTGAAGTCTCCGCTCAAGGAGCTGTTCAAG  
ACTTCCCCTGCGCCTGTTGTGCAAGGCTACTTTGATCATGCTGTCCACTTATACCTTGTTT  
TACCTGGTTACCACGTGGATTCTGTGCTATGGCATCGGTAATCGCAGCACCGGAAACGGC  
CTGTCTATTCCGTACTTTGAGTTCTTGAGTTGCGAGTTGCGAGCTGGCCACCATCGTGTCTTCGCC  
ATCATGATCCCTGTGTGAGGCTGGTTGGCTGATGTGTGGGGTCTGTAACACACCTGACC  
TTGGCTTCTGTGCTGCTTCTCGGCTTTGGTCTGACGTTTAACTGCTTCTCGATCCAGAG  
ACCGCCACCAAGACCACCGTGTTCATCTTCTGTTGCTGGGCATGAGCATCATGGGTCTG  
ATCTTTGGACCCATGTGCGCAATTTTGCCGGAGCTCTTCCCCACCAACGTCCGCTACACG  
GGCTCCGGAATCGCTACAATGTCTCCTCGATCCTCGGTGCAGCTATTGCACCGTTTCATC  
GCAACGTGGCTGGTGTCCGAGTTTTTCAGTGGCGTACGTGCGCTATTACCTCATCATGCTC  
ACCGCAATTACCTTTGTTGCGGTGCTGACGATGAAGGAAAACAAAAACCACGACCTCCGA  
GAGGTC

>RXA02030-downstream  
TAAAAGATTTTGTCTTATCGACG

>RXA02073-upstream  
TCATTGTTTTAGAGGATGGCCAATTGACCATGATGGATACACCCAGCAACGTTTCCCAGC  
ACAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAACA

>RXA02073  
ATGATTTCCCGACTTCTCCAATTGGCTAAGAAAGTATGGCCGGAAGTGGAGCCTCCACG  
CTCCTGCGACTGCTCAATCAGCTACTCACCGCAGCACTCATTGTGTTCCCGCCTGGGTG  
CTAAGCCGCAAACAGACATCTCCCTGCTCGCCGTCGCCATCATCATGGCGCTCATCGCG  
CTGACAGCAGCTGTCTGTGCTGGGGTGGAGGATATGCGGCCACCGCGCTGCCTTTGGG  
CTGCTTGCCACATGCGCGTTATGCTTTACGACGCCCTCGTCCACAAAGGTTCCCTCTCG  
CCGATCCACGGCAGCGGTTGATCATGTCTGTTGCCACCCGTGACATTAACTCCATCGAA



GTATTCTTCGCGCACACCATTGGGCTACAGTCACCGCAGTGCTGCTCAGTGCGGGAGGC  
 GTGATCACGCTGGCAACGCTCGATCCCGTTGCTGGTCTAATTGGTTTACTCGGTGTCTC  
 ATCGCGTGGTTGATCCCTTGATTGGAAAACAATCCTCAAGCAGTGAAGCCACATCACGT  
 GGACACATCGCCAGCACCTCACCGAAGATGCCGCCGGCAGGCTTGAAATCAACTCACAT  
 GGAGCGCAAGCCACACGGTTAAATGCGCTCGAGGTGAAAGAGCAACAACCTGGAACAAGTT  
 GTGACCCGACAGGGCTTGATCGTCGGTATCCGTGAGGGCGCAGCACTTTTATGGCCGTGG  
 ATATCAGCTGTGTGTGGTTGCTCTGGTTCCCTCATGTGGGCATTGTTGCAGCCGCGATT  
 ATCCTGGGCATCTCCCTGCGTTGGATGCAGTTGAGGGATTTGCTCGCACCATGCCTACC  
 GCGTTAAACAGTGCGCAGCGGTATTTCCAGATCATCGATGCCCTGTTGCTATCGCTGAA  
 CCTGACGAGCCGAAGCCTTTGCCAAAGGCCGCTTAAGCTGCGAATTTCTAGAGTTCCA  
 GTCAGCGCAAAGGGCACCCTGTCTTTAGAGGTTGAGCTGGTGAACACATCGGCATCATC  
 GGATCCAGCGGTAGTGGAAAATCCACTTTGGCCAAACTCATCCTCAAGCTGGCGCAACTA  
 CGGTCTGGAACCATCACCATCGGTGGTGTGATATCGCAGAGGTTTCATCGGCGGAGCTT  
 CGCAAATCCGTACGCTGGTTGAGCAGAAATCTGTGCTGTTTAGAGCAAGCGTGCTGGAG  
 AATTTACGGATGGGCAATCCAGAGCTGTCTGAAGATGAAGCAAGGGAAGCCTTGAGGTTG  
 GCGTCGATAAGCGAACTGCCTTTAGATGCTGACGCCCTGCGCCTATCTGGCGGACAGCAA  
 CAACGGCTCTGCCTGGCGCGTGCTTTGGCACGACCCCTCAGGTACTGATTGTGATGAA  
 GCCACCAGCCACCAAGATGCGCTCAATCAAGCGGATCTTTCCAGACTCTGGCCACGCTT  
 AAAGACACCACGGTGATCATATTGCGCACCGCACAGCTGCATTAACCCATGTGGATCGG  
 ATAATTGACCTGGAAGAAATCAAAAATCC

>RXA02073-downstream  
 TGATCCTTAACGCGGATCAGGGG

>RXA02074-upstream  
 CGGGGGAAGGCCGTGTCGATGCTCGGGCTAGCCTTGGATCTCAAGAAGAATTCGACTGG  
 TTTAAAGTCTGGGCTTTAAGTGCAGAAAGGTTGTGGATTG

>RXA02074  
 ATGCGCTCCCTGCTTCGTGATATCCCTGCGGTGGGTTGGCTAATCACCGCGACGATTGTT  
 GTGCGCACGCTCGTTGTTGCGCTGGTCATCGTTGGGATCGGCTTGCTTATCGACGTCCCC  
 TCGCCCGCTCATTACGCCATGTTGTGGTGGGTTCTGGCAGGTGCCACGGCAGCAGCTGCG  
 CTGCTGTGCGCGGAAGCGGTGCTCCCCAACGTATTCGTGCACGAGTTGAACGATCCTGG  
 CGGCGGCAGTTGGCTGCTAAAAATCTGGAGCTGAATTCCAGTTCGTGAGATGATGCCAG  
 TTGATCACACTGGCAACTGAAGCCACCTCAAAAGCATCCACTTACACAGTGATGTTTCTG  
 GGGCCTTACTTTGCAGTATTTTTGGCCCCACTGACAGTTATTGCCGTTGTGCGCGCGGCT  
 ATTTCCCTGGCCGATGTTGAAAGGCGCTGGCGCGGGATACGGGCGAGCATCTGGGCAG  
 TTGGCAGGCGTGTTTTTGGAAATCGGTGCGCACACTAGGCACACGATGATGCTGAATGCC  
 GCTGGGCAGCGCAGGCAGATCATCACACAGCGCGCAGAGAATATGCGCTCCCAAGTGATG  
 TCATTGCTGTACCGAAATCAGTTGATGATTCTGGTGACCGACGGCGTGTTTGGAGTTGCC  
 ACCACAATGGTTGCTGCGGTGTTTGCCATTGGAGGATTCTTTTCAGGCTCTCTTACTCTC  
 GGCCAAGCTGTAGCACTCGTATTGCTGGCCAGGCTGCTTATTGATCCCATCAACCGCATG  
 GGTGCGACGTTTTACACCGCATGGCAGGCAACCCCTCGCTGATCGCCATTGAAAAAGCC  
 CTCGCGACAACCTTTACTGATCAGCCAACTCAACAGGGACAGCGCCACGATGGGGATCTG  
 GTGGTCAACAACCTGAAGATCGCCGCGATCACAGGGACATTGTGCACGGTATCTCTTTC  
 AGCATTTCCCGCGGTTCCACATCGCGGTGGTAGGTCCCAGTGGCGCTGGTAAATCCCTCT  
 GTGGCTCTAGCGTTGTCCGACTTTTAGAGTTTGTGTTGCGATTTCCTCGGCGGCGAC  
 AACTGTGAGATGTTAGATCTTCGCGCCTCAGTCAGTTTCGTGCCCCAATCCCCCACGCTG  
 TTTAGCGGAAGCATCAAAAGCAATATCGATCTGGCGCGCACGGGTGTTGATTCTGATCAC  
 ATCCACGCAGCACTTTTAGGCGAAGAACTCCCCGCGGACCTCAAAGTCGGTGAAACCGGC  
 AAAGGTGTCTCCGGCGGCCAAGCAGCACGATTTCCATTGCCCCGAGGTTTAGTAAAGAAT  
 GCTGCCGTGATTGTTCTCGACGAGGCGACCGCACAACCTCGACTACACCAACGCCCCGCGAG  
 GTTCGACATCTTGCCAAATCCCTTGAGTGCACGTTGGTTGAGATACCCACCGCCCATCA  
 GAAGCCCTCGATGCAGACTTCATATTGTTTTAGAGGATGGCCAATTGACCATGATGGAT  
 ACACCCAGCAACGTTTCCAGCACAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAA  
 CAA

>RXA02074-downstream  
 TGATTTCGCGACTTCTCCAATTG

>RXA02095-upstream  
CTCTCTTGGTCCTCTCCCCACCCATTTTAAAGTACTCAAGACCCTTCCAACAGAAAGGAT  
TACTCCCCAACAGGCTCAAAAATACTGAAAGGCTCACGC

>RXA02095  
ATGAAAACCTGAGCAATCCCAAAAAGCACAATTAGCCCCTAAGAAAGCACCTGAAAAGCCA  
CAACGCATCCGCCAACTTATTTCCGTGGCGTGGCAGCGACCTTGGCTCACCTCATTACCC  
GTAATCAGCGCTTTAGCTGCAACGTTGTTTGAACCTACACTTCCTCTTTTGACCGGTGGC  
GCCATCGATATCGCGCTCGGAAATACCGGAGATACTTTAACCCTGACCTGCTGGACCGG  
TTCACTCCGAGTGGATTAAGCGTGTTGACCAGCGTCATTGCCCTTATCGTGCTTCTCGCG  
TTGCTTCCGTATGCCAGTCAATTTGGACGGCGATACACCGCAGGCAAGCTCAGCATGGGG  
GTACAGCATGATGTCCGGCTTAAACGATGCGCTCATTGCAGAACCTCGATGGGCCAGGT  
CAGGACTCTATTTCGCACAGGCCAAGTAGTCAGTCGGTCCATTTTCGGATATCAACATGGTG  
CAAAGCCTTGTGGCGATGTTGCCGATGTTGATCGGAAATGTGGTCAAGCTTGTGCTCACT  
TTGGTGATCATGCTGGCTATTTCCCCGCCGCTGACCATCATCGCTGCAGTGTTGGTGCCCT  
TTGCTGTTGTGGGCCGTGGCCTATTTCGCGAAAAGCGCTTTTTCGCTCCACGTGGTTCGGCC  
CAGCAAAAGGCTGCGGATCTGACCACTCATGTGGAAGAACTGTCACGGGTATCCGCGTG  
GTCAAGGCATTTGCGCAGGAAGACCGCGAGACCGACAAATTGGATCTCACCGCACGTGAG  
TTATTTGCCAGCGCATGCGCACTGCACGTCTGACGGCAAAGTTCATCCCCATGGTTGAG  
CAGCTTCCGCAGCTTGCTTTGGTGGTCAACATTGTTGGCGGTGGCTATTTGGCCATGACT  
GGTCACATCACGGTGGGCACGTTTGTGGCGTTTTCTTCTATCTCACTAGCTTGTTCGGCG  
GTGGCTAGGTCCCTGTGCGGCATGCTCATGCGCGTGCAGTTGGCGCTGTCTTCTGTGGAG  
CGCATTTGAAGTCATTGATCTTCAGCCTGAACGCACCGATCCTGCACACCCCTGTCA  
CTTCCCGACACTCCCCCTGGGTCTGTGCTTCAACAACGTAGATTTCCGTGGGATTCTCAAC  
GGTTTTGAGCTGGGTGTTTCAAGCCGGTGAAACCGTTGTGTTGGTGGGCCCTCCAGGTTCA  
GGCAAGACCATGGCTGTGCAGCTTGTGGAACCTTTTATCAACCAGACAGCGGCCACATC  
GCCTTTGATAGCAACGGCCATCGCACTCGCTTCGACGACCTCACCCACAGCGATATCCGC  
AGGAATCTCATCGCGTTTTTGTATGAGCCGTTCTTGTACTCCTCCTCCATACCGCGAGAA  
CATCTCGATGGGTTTGGATGTCAG

>RXA02095-downstream  
TGATGAGCAGATCGAACACGCAG

>RXA02099-upstream  
TAGTTAGAGCTGGTTCAAGGGGTGTCAATCCCAAAAGGCACTCCTTGAACCTCATGAAAA  
GCTTGACAAAACCTTCAACGTCAAAGGAGGTATCCACGCT

>RXA02099  
ATGGGTGCAGATCAAATTGCAGCAGTCTCCGGCAATTGAGCTTGGATGCTGATGTCCGCG  
TCGCTCGTGCTGCTAATGACACCAGCACTGGCACTTTTCTATGGCGGCATGTCTCGTCAA  
AAGTCCGTGCTCAACATGATGATGATGTCTTTGGAGCATTGGGCGTCGTTACTGTTATT  
TACCTCTTGTGGGGATGGTCGATGTCTTATGGAACCCAATCAATCGCGGGAATCTTTGCT  
AACCCTTTTGTAGTTCTTCGGTCTTAAAGATTCC

>RXA02115  
ACCCGCGCAACCAAAAGTGTGGAACAGTTCTCGCACTCCTGTGGTTCGCAATTGTCCTC  
GACGGCTTTGACCTAGTCGTCCTGGGTGCAACAATCCCGTCCATGCTGGAGGATCCCGCG  
TGGGATCTCACTGCTGGACAGGCCACACAGATTTCCACCATCGGCCTCGTCGGCATGACC  
ATTGGCGCACTGACCATCGGTTTCTTAACGGACCGTCTGGGTGACGCGGTGTGATGCTG  
TTCTCTGTGGCAGTATTTTCTGTATTCACTCTCCTGCTGGCATTACCAACCAACGTCCAG  
CTCTTCAGCCTGTGGCGTTTCTTCGAGGTGTTGGCCTTGGTGGAGCACTCCCCACCGCA  
ATTGCCATGGTGACCGAGTTCCGCCCCGGCACCAAGCGGGCTCTGCATCCACCACCTTG  
ATGACCGGTACACGTCGGCGCAGTAGCAACCGCTTCCCTGGCCTCTTCTTATCGAC  
GGCTTTGGTTGGCACTCCATGTTTCATCGCAGGTGCCGTACCAAGGACTGATCTGTACCA  
CTGCTGTACTTCTTCTTCCAGAATCCCCGCACTACCTCAAAATCTCCGGCAAGTTGGAT  
GAGGCGCAGGAGTTGCAGCATCTTATGGACTTTCCCTGGATGATGATCTTGATCGCGAA  
CACGAAGAAGAACTCGGCGAGTCTCCTCACTTTCTCCTGTTCAAGCCCTCGTTCCGC  
CGCAACACCCTGGCGATTTGGGGCACCTCATTCATGGGACTCCTCCTGGTCTACGGCCTG  
AACACATGGCTGCCACAAATCATGCGCCAAGCAGACTACGACATGGGTAACTCGCTTGGA  
TTCTCATGGTGCTCAACATCGGCGCAGTGATCGGCCTTTATATTGCAGGGCGAATTGCC  
GATAAGAACTCCCCCTCGCAAAACAGCACTCGTATGGTTCGTGTTCTCTGCATTTTCCCTC

CGCTTGCTTGCTGTCCGGATGCCACTGATCGGTCTGTATGGCATCGTGCTGCTCACC  
 ATCTTTGTGTTACAGTCCCAGGTACTCATCTACGCCTTCGTTGGTGAGAATCACCCTGCC  
 AAGATGCGCGCAACCGCCATGGGATTCTCCGCAGGAATTGGTGCCTCGGCGCCATCTCT  
 GGCCCGTTGCTTGGTGGTCTGCTTGTCTAGTGCCAACCTTGCTTACCCATGGGGCTTC

>RXA02128-upstream

TATTAGCAAACTTCTTAAAGAGCCTTTTTGTGCCTTTATCCGAGTATCTTTAAAGCAT  
 GAGTATTAAGTGGGCGCGCTTTGTACCGGGGATAACCGCG

>RXA02128

ATGCGGGGCTATCAACGATCCTGGTTGAAGGGTGATGTCATCGCGGGGTATAACCGTGGCC  
 GCGTACTTGGTTCCACAAGTCATGGCTTATGCCGTGATTGCGGGGCTGCCAGCTGTCGTT  
 GGTCTGTGGGGAGTTCTGGCTCCCATGGCGCTGACTTTTTCTTGGGCACGTCTCGAAAT  
 CTCTCGGTTGGTCTGAATCAACCACCGCTCTGATGACGGCTGCAGGTGTGGGAGCTTTA  
 GTCGGGGCAGCTGGCGGGCCTGAACGATACGCAGAAGTAGCGGCACTATTGGCTATTGCA  
 GTGGGCATTGTATGCGCTGTTGGTTTTATTGGCCGATTGGGATTCTTACCAGGCTGTTG  
 TCTCGACCGGTGCTCGTTGGATATTTGATCGGTATTGCAGTCTTGATGATCGTCAGTCAG  
 CTGTCCAAAGTCACCCAGGTGAATGTGGAGAGCGGTCAGACGTGGCAGGAAATAATATCG  
 TTTATCAAAGTAGCTGGCCAGGCACATATTCCTACAGTGATTTTGGCAGTCGTGGTGTG  
 AGCTTGCTGTATCTGGCAAATTGGTTGACGCCTAAATTTCCAGCACACTCATGGTTCTT  
 CTGCTTTTCGGCAGCCGCGGTGGGGTTTTTTCATCTGGATAGGTTTGGTCTTGAGGTCATT  
 GGTGAGGTGCCCCGTGGCCTGCCTCAACCAAGTATTCCTCGATTGGCGATCTAGAGATC  
 TGGTCGTTGTTGCCCTATGCCGTGGGTATTGCCATCGTTGGTTTTTTCAGACAATGTGTTG  
 ACTGCTCGTGCATTGCGCTCGGGAAAGATGAGGTGATTGATTCCAACCAGGAGCTGCTC  
 GCACTGGGAACCGCAAACCTGGCGAATGGGTCTTCCAGGGATTTCCTGTGTCATCGAGT  
 GGCTCCCGAAGTGTCTTGGAGACACGGCAGGTGCTCGCACTCAGGTGCATTCACTTGTG  
 GTGGTGGCGCTGGTGATCATGGTGCTGTTGTTTGTGCTGGTCTGTGCTCGAGTCTTTCCCA  
 GATGCGGCACTTGGCGCCTTAGTTATTTATGCAGCAACGCAGTTGATTGATATCGCAGAG  
 ATCAAAAGGATCGCACGTTTCCGCAAGAGCGAGTTGGTCATCACAGCGGCTACTGCTGCA  
 TCCGTTGTGGCTTCTGGCGTGCTCGCGGGGATCGGCGTTGCGGTTACGTTGTCCATCTTG  
 GATCTCATCAGACGTTTGGAGGATTATCCTGAGTCGACAGCAGTCGAAGGGCTCGTGGTT  
 GCTGGAATGCACAGCTTGGAGGATTATCCTGAGTCGACAGCAGTCGAAGGGCTCGTGGTT  
 TTTAGATACGATTCCCCACTGTTTTTCGCCAACGCTGATGATTTTTCCAAACGTGCCATC  
 GAAGCCGTTGATGAAGCAACTCAACCCGTGCATTGGTTTTTACTGAATGCTGAAGCGAAT  
 ACGGAAGTTGATCTCACGGCCGTCGATGCCATGGAAGCACTTCGCAAAACCTGGAGGAA  
 CGGGGTATCCGATTTGCGATGGCCCCGGGTGAAGCAAGATCTACGCCGAAGCCTCGAGCCT  
 GCAGGTTTCATTGAATCCGTGGGGGAGGAGTACATTTTCGCCACACTCCCCACTGCAGTC  
 AAGGGGTATTCCGTGGAGTTTCGCGATCGTTTTTGAAACTATCCAGAAGGCGTTCCGAAA  
 GAAATTTTGGAACCT

>RXA02128-downstream

TAAGCTGCCTGGTTGGCGGACTT

>RXA02133

GAAAACCCCTACATTGGCGGAGCTGGATACAACGCAGCAAAATTCGGTGTAGCAGCATTC  
 AACCGTGTGCTTCGCTTGGAAACCCACCAGCAGACCCTTCGCGTATCTGAGATCGATCCA  
 GGTGAGTTGCCACGGAAGAATTCCTCGTTTCGTTTCGGCGGAGATAAAGAACGCGCA  
 GAAGCAGTCTATGACGACGTCCTCAACCTCACCGCTGAAGACATCGCAGAGTCTGTGCGT  
 TGGGTCGCGAGCCTTCCAAAGCACATGAACATTGACCGCATGCGTATTACACCTCGCGAT  
 CAGGTC

>RXA02133-downstream

TAAAACCCGCACTCTTTTGAAAT

>RXA02150-upstream

GTGTTTTTCGGTGGGCTGCGATGACGCATGTCCACCAAAGAGCCACCCCTTAAAGAAAT  
 TAAAAAGTGGTTTTGGTAGCTTCGCAGCAAAATACACATC

>RXA02150

GTGGGTAACGTATTCTTAGAAGTTCCTACAGCAGTAAAGCGCGAAGAAGGGGTAAACCCA  
 AACATCATGAAAAACAACCTGGTATCGGCTTTTCAAGTATGTGCTAATTGGCCCCGTTTTTG

CGTGTGTACAACCGCCCCGAGATCGAAGGCCAAAGAAAACATCCCTGCAGAAGGTGCCGCG  
ATCATGGCGTCCAACCACGAAGCAGTGATGGATTCCCTTTTATTTTCCCCTGCTGTGCCCA  
CGGCAGCTGACCTTCCCAGCGAAGGCCGAATACTTCACATCACCAGGTATTAAAGGCAAG  
ATGCAGAAGTGGTTTTTACTTCTGTGGGGCAAGTACCCCTGGACCGCACCGCAGATAAT  
GCCATGGATTCTTTGATGAATACCGCCAAAATGGTGGTGGATCGGGGAGACCTCTTCGGT  
ATTTACCCCTGAAGGATCTCGTTTCGCCCCGATGGTTCGCATCTACAAGGGCAAACCGGAATG  
GCCTATGTTGCGATGGAACTGGTACGACAGTTATCCCCGTGGCATGATTGGCAGCCGG  
GACGCGAACCCTATCGGAAGTTGGTTTCCGAAACCCGCAAAAGTCAGGATCAAGGTAGGA  
AGCCCAATTGATCCCCTCGCATTTCGTCAAAGAACATGGGTTGAAGCCTGGAACCTACGAA  
GCAGCGCGCAAGCTGACAGATCACGTTATGTTTCATTCTTGCTGATCTCACTGGTCAGCCG  
TATGTTGATGCGTACTCTAAAGATGTGAAAAACGCTCTGGAGGAAGGAAAAGGATACCCG  
GAGGGCACAGCTCCTTCACAG

>RXA02150-downstream  
TAATCGGGTCTTTTCTGTAAAA

>RXA02171-upstream  
AACCACATTTCGTCACTTACTTACATCTATGTCATGTTTGCGAACAAGAACTTGGAGCCTCG  
TCAGGCTGCTATTCGCCAGAAGATGGAAGGTTAATCAGAT

>RXA02171  
ATGAATTCCACTATTCTCCTTGACACAAGACGCTGTTTCTGAGGGCGTCGGTAATCCGATT  
CTTAACATCAGTGTCTTCGTCTCTTCACTATTGTTGACGATGACCGTGGTGCTTCGCGTG  
GGCAAGAGCACCAGCGAATCCACCGACTTCTACACCGGTGGTGCTTCCTTCTCCGGAACC  
CAGAACGGTCTGGCTATCGCAGGTGACTACCTGTCTGCAGCGTCCCTCCTCGGAATCGTT  
GGTGCAATTTCACTCAACGGTTACGACGGATTCCCTTACTCCATCGGCTTCTTCGTGCA  
TGGCTTGTGCACTGCTGCTCGTGGCAGAGCCACTTCGTAACGTGGGCCGCTTCACCATG  
GCTGACGTGCTGCTTCCTCCGACTGCGTCAGAAACAGTCCGCGTCGCTGCGGCCTGCGGT  
ACCTTCGCGGTTACCCCTCTTTACTTGTATCGCTCAGATGGCTGGTGCAAGTTTCGTTGTG  
TCCGTTCTGCTGGACATCCACGAGTTCAAGTGGCAGGCAGTTGTTGTGCGGTATCGTTGGC  
ATTGTCATGATCGCTACGTTCTTCTTGGCGGTATGAAGGGCACCATACGTTTCAGATG  
ATTAAGGCAGTTCTGCTGGTGGTGGCGTTGCCATTATGACCGTTCTGACCTTCGTCAAG  
GTGTCTGGTGGCCTGACCACCCTTTTAAATGACGCTGTTGAGAAGCACGCCGCTTCAGAT  
TACGCTGCCACCAAGGGGTACGATCCAACCCAGATCCTGGAGCCTGGTCTGCAGTACGGT  
GCAACTCTGACCACTCAGCTGGACTTCATTTCTTGGCTCTCGCTCTGTGTCTTGGAACC  
GCTGGTCTGCCACACGTTCTGATGCGCTTCTACACCGTTCCTACCGCCAAGGAAGCACGT  
AAGTCTGTGACCTAGGCTATCGTCTCATTGGTGGCTTCTACCTGATGACCTGGTTCCTT  
GGTTACGGCGCTGCGGCACTGGTGGTCCAGACCGCGTCATTGCCGCACCAGGTGCTGCT  
AATGCTGCTGCTCCTCTGCTGGCCTTCGAGCTTGGTGGTTCATCTTCATGGCGCTGATT  
TCCGCAGTTGCGTTTCGCTACCGTTCTCGCCGTGGTTCGAGGTCTTGCAATTACCGCATCC  
GCTGCTGTTGGTACGACATCTACAACGCTGTTATCCGCAACGGTCAGTCCACCGAAGCG  
GAGCAGGTCCGAGTATCCCGCATCACCGTTGTCGTCATTGGCCTGATTTCCATTGTCCTG  
GGAATCTTGCAATGACCCAGAACGTTGCGTTCCCTCGTGGCCCTGGCCTTCGCAGTTGCA  
GCATCCGCTAACCTGCCAACCATCCTGTACTCCCTGTACTGGAAGAAGTTCAACACCACC  
GGCGCTGTGGCCGCTATCTACACCGGTCTCATCTCCGCGCTGCTGCTGATCTTCTGTCC  
CCAGCAGTCTCCGGTAATGACAGCGCAATGGTTCCAGGTGCAGACTGGGCAATCTTCCCA  
CTGAAGAACCAGGCCTCGTCTCCATCCCACTGGCATTCATCGCTGGTTGGATCGGCACT  
TTGGTTGGCAAGCCAGACAACATGGATGATCTTGCTGCCGAAATGGAAGTTTCGTTCCCTC  
ACCGGTGTCGGTGTGAAAAGGCTGTTGATCAC

>RXA02171-downstream  
TAAATCTAGTTTCTGAAGTTATT

>RXA02173-upstream  
CTAAATTGGGCTTAGATCTTCGCTCTAAATAGGTATGCAGAGACATTCTGAATTAATTA  
ACAAAGCCATTTTTCGGCCGTGGAGAAGCGTTTTCCGACT

>RXA02173  
ATGGTGTGGGGCATGGAACACACTTCAGCATTGACGCTCATAGACTCGGTTTTGGACCCT  
GACAGCTTCATTTCTTGGAATGAAACTCCCCAATATGACAACCTCAATCAAGGCTATGCA  
GAGACCTTGAGCGGGCTCGAAGCAAGGCCAAATGCGATGAATCGGTAATTACTGGAGAA

GGCACCGTGGAGGGCATTCCGGTAGCCGTTATTTGTCCGATTTTTCCTTCCTCGGCGGT  
TCTTTGGGCACGGTCGCGTCGGTGCGCATCATGAAGGCGATTACCCGCCACAGAGCTG  
AAACTCCCCTGCTGGTCTCCCTGCTTCCGGTGGTGCGCGCATGCAGGAAGACAATCGA  
GCTTTTGTGTCATGATGGTGTCCATAACCGCGGCTGTGCAGCGTCACCGCGAGGCGCATTTG  
CCGTTCTGCTGATTTTGCAGCAATCCACGATGGGTGGCGCCATGGCCTCGTGGGGTTCA  
TCTGGGCATCTCACTTTTGCAGAACCCGGCGCGCAGATAGGTTTCTGGGTCTCGCGTG  
GTGGAGTTAACCCTGGGCATGCGCTTCCAGACGGTGTGCAGCAGGCGGAGAATTTGGTG  
AAACTGGTGTGATTGATGGAATTGTGTGCCACTCCAATTGCGTGCAGCGGTGGCAAAA  
ACCCTCAAGGTTATTACGCCGGTAGAGGCAACGGATCGTTTTTCTCCAACAACCTCTGGC  
GTGGCACTTCCGGTGATGGAGGCGATTGCGCGTTCTCGTGACCCGCAGAGGCTGGAATC  
GGGAGATTATGGAACGTTGGGGGCAGACGTCGTCAAGCTTTCTGGTGCGCGTGCTGGC  
GCATTGAGCCCCGGCTGTGCGCGTTGCCCTGGCGCGCATCGGGGGCCGGCCCGTGGTGTG  
ATTGGGCAGGATCGCCGCTTACGCTTGGGGCCGAGGAGCTGCGTTTTTGGCGCTCGTGGC  
ATTTGCGTGGCGCGCAGCTAAACCTGCCGATCGTGTCCATCATCGACACCTCCGGCGCC  
GAATTGTGCGAGGCGGCTGAGGAGCTCGGCATCGCAAGCTCGATTGCGCGCACCTTGTCC  
AAGCTTATCGACGCTCCCTCCCCACCGTTTCCGGTCATTATTGGTCAGGGCGTTGGCGGT  
GGCGCGCTGGCCATGCTGCCCCCGCATCTGGTCTACGCGGCCGAAAACGCGTGGCTGTCC  
GCATTGCCACCAGAGGGCGCCTCGGCCATCCTCTTCCGCGACACCAACCACGCCGCGGAA  
ATCATAGAGCGACAAGGCGTGAGGCGCACGCACTTTTAAGCCAAGGGCTTATCGACGGG  
ATCGTCGCGGAAACCGAGCACTTTGTTGAAGAAATCTCGGCACAATCAGCAACGCCCTC  
TCCGAATTGGATAACAATCCGAGAGGGCGGGACGCGACAGTCGCTTACACGATTTGAG  
CGTTTAGCGCAG

>RXA02173-downstream  
TAAAGAAAATTATGCGCTGATCA

>RXA02224-upstream  
GCTTCGTCGAGGCGGAAACCGTCGTCATTACGTCGAACCCGACGTGGCACGGCGTCGC  
AAAGCAGATGCAATCTGATTTTTCGGAAGGGTGAAGTAG

>RXA02224  
ATGGCGCAGCATGAGCGGTTGCGGATGCGCTGCAGCCGGCGTCGTTGGCGGAGTCGTGG  
CGTGAGCTGAAAACGATGCCTTCCGGGGCCCAAGGCCTGGTGGTATGTGAGTTTTCGTGGTT  
ATTAGCGTGGTCACGGTCGTGGCGATGGTCCGCACGTCCAACCTGTTGGGCTATTCCGTT  
GATCTGATCAATGGGCAGTCGTTGCCGCTGATCGGTTCAAGATCGACCGCAATGATCTGG  
TTGCTTGGTTTGGTGCGCTGGAATTTTAGCAGAAACTGCCGGTCGCGCGCTGCTGCAA  
TTGGTGATCAACACCTTGGCACGTCGCTGTGCGGTGGATCTGCGGAAAGCTGCGCTGTCT  
TCGGCGTTGCGTGACCGGTTCTGATGTGATGGAATTGGGCACGGGAAACGTGATTAGC  
CGCCTGACGCAAGACATCGATAACACTGTGCGCATCGTCGGCATGGTAGGTGTGCGTTTG  
GTGATCACCATTTTGATTCTGCCCAGCTCCTTGTTCGCGTTGATGACCATTCACTGGACC  
TTTGTGATCCTGTTTCATCGCAGTGATTGTGGTGCTGATTCCCAGCGGTGCGAAAGCCGTG  
CGAGCTATTCTTCCGGCAACAAATATTGTGTCCAGTACGGAGGCGCGTCGAAACAATCTG  
CTCCTCGATACGATCCGTGGCATTGAAACACTGCGTGTGCTCAAGCTCGGTGCGTGGGT  
GTGCAGCGGATGCGCCAAGCGTCGTGGACTGCGGTGCAAGCAACAGCTGATCGCGCGCCG  
ATTTTCACTCGTCTGCTCGCCCTTGGTTTCGATTGCTTATGGCCTGCTGCTAATTGGCGTG  
TTTGGGCTCAGTGCGTTTTTGGGTTGCCAGGATGCGATGAGCATTGGAGCGGCAACGGCA  
GCAGTTTTTCTGGTTGTGCGCATGGAATTCACGTGTTCAACGTGCTGTTCTTCGCATCG  
GAAATTACAGAGTGCGTCTACTTCTTGGTTCGCGCGGTGTCCCTTGGCCAGATGGCTCGT  
CGCACCGAACAGCTGTCTGAGTCTGCCGATTGCACAGAACCACCTCCGTGACTGTGCAG  
GACGTGACGTTTAAATATCCCGGCGGCGTGGCCATTTTGGAGGATTTCAATCTGGTCTTG  
GAAGCAGGAACAACCACAGCGCTGGTCCGTACTTCTGGTGCGGGAAAATCCACGCTCGCG  
GGCGTCATTGCGGGGCTGCAGCGCCCTGATTCCGGCGCCGTTTTTGGTCGGGGGCATCAAC  
ACCGCCACCGTCACCGACACGTGGACTACCGCCAGGTTGCGCTGATCAGCCAGGAAGTC  
CACCTTTTTCGAGGCACTCTGGCAGAGGATCTTCGCATGGCCAATGCGCACGCCACCGAC  
GCGCAGCTCCACGCGCGCTCGAGTCGGTCCGGCTCGGGCAAATGACAACCTGCTTTTCGA  
CGTTTCTTTCCATCCGATTAGACACCAAAATTTGGCGCCGGCGCAGAAGAATCACCCCT  
GAAATCCAACAGCAAATCTCTTGTCCCGCATCGTGTCCGCAATCCACCTGTGTTGATC  
ATGGATGAAGCCACAGTGAAGCCGGCAGCGATGATGCCCGCATGTTGGAAAAAGCCGCC  
ACAGAAATCGCACGAAACCGCACCACTTGGTTGTTGCGCACCGCCTTGACCAAGCAGTT  
GTCGAGATCGCATCATCGTGATGGAACAAGGCACAATCACCGAAGACGGCACTCACCAAG  
GAATTACTTGCTTTTGGAGGCGCTACGCGCAGCTGTATCAACGATGGAGTGCTCAA

>RXA02224-downstream  
TAGTTCAAATCCACCACAACTC

>RXA02225  
CAAACGTAGGAGCGCTTTGGCGCAGCGGCTGATGAAGCCTTGGCAATCATGTTGAAGGAA  
GCTCGTCTGCAGTCGTTGCTGACTTTTGTGCGCCAACTTGTCAGCGGTGTTTTCTGTG  
GGTCTTTTGGCTTATGCGTCACTGTTGGCTTTTGACGGTGACATAACTGGTGGTGAGATG  
ATCTCGGTGACGTTGCTGGTGCCACCTTCGTTGACTGTGTTGGGTGTGTCGCTTGGCATG  
ATGACAGAGATTTGGGCTAGGGGACAGGCTTCGACAAAAAGGGTCCAAACTTAGTCACT  
GAACTGGATAAGGCGGCCGCTGAGCCACGACCTCAGCCTGCCACCTTTGAATTTGAAGAG  
GGGATCACGGTGTGGGATCCTTCGACACCTGAGGCACGCGATGTGATTGATCGGGAGTTG  
GAGGCGCTTCAGGTTGCGGAAGATGTCATTGTGGCTCCTCACC GCGTCAGCGTGTGTTGAA  
GGTGTGCTGAAGGATAATTTGAATCCGATGGGCACTATCGCACCGGAGATGCTGCGCGCT  
GCTCTTCATGCTGCAAGTTGTGAGGACATCTTGAGCCGATTGGGTGCTGATCTGAACATG  
CCGGGGGAGTTTGAGCTTCCAGATACCTTGATCGGCGAGGCCGGATTGAATCTCTCCGGT  
GGCCAACGCCAGAGGATTGCTTTGGCACGATTCTTGCTGTTGATCCTGAGGTGCTCATT  
TTGGATGAACCGACCACGGGGTTGGATGCGGTGACCCTGGATGAAGTGGCACATCGCGTC  
GAAAAGCTTCGTCGAGGCCGAAAACCGTCGTCATTACGTGCAACCCGACGTGGCACGGC  
GTCGCAAAGCAGATGCAATCTGATTTTTTCGGAAGGGGTGAAG

>RXA02225-downstream  
TAGATGGCGCAGCATGAGCGCGT

>RXA02233-upstream  
ATCCCCACCCAATTGGCCCAAGAGCTGCAGAGTTACGTTGTAGAACCACCTCTGCCTAA  
CTGTCGATTTCCTCAAGAGCCCCCTTGGGAGTCGATAATTA

>RXA02233  
GTGCTCGTGACTTCAACATGGGGATGGACCGTCCACGGAGACGGCAAAAAGATCGAACCC  
GGCGCAGTTGTCGCTCCTAAAGAGCGCCTGAGCTGGGGGCGCACAATTGGAATCGGTATG  
CAGCACGTGATCGCCATGTTGCGCGCCACGCTCCTGGTTCCCACACTCACC GGATTTCG  
GTCAACACCACACTTTTTATTCTCTGGTCTGGGAACAATCCTGTTCTGTTGATCACCAGA  
AACCGACTACCTCTGACCTGGGTAGTTCTTTTGTCTTTCATTGCACCTTTAACCGCAACC  
CAAGTCCATGGCATTGGCGTGCAGATCGGTGGCATTCTTGTGCGAGGTCTCGTGCTCGTC  
GCCATTGGATTTGTGGTGAAAGCAGCGGGCAAACGCGTTATTGATGCTGTCATGCCACCC  
GCTGTACCCGGTGGCATCGTGGCACTCATCGGCCTGAACCTGGCACCAACCGCGGCAGGA  
AACTTCTCCAGCCAACCACTGGTTGCCACGGCGACCCTCTTTGCCATTTTGATCGCTACC  
GTTGCAGGCCCGGGAATGATTGCTCGCCTGGGCATTTTGATCGGTGTGGTGATCGGCTGG  
GTTTTGCGCAGCTATCACC GGCAACCTCTCAGAAGGCGCAGCAGACACCATCCGTGAAGCA  
GCATGGTTGCGACTGCCACAGTTCACAAAGCCGGAATTCCAGCTCTCTGCCATTTTGGTG  
ACACTGCCAGTCATCATCGTGTCTCATCGCTGAAAACGTGCGCCACGTCAAAGCAGTCTCA  
GAGATGACAGGGGAGGACCTCGACGACCTCGCCGGCGACGCACTTATCGCAGACGGATTC  
GGCACACCCCTCGCAGGTGCCTTCGGTGGATCCGGCACCAACCACTACGCAGAAAACATC  
GGCGTCATGGCGGCCACCCGCGTATATTCCACCGCTGCGTACTGGGTTGCCGCGTGCACT  
GCCATCGCCCTTGCCCTTCATCCCCAAATTCGGTGCATGATCTTCACCATCCCCGCCGGC  
GTGCTGGGTGGGGCATGTTTGGTTCTTTACGGCCTAATCGGTATGCTCGGCATTTCGTATC  
TGGCAAGACAACAAGGTCAACTTCAACAATCCAGTGAATCTGACCATGGCTGCCGTTGCT  
TTGGTTGCAGGCATTGGTAACCTCACCTCACCGTTTTTCGGAGTCACTCTTGAAGGCATC  
GCATGGGCTCTG

>RXA02233-downstream  
TAGGCATCATTGTGCTGTACCCA

>RXA02253-upstream  
TGAGGACATTTCCCAAGTGAAAGGCTTCGGCCCGAAACTTGCGGAGGCTGTCTATGAAG  
TCTTCACGCGTCAAAATAAGTAGATCGCTAGGATGTAACC

>RXA02253  
ATGATTCAATCCACTGGGGTCACGCACACTGATAAGTCTGCACAAGAAAATCCTGTGAAG  
TACAGGGACAATTTACACCTGTCATCATCACCGGTATGTCAGGCGCAGGTCTGAGCACA

GCAGCCCGAGTCCTCGAAGACTTGGGTTGGTATGTGGCGCACAAATATTCCACCACAGATC  
ATCCTGGAATTAATTGATATGTGCGCTCGGGAAGATTCTCCGTCGACAAAGTTGCAGTC  
GTGTGCGATGTGCGCTCCCGTGAATTCGCGGAAGCCTCACCAGGTTGTTTCAGAGCTG  
CGTGATAAGCAGCTCGATCCCACGGTGTTATTTCTGGAAGCACGCGATGAGGTGCTGATC  
AAGCGATTTCGATAATGTGCGCCGCACCCATCCTTTGCAGGGCAGCCAAACCTTCAGGTG  
GGTATTGAACGTGAACGAACCGTGCTGTCTCCTGTGAAGGAAGACGCTTCAGTGGTCATC  
GATACCTCGGATCTGTCCGTGCATGATTTGCGCCGCGCCATCGAATCCTCGTTTAGGACA  
ATCGCCACGCGCACCCAGCACGTACCATTGAATCATTCGGTTTTCAAACACGGCTCACCA  
CGCGACGCCGACTTTGTTGTGGACGTGCGTTTCTTGCCGAACCCATTCTGGGTTCCAGAG  
CTGCGCCCATTTAGGGGAGTGGACAAGCCAGTATCTGACTATGTGCTCTCCCAAAAAGGC  
GCAGAAGAATTTTTGAACAACCTTGTGGACATGCTCAAAGACATGCTTCCGGGATACCGC  
CACGAAGGAAAAAATTCATCACAAATCGGTGTGCGCTGCACCGGTGGACACCACAGATCA  
GTTGCGGTGTCTGAAGAACTAGCCAAAAGAATCGCAGATCAGACCACGCTCGACGTGTCT  
GTAGTACACCGCGATATTAACCGCCAC

>RXA02253-downstream  
TAGGAAAGGGGCCAACTAATTGA

>RXA02261-upstream  
GAAATCTATAGAACGATAGGTAAAACTGGACTAGGTTTATCTATAGCGGAATAGAAAAT  
ACTCCGCTCGACAGCATCACTTAGCTGAAAGGCCTTTAAC

>RXA02261  
ATGGACCCCTCAGATCTAGCCTGGATTCTCGCAGCTTTTTCGCTTGGTAAGCCTGATGTTT  
CCCGGATTGTCCCTGCTCTACGGCGGCATGCTGGGTGGGCAACACGTTCTTAACACGTTT  
ATGATGGTTATGAGCTCACTTGAATCATCAGCCTTGTGTACATCATTTATGGACACGGA  
CTTGTCTTAGGAACTCCATCGGTGGGTGGGGAATTATCGGAAATCCCCTTGAATACTTC  
GGCTTCCGCAACATTATGGAAGATGACGGCACCGGAGACCTCATGTGGGCCGGCTTCTAC  
ATTCTGTTTCGCTGCAATCTCACTCGCACTTGTTCATCTGGTGCAGCGGGGCGCATGCGC  
TTTGGAGCGTGGCTGGTCTTTCGGTGTCTGTGGTTACCTTTGTGTACGCGCCACTGGCA  
CACTGGGTTTTTCGCTATCGATGATCCTGAGTCCGGCTACGTGGGTGGCTGGATGAAAAAT  
GTGCTTGAGTTCCACGACTTTGCTGGTGGAAACGGCAGTGCACATGAATGCGGGTGCCTCT  
GGACTCGCGCTGGCAATAGTGTGGGACGCCGCCACTCCATGGCTGTGCGTCCACACAAC  
CTTCCACTGATTTTATTGGTGCAGGACTGATCGTTGCGGGCTGGTTCCGATTCAATGGT  
GGTACCGCAGGTGGTGCCAACCTCCTCGCAAGCTACGTGGTTCGTTACCTCTCTCATTGCT  
GCAGCTGGCGGAATGATGGGCTTCATGCTCGTTGAACGTGTGTTTCAGCGGAAAACCCACT  
TTCTTTGGCTCGGCAACCGGCACAATCGCAGGCCTTGTGGCTATCACCCCGGCCGCGGAT  
GCAGTGAGCCCGCTCGGAGCATTTCGCGCTCGGAGCGCTCGGCGCAGTTGTCTCCTTCTGG  
GCAATTAGCTGGAAGAAGGACACCGAGTCGATGATTCCTTCGATGTGTTTCGACGTCAC  
GGAATGGCCGGCATTGCAGGTGCACTGTTTGTGATGCTCTTTGGCGATCCACTAGCACCA  
GCGGGAGTTTCCGGAGTCTTCTTCGGTGGCGAACTCTCCCTGCTGTGGAGGGAACCACTG  
GCCATCATCGTGACCTTACATACGCATTTCGGCGTGACCTGGTTGATTGCCACGATCTTG  
AACAAGTTCATGACTCTGCGCATCACCTCCGAAGCCGAATATGAAGGCATTGACCGCGCA  
GAACACGCAGAATCTGCCTACCACCTCAATTCCAACGGAATTGGGATGGCAACCCGCAAC  
AATTTCCGACCTGAAATCCCCGAGGAAACCGTGCCCGACGCCGTGCAGGTGGGCGTCGAT  
AAGCAAAAAATCGCTGATACTCGAAAGGCCTCAAAA

>RXA02261-downstream  
TGACCGCAACCTACACCACTGAA

>RXA02268-upstream  
TGAATCGTTGGTGTCTCGAGTTGGGATTGTTATGTGGGGAGACGTCGATAAGCAAAACAC  
TTGCCGAGCGCAAGCCGGCCTACGGCGCTAGTGTGAGCAC

>RXA02268  
ATGTCCCAGGAAAATTCTGGTTTGTTCAGCGCGGATTACACGTGGGGTGGCTAAGGTG  
CGCCGGAATCCGCGCGAGGATTTTTCGGAGGAATTCACCCAAGAACTCTACGATCACGCA  
ACAAATATCACCTGCCCCGACGGCGCGGCTGAAGCCGAATGGGTTTTTCCAGGATGAT  
TGGCGGGCGCGACCAAGTGGTGCAGCACCGTGGCCGATCGTGCTAATTCACGGATCCGGG  
GCCAGCAAGGGTTCATGGGAGGAAATGGGCGCTGAGCTGCGCAGCAAAGGTTGGGCCGTG  
TTTGCCCTGACTTTGGAACGCGTGCCACCGAGCCAATTGCGGCGTCCGCTGCCCAATT

GGTGGTATATTGATGCCGTTTTGTTGGTGACGGGCGCTGCGCAGATTGTGCTGGTTGGG  
 CATTGCAAGGCGGTGTCGTGGCGCGGTATTGGATGCGCACCTACGGCGGATACATGAAG  
 GTCAGGCACATGATTTCCATCTCTACGCCAAATCACGGAACGCTCATGGGAGGCATTTTA  
 AACCCGATGACGAAGGTGAAATCGGGAGAGGGAACGATCGAAAAGCTGATGCACAGACTA  
 TTCGGGGCCCACTGGTTTTGAACAGCTGCGCGGACACGACATCATCGAGTTTTTGGCCGAC  
 GGTGGGGACCTCGATCCAGGCGTCACCTACACCTGCATTGGTACCCATTTTGATCCTTTT  
 ATCCAACCTCCGGAGGTGGCCTTTTTGGAGGTCAACGAGGACGATGATCCAAATCGAGTC  
 CACAATATTTGGGTGCAAGATGAACACCCGCGCGCAATGATTGCCCAACGATATGGTG  
 CGCGATCCAGGGTGATCGAAATCGTACGCGCAGAGCTCGACCGGGTGGCACGCCTCGGC

>RXA02268-downstream  
 TAAGTTGGGGACATGGTTGACGC

>RXA02269-upstream  
 CGCAATGATTGCCCACAACGATATGGTGCGCGATCCCAGGGTGATCGAAATCGTACGCGC  
 AGAGCTCGACCGGGTGGCACGCCTCGGCTAAGTTGGGGAC

>RXA02269  
 ATGGTTGACGCCCTCAATGATCTCCGCCGAGAACTCACAAACGCGTTAAGGTCCGTGTGG  
 AAAAACCTCCCCACTGATAACGCCCGCAGGCCGATGCCTTGCCAGACGATGTAGTGGA  
 GAGATTGCGATAAATTTCTACCGTGATCCCAAAAACCGCGGCAAACTCAACGAAGACAAA  
 ACAGATTCTTGGCGATGCTCGCGGCATACGTTACGTGGACTTTTTGAAGACGATTGG  
 CGCGCCCGCCCAACCGAAGACCGCCCTGGCCAGTGGTATTAGTCCACGGAACCTGGATCA  
 ACAAAGGTGATTGGCAAGACTTGGGAGCCGATCTACGCCGCGACGGCTGGGCAGTGTTC  
 GCACCCGAATTTGGCCAACGCGCCACCGGTTCACTCGCAGAATCATCCGCACAAATTGGC  
 GCCTATATAGATACAGTATTGCTTGCTACAGGAGCCTCAAAGTCATTGTCGTTGGCCAC  
 TCCCAAGGCGCGCTGTTGCTGAGATACTGGATGCGTGTTTTGGGTGGTGCATCCAAAGTC  
 AAACACATGGTCTCCCTCGCTGTCCCAATCACGGCACCCATGGGCGGAATCGTCAGC  
 CCGCTAATCCGTAACAATCGTGGCGAAAGTGTGGTTAATTCTGTCGTTCAATCATGGTTC  
 GGCGAAGCTGGATTGTGAAATGATCCGCGGACACGACACCATCAACGCCATCAATGAAGGC  
 GGCGATTTGGATCCAGACGTGACATATCTGTGCATCGCCACCCACTTTGACACCGTGATT  
 CAGCCCCCTGAAACCTGCTTCCTAGAGGCCCGGAACCCCGAAGAACTCAAGCGGGTCCAA  
 AACATCTGGGTGGAACCTCGACCCCAATTCACTGCTGCTCCACGAAGCAATGCCTTAC  
 GATCCCCGCGTACGCGCACTGGTCAGGGCGGATTTGAGCAAATTGGTGGAGATTTCCGAG  
 ACTGCGGAGAAC

>RXA02269-downstream  
 TAGGGGTTTTGGTGGTTGTCTAA

>RXA02309-upstream  
 GTGCCTTCCGTCGACTACGGTTAAACAAAAGCTTTTTGTCCATTTCACTGGATTACCCG  
 AAAGAATGAATCCACACTCGATCACCAAGGTAGCGATGA

>RXA02309  
 ATGAGTAGCGGCCGAACCGTTCCAACCCGTTCCACGGGCTCGGAAAAGAAGGTGTATCC  
 ACCACAGGAGCATCTCAGGTCGAGTTTGGTGATCCCGAGCTAACGGCCAGGATCAATGAC  
 GCCATGGTGCAGGTAGAAGAACTCCTGCACACTGAACTATCGTCCGGGGGAAGACTTCCTC  
 GTCGATATCGTCATGCACCTAACACGAGCCGGCGGCAACGATTCCGCCCCATGTTTGCA  
 CTGCTGGCCTCCGAGTTCGGTGAAAAACCACTCTCCGAAAACGTCATCAAAGCCGCCGTT  
 GTCGTAGAGATCACCCACCTGGCCACCCTGTACCACGACGATGTCATGGACGAGGCATCC  
 ATGCGCCGCGGCGTCCCAAGTGCTAACGCGCGATGGGACAACTCCGTAGCCATCCTCGCA  
 GGCGACATCCTCCTAGCACATGCATCAGGTCTGATGAGTCAGCTGGGTACCGACACAGTC  
 GCCCCTTTGCCGAAACATTCCGGCAACTAGTCACCGGCCAAATGCGCGAAACAGTCGGG  
 CCACGCGACACCGACCCGATCGAGCACTACCAACGTAATCCGTGAAAAAATGGTGTC  
 CTCATCGCCTCCGCAGGCTATTTGGGAGCCATGCACGCAGGCGCCGCACCTGAACACATC  
 GACGCCCTGAAGAACTTCGGCGCAGCCGTGGCATGATCTTCCAAATCGTCGACGACATC  
 ATCGACATCTTCTCGGAAACCCACGAATCCGGAACACGCCCCGACCGACCTCCGCGAA  
 GGTGTATTACCCCTCCAGTGCTCTACGCACTCCGTGAAGACACCCCGTCGGCGCAGAA  
 CTCCGCGACATCCTCACCGGCCCTCTAGAAGACGACGAGACCGTCAACCACGTCCTCGAG  
 CTCTCTCCCAATCCGGCGGACGCCAAGCAGCCCTCGACGAGGTCTACCGCTACATGGAC  
 ATCGCCAACGCAGAA



>RXA02310-upstream

GAAATGGACAAAAAGCTTTTTGTTTAACCGTAGTCGACGGAAGGCACTTGAAGCACCTTG  
GGTTAGTCTTCTTGCTCTCCGGACTGAGACAATGGGGTTT

>RXA02310

GTGTCTACAACTTTTGATGTGTTGATCATCGGCGCGGGCCCTCAGGTGCCAGCGCCGCC  
GTCCATGCGGCCAGGACTGGGCTTCAAACATTGCTTATCGACGCCTCCTCCTTCCCGCGG  
GATAAAACGTGTGGCGATGGCCTTACTCCCCGTGCGATTACACAGCTAGAAGTTCTAGGT  
GTTGCTGATCAGGTTACCGGGGATTATTTCAACAAGGGCTTGAACTGCATGGTTTTGGT  
GGCTCTGTTGAGGCGCCGTGGCCGGAGACATATTTACGAATAAGGGTTCCGCGATGTGCG  
CGGATGGAGTTCGATGATTTGTTATTCGCTTGGCAAAATCTCATGAGGAAGTAACCACG  
TGGGAGAACGCGAGCGCCCAAGACCCCATTTTGAGGGGAATTTCTTGGAAGGCGTTGTG  
ATTAATCACGCAGGGCAAGAGAAAACCGTCAAGGCGAAGCATGTGATTATTGCCGATGGT  
GTCCGCTCCCCCTTTCCGTAAGAACTGGGTAGGCAGTGGCAACGCGATGAGGTGTATGGC  
ATTGCGGCTCGTGCTTATTGTGAACTCCGCTGTCTGATGAACCGTGGATTCACTCCCAT  
GTGGAAGTGCAGGATGAAGATGGTGTGGTGCAGCCAGGATATGGGTGGATTTTCCCGCTG  
GGCAACGGCACGGTGAATTTGGGTGTGGCGCGCTCTCGACGGATACGAGACCAGCGAAG  
ATCAATACGAAGAAATTGTTGAGCTTCTATGCGGGTCAGCGTCGTAAAGCATGGCAACTC  
GGGCCCCGAGCACGACGTCGCTCTGCCCTGCTGCCTATGGGCGGCGCGGTGTGCAATGTG  
GCTGGCGCAACTGGATGCTGATCGGCGATTCCGCCGCGTGTGTGAACCGCTGAACGGC  
GAAGGCATCGCATATGGCCTGGAAACCGCGCGATGGCCGTCGACACGCTTGTGGAAGAAC  
CCCAAGCGCGATTTGACCTTGGTATGGCCACATAGGTTGCGCGACGCGTACGGCGAGACC  
TTCATGTTGGCGCGCACGGCTGCTCGACTGCTGACGTACCCGCGATTTTTGCGGATGGCT  
GGGCCGCTCGCATTCCGCGGGCCGCTGCAAAAGGCCATCATGCCGGCGGCTGCGCGTTTG  
ATGGGCAACCTGATCACAGAGGAGGATAAAGACCTGCTCGCCAGGGGTTGGCAGGCCGCC  
GGATCCGCGATTAGTTGGGCGCGGAAGGGCTCCCCTCTGTGGGACTCGACTAGTTCTCTG  
GTT

>RXA02310-downstream

TAATCGCCGAGTGACGCGCGACG

>RXA02320-upstream

GTATGTTACACAAGAACCCTGCACAACGCCTTCAAAGTACGTCGACCACGACCAAGCGC  
ATTATTCACTCTCACCTTCAGGATTTAGACTAAGAAACC

>RXA02320

ATGACTGCAGCACAGACCAAACCTGACCTCACCACCACGGCTGGAAAGCTGTCCGATCTT  
CGCTCCCGTCTTGAGAAGCTCAAGCTCCAATGGGCGAAGCAACTGTAGAAAAAGTGCAC  
GCTGCTGGCAGGAAGACTGCCCGGAACGTATCGAGTATTTGCTCGATGAGGGCTCTTTC  
GTAGAGATCGATGCTCTTGCTCGTCACCGTTCCAAGAACTTCGGCCTGGATGCCAAGCGT  
CCAGTTACTGACGGTGTGTGACTGGTTACGGCACCATCGATGGCCGTAAGGTCTGTGTG  
TTCTCCCAGGACGGCGCTGTATTCGGTGGCGCTTTGGGTGAAGTTTATGGTGAAAAGATC  
GTTAAGGTTATGGATCTTGCATCAAGACCGGTGTGCCTTTGATCGGAATCAATGAGGGT  
GCTGGTGCAGTATCCAGGAAGGTGTGTGTCTCTGGGTCTGTACTCACAGATCTTCTAC  
CGCAACACCCAGGCGTCTGGCGTTATCCACAGATCTCTTTGATCATGGGTGCCTGCGCT  
GGTGGTCACGTGTACTCCCCTGCTCTGACTGACTTCATCGTCATGGTG

>RXA02321

GAGTACGGTGGCATTCTGCGTCGTGGCGCAAAGCTGCTCTACGCATCGGNNGAAGCACCG  
GTTCCAAAGATCACCGTCAACATGCGTAAGGCTTACGGCGGAGCGTACTGCGTGATGGGT  
TCCAAGGGCTTGGGCTCTGACATCAACCTTGCATGGCCAACCGCACAGATCGCCGTCATG  
GGCGCTGCTGGCGAGTTGGATTCACTACCGCAAGGAGCTCATGGCAGCTGATGCCAAG  
GGCCTCGATACCGTAGCTCTGGCTAAGTCCCTTCGAGCGCGAGTATGAAGACCACATGCTC  
AACCCGTACCACGCTGCAGAACGTGGCCTGATCGACGCCGTGATCCTGCCAAGCGAAACC  
CGCGGACAGATTTCCCGCAACCTTCGCCTGCTCAAGCACAAGAACGTCACTCGCCCTGCT  
CGCAAGCACGGCAACATGCCACTG

>RXA02321-downstream

TAAATCGGCGAATCCATAAAGGT

>RXA02335-upstream  
TGGTTGAGTTCTTCGGGGTTGAGTGTGCAAGAATATTTACTATTGGTCAGGCAACTATGT  
GTCTACCCACTGAGTCATCAATTTAAATCAGGAGTTATTA

>RXA02335  
GTGTCAGTCGAGACTAGGAAGATCACCAAGGTTCTTGTGCTAACCGTGGTGAGATTGCA  
ATCCGCGTGTTCGGTGCAGCTCGAGATGAAGGCATGGGATCTGTGCGCGTCTACGCAGAG  
CCAGATGCAGATGCACCATTCGTGTTCATATGCAGACGAGGCTTTTGCCCTCGGTGGCCAA  
ACATCCGCTGAGTCTACCTTGTTCATTGACAAGATCATCGATGCGGCCCCGCAAGTCCGGC  
GCGGACGCCATCCACCCCGCTACGGCTTCCTCGCAGAAAACGCTGACTTCGCAGAAGCA  
GTCATCAACGAAGGCCTGATCTGGATTGGACCTTCACCTGAGTCCATCCGCTCCCTCGGC  
GACAAGGTACCCGCTCGCCACATCGCAGATACCGCCAAGGCTCCAATGGCTCCTGGCACC  
AAGGAACCAGTAAAGACGCAGCAGAAAGTTGTGGCTTTTCGCTGAAGAATTCGGTCTCCCA  
ATCGCCATCAAGGCAGCTTTTCGGTGGCGGGACGTGGCATGAAGGTTGCCTACAAGATG  
GAAGAAGTCGATGACCTCTTCGAGTCCGCAACCCGTGAAGCAACCGCAGCGTTCCGGCCG  
GGCGAGTGCTTCGTGGAGCGCTACCTGGACAAGGCACGCCACGTTGAGGCTCAGGTTCATC  
GCCGATAAGCACGGCAACGTTGTTGTGCGCCGGAACCCGTGACTGCTCCCTGCAGCGCCGT  
TTCCAGAAGCTCGTCGAAGAAGCACCCAGCACCATTTCCTACCGATGACCAGCGCGAGCGT  
CTCCACTCCTCCGCGAAGGCTATCTGTAAGGAAGCTGGCTACTACGGTGCAGGCACCGTT  
GAGTACCTCGTTGGCTCCGACGGCTGATCTCCTTCCTCGAGGTCAACACCCGCCTCCAG  
GTGGAACACCCAGTACCCGAAGAGACACCCGGCATCGACCTGGTCCGCGAAATGTTCCGC  
ATCGCAGAAGGCCACGAGCTCTCCATCAAGGAAGATCCAGCTCCACGCGGCCACGCATT  
GAGTTCCGCATCAACGGCGAAGACGCTGGCTCCAACCTTCATGCCTGCACCAGGCAAGATC  
ACCAGCTACCCGCGAGCCACAGGGCCAGGCGTCCGCGATGGACTCCGGTGTGCTTGAAGGT  
TCCGAAATCTCCGACAGTTTCGACTCCATGCTGGCAAAGCTGATCGTTTGGGGCGACACC  
CGCGAGCAGGCTCTCCAGCGCTCCCGCCGTGCACCTGCAGAGTACGTTGTGAGGGCATG  
CCAACCGTTATCCATTCCACCAGCACATCGTGAAAACCCAGCATTCGTGGGCAACGAC  
GAAGGCTTCGAGATCTACACCAAGTGGATCGAAGAGGTTTGGGATAACCCAATCGCACCT  
TACGTTGACGCTTCCGAGCTCGACGAAGATGAGGACAAGACCCAGCACAGAAGGTTGTT  
GTGGAGATCAACGGCCGTCGCGTTGAGGTTGCACTCCAGGGCGATCTGGCACTCGGTGGC  
ACCGCTGGTCCTAAGAAGAAGGCCAAGAAGCGTCGCGCAGGTGGTGCAAAGGCTGGCGTA  
TCCGGCGATGCAGTGGCAGCTCCAATGCAGGGCACTGTATCAAGGTCAACGTCGAAGAA  
GGCGCTGAAGTCAACGAAGGCGACACCGTTGTTGTCTCGAGGCTATGAAGATGGAAAAC  
CCTGTGAAGGCTCATAAGTCCGGAACCGTAACCGGCCCTTACTGTCGCTGCAGGCGAGGGT  
GTCAACAAGGGCGTTGTTCTCCTCGAGATCAAG

>RXA02335-downstream  
TAAGTTCTTGGATTTCCTGTTAGT

>RXA02343-upstream  
TTTAAAACTACCCGCACGCAGCACGAACCTGTTCAAGTGATGTAAATCACCGCGGAAATA  
TTGTGGACGTTACCCCCGCCTACCGCTACGATTTCAAAAC

>RXA02343  
ATGACCATTTTCCTCACCTTTGATTGACGTCGCCAACCTTCCAGACATCAACACCACTGCC  
GGCAAGATCGCCGACCTTAAGGCTCGCCGCGCGGAAGCCCATTTCCCATGGGTGAAAAG  
GCAGTAGAGAAGGTCCACGCTGCTGGACGCCCTCACTGCCCCGTGAGCGCTTGATTACTTA  
CTCGATGAGGGCTCCTTCATCGAGACCGATCAGCTGGCTCGCCACCGCACCACCGTTTC  
TGCTGGGCGCTAAGCGTCTGCAACCGACGGCATCGTGACCGGCTGGGGCACCATTGAT  
GGACGCGAAGTCTGCATCTTCTCGCAGGACGGCACCGTATTTCGGTGGCGCGCTTGGTGA  
GTGTACGGCGAAAAGATGATCAAGATCATGGAGCTGGCAATCGACACCGGCCG

>RXA02364-upstream  
GCGAAAGTATCTAAGGTCGTTTGATTGGTTTACTACCCCCGAAGTGGGGGTTATTGGCAG  
CATCGAGCACCAATGAGCGTGATCCGGGATCAGGATCTG

>RXA02364  
ATGGAGCCACTGTTCCAAAGTCTTGCGGAATCGGACAATATTTCTGTCATTGGTGGATTT  
ACCCAAGGCACCCGAAATCTGTACACCACTGATGCGCCGGTGAAAAGACCCGCTGACCTG  
GCTGGAAAAGAAGATTTCGCGTCCAGGAATCCGCCATGCACATCCGCATGATTGAACTCATG  
GGTGGCTCGGCAACCCCGTTGACTTACGGCGAGGTATATACCGCGATGCAGTCTGGTGTG

CTGGATGGCGCGGAAAATAACGAGATCAGTTACGTTACCCAAAACCACTTCGAGGTTGCT  
CGCTACAACAGCAACACCAATCACCTTGTGCGTTTGGATTACATGGTCATGCGACACGAT  
CTGCTTGACGCCATGAGCGAGCCAGACCGTGAATTGTTTCCTGGAAGAATGGGACGCCGCG  
ATGACTGAGCACACGGATCTGTGGAACACAGAACTGATGCCGTTATTGAAAAGGCGAAA  
GCTGGGGGAGCGGAGTTCTGTTGAGGTGGATGCGCAAGCATTACCGATGCACTGGCTCCC  
ATCAAAGACGAATTCTTGACCTCAGAATTCCAGCGTGAACCTCTACGAAGCAGTGCGCGCC  
GCTGATACTTCAGGAGGTGCGGCATCA

>RXA02364-downstream  
TGATGAATTTTAAGTCCATCGTG

>RXA02372  
GATGCGGTCAACAAGATGGATCGCACCGACTTCGTAGAAACCTTCGCACCGCTGTTCAAC  
AGCAAGACCTGGCCTTTGGAAACCGCATGGGAATCCCAGCCATTGCGCAACGTACGGAA  
CTGCGCGAAGCCATCCAAGTCGCTGTGCTACCGCACCGTTGTCCGACCGCGAAGAGCTC  
ATCCACGACTACCCCGACATGGCACAGCTCATTTTGGCCACCGAAGAGGAAGCCGCCACC  
ATCTCTCAAGACCGTGGTTCGATCGGTCTTGATGATCTCGATGACGTGGATCAAGAAAAG  
CTCATCACCGTCACCGAGCAGTACCGCGAACGGTTCAACATGCCGTATGTTGCGTACTTC  
GACACCATGGATTCTGTGGATACCGTCGTAGCCGCCGGCTTGCGCCGCCCTCGACAACTCC  
GACGAGCAGGAGCACCGCCAAGCGCTATCGGAAATCATTGAGATTGCCAATGACCGCTTC  
GATATATTGCTTGCCGACGCTAACCCAGCCCGTTTTCAGCTTTTCGATCGCAAGTTTACCGAG  
ACTGACTTCCTCGGC

>RXA02372-downstream  
TAAAACACCAAAAACAAATTAAG

>RXA02377-upstream  
GACAATACTGATGGATAAATTTTCATATCGAGGACGAAGGGACAACCCCGAACGCCGTGAC  
AACATCAACCACAACCCGGGTGAAACATCCGGTAGACCAG

>RXA02377  
GTGCCACCCGCACCCAACTTGCAGCCCTAGGGCTCCAACACGTTCTTGCTTTCTACGCA  
GGAGCCGTCATTGTTCCGCTGCTGATTGCACAGTCGCTGAACTTGGACACTGCGACCACC  
ATTCACCTGATTAACGCTGACTTGTGACATGTGGCATCGCCACGTTGATTGAGTCTGTG  
GGCATTGGTCGCCACATTGGTGTGCGCCTACCGATCGTTCAAGGTGTCACCACTACTGCT  
GTTGCTCCCATCATCGCCATTGGTTTGGGCGTTACTGATGGTCAAGGTGGCGTTGCGTCG  
CTGCCCTGCCATTACGGTGCAGTCATTGTCTCCGGCATTTCACGTTCTTTGCAGCGCCG  
GTGTTTGCAGCGTTTCCCTCAAGTTCTTCCCACAGTTGTACCCGTAAGTGTGCTGTTGGTT  
ATGGGTGCTTCCCTGCTGTCGGTATCTGCAAATGACTTTGTGAACTACGCCGATGGGGTG  
CCTGCTGCCCCGCGATCTTGCTTACGGTTTGGCACCTTGGCGGTGATCATTTTGGCGCAG  
CGCTTCTTCCGTGGATTTCATGGGCACCTTGGCTGTGTTGATCGGCCTGGTTGGTGGCACC  
GCAGTTGCTCTGATCTTGGGCGATGCCAATTTGGATGAGGTGGGAAATGCTGAAGCGTTC  
GACATCACCACTCCGTTTTATTTTGGTGTTCAGAAATTTAACGCTGTTGCCATTTTCTCC  
ATGATTATCGTCATGATCATCACCATGGTGGAGACCACCGGTGATGTGTTTGAACGGGG  
GAAATCGTCGGCAAGCGAACTCGCCGAGTGATGTACCCGCGCACTGCGCGCTGACGGC  
CTGTCCACCTGATGGGTGGCGTCATGAACCTTCCCGTACACGTGCTTCGCGCAAAAC  
GTTGGCCTGGTGCGCATCACGGGCGTGAATCTCGCTGGGTTGCGGCAGCTGCTGCCGGC  
TTCATGATCATCCTCGGTGTGCTGCCAAGGCTGGCGCGATCGTCGCTTCCATCCCTTCC  
CCAGTCCCTCGGTGGCGCATCCTTGGCACTGTTCCGCCAACGTTGCATGGGTGGGCATCCAG  
ACCATCGCCAAGTCTGACCTCGCTGATAGCCGCAACTCCGTCATCGTGACCTCCGCACTT  
GGCCTAGCCATGCTGGTGTCTTCCGCCCGATGTTGCTCAAGGCGTTCCC

>RXA02377-downstream  
TGAGTGGGCGCGTATCTTCGTCT

>RXA02397-upstream  
GTGTGAATAAACTTGTTCCTGGTCATTTCCCCTACTGAACTGCGCTTATGCCTATGCT  
TAGAAACCAGAGACAAGCTTAAGAAGGACAGGGGCCGGCC

>RXA02397  
ATGAATGATTTCGAAACAACCATCGATCGGATCTCTAAAGAACAAGATCCCGCAGCCCGA

AGCCGCGTGGAACAGTTCATTGTGGAAACAGTACGTGCACTACCCAACTTGACCACCAAA  
 CAAGGTGCATCGTTGGCTATCCAACCTTCTTGATGCGGTACAGCTCGCGGATGCGGCGGGA  
 ACCAAGGGGGGTGCGTCGACAAGCAATGCTTCATCGCTGCCTGACACCTTTGACGCGCTG  
 ACCAGCCTGATTGGCAAGCTCGATGTGCGCAGCGATTCTGAATGGCGCTCGTTTGGGTTTC  
 CAGCCTTCTGAAACTGCGCACCCGCTAATGATCGCTATCCCTGAGATTGAGATTTTTAT  
 CAGCACACCGATGTGGAGCCGGGAAGCGATGACGCCGTGGCGCCGGACTTTCAGGAAAAT  
 CAGGATATGTGGCGCAGGCGTCTCGGATCTGTACCGAACCACAACTTATATATAAAGAG  
 TTTTCCGGACCCGGCAAAGCGCAGCGTGCCGTAGAAATGCTGGGCAATCTGTGGAAGATC  
 GCGTGGTGGTGGTAGGAAATACGGAAGTCGCCTTGGGTTAACTCGTGTGGAATACACC  
 CCCACCCCTGGCGAAGTACCCGTGCCGTGATGTGCGAGAAGAACTGTTGGTACAGCATT  
 CGGGTGTCTGAAACCATTGGTGAGAACCAGGTTCCGGAAATTGTGCGCTGCTTAGGCGAG  
 ATTTTCTGTGGCTATCTTCCCCAGATGTGGCTCAAAGAACCAGTAAAGGCCGGCAAGTTG  
 CGAATCCAAGAAATCGGAAGCAGCAGCGTATATCGCGATGGCGCGACTAGATCTTCCCCA  
 CGCACCGGCAACACCACTTGGACCAACAGCTATATTTCCACGCGTCTCTCTCCCCCGCT  
 TTTAGGTGGGACGTGGTGTGGAGGCTTCCACCAATTGGAGAACCTGCTGCGTGGAGAC  
 ACAGGGCCGGTCACTGCCACACAATCGGCAGCTGGT

>RXA02397-downstream  
 TAACCAAAAGTTCACGTGGAGAT

>RXA02424  
 ACCGGAGCAACTACTACGCGCCTTTCCTTGAGGTGCCAGCTTTGCCCTCCGCTGTTGAT  
 GTGGAAGTGCATCATGGTGATTCAATTGAATTTGAGGGTCATGTATTCCCTATCAGCATT  
 CTGCGCGGCCACACCCAGGCGGTGCAGTACTACCGCTGAGATCGACGGTAAACTCAC  
 CTTTTCTGTGGGTGACAGCCTCTTCCCCGGCGGTTTGGGCAAAACCAGCAGCGAAGGCGAC  
 TTCGTCCGACTGTTCAACGATGTCAAAGAGCGCATCTTTGACACCTACGACGATGACAGC  
 ATCGTGTGGCCAGGTACGGCAAGGAAACCACCTTGGAGCCGAGCGTCCACAGCTGGAA  
 ATCTGGTGGGAGCGTCGCTGG

>RXA02424-downstream  
 TAAGCGCTTTTCTCAACCAGGCA

>RXA02426-upstream  
 TGCAGCAGCATAATCAGGGAAAAATAGGAACTGTTTACTGAAAACTGACAAACCTGACA  
 GACCTGACCCGAAGAGACCTTATTCATGACGATATTGTTT

>RXA02426  
 ATGCTCATTACATTGCTGCTCGCCACCGTGATTGTGGTGGCCATCGGCGATAAAACCGGA  
 CTCCCCTGGCTGCTTTGATGACTATTGTCGCCGCGAGGTGGAGCGTTGTTGCCATTTTTG  
 CCGGAATTTACTATCCCGGCCGATCTGATGTTGCCTATTTTCATTCCGCCGCTGCTGTGG  
 GCGCTGGCGAGGAAGTCATCGTGGGCGGTGATTAGGTGCGAGATGTCTACCATCATCACG  
 ATGTCGGTGTGTTGGTGTTCGTGACCATCGCGGCACTCACGGGTGCATCCATGCTGTTG  
 CTTCCTGGCATTGGTCTTGCTGGTGCGATCATGTTGGCTGCGGCTATTGCTCCACCGGAT  
 CCTGTTGCTGTTGATGCAGTGGCGGAACCTGCGGGAATCCCGAAGCGCATCACCACTT  
 TTGCAGACGGAGGGTCTGTTTAAATGATGCAGCCAGCATCGTGGCGTTCCATGTGGCTTTA  
 GCTGCCCTGGTCTGCTGGTGAGGATTTGTCCTGGTCAACGGGTGTTTTGGAATTCTTGTTG  
 TCGTGTCTTCTGCTGCCGTTATTTTGGGCTTGGTTATTGGCCGGGCGGCTGCGTGGTTTACC  
 GATCACGTGAGTTCCGTTGAGGCTCGAAATGCGTTTACGTGGGTGCTGCCGTTTGCCATT  
 TATGTGGTGGCGGAAGAAATCGGCGGATCGGGCGTTATCGCCATTGTGATCGCTGCAGTG  
 GAGATGAATTCAGGGCGTCGATTGGTGCGGAGGATCGTCTAACGGGTTCTGCGTTCTGG  
 GGAACCATTGAGGTGCTGTTTACTGGCGTTGCCCTTGGTTTGATCGGCCTGAATGTGCGC  
 GCTGCGATTGATGAAGTTGGATCTGAGCTGTGGCATGCCGTGGTCTGTTGGGCAATGCTC  
 TCGGTGGTGGCGATCGTTGTCCGTGGTGTGTTGATGTTTCGCGGCGTATAAGCGCAATCGT  
 TTCAAGATCGATAAGAAGGGTGCACCAATAGTTTCATTGCGGGCGCCTCTTCGACTGCAG  
 GAATCGTTGCTGATGACGTGGGCGGGCATGCGCGGTTTGGTGACGTTGGCGCTGGTGCTG  
 TCTATTCCGGAGGATATTTTCCCGTATCACACGAGTTGCAGGTCATTGCGCTGGTCTGTT  
 CTCTTAATCACCATGGTGGGCCCTGGTTTACGTTGCCGTGGCTGATGCGGAAGCTCAGC  
 TTGGATAAGGGTCCCGATGCTGCGGGCGATGAGAGTATCGCCGCGCTGACAGAGAGGGCT  
 CACAAGGCCGCAACAACGTATTTGGTGGATACCACGGAGTTGCCGATGGAGCAGATGGTG  
 GCGATCAAGAATTGGTTCTCGCAAGAAATTGACGCTGATGAACTGCAGGAGAAGCTCGAT  
 AAGCTGCATCAGCGCGCATCATGCGCGTGTGCGGGCAATTAAGGCGGCCAGGAGGAG

CTGTTGAAGGCGCGGCGGGAGCGCGGCGTTAATCCGGCCTATGTTGATGAGGTGTTGACC  
AACATTGACCGGATGCTTGTTCGGGCTGAACGC

>RXA02426-downstream  
TAGATAAACAGCAGCAGGCTGAT

>RXA02487-upstream  
GGCGAGTGGTACCGCACCGCGACGTCGGAGTGATGAAGAAGCCGGGTTTCATCCGCCTAGT  
TGCTCGCATCAAGAAAGTCATCATCACTGGCGGTTTCAAC

>RXA02487  
GTGTACCCAGCTGAGGTTGAAGAAGTCCTCGCAGAGCACCCAGACATTGAAGATTCCGCA  
GTCGTTGGTATCCCGCGTGAAGACGGCTCCGAAAACGTCGTTGCTGCCATCACTTTGGTG  
GAAGGTGCAGCGCTGGATCCGGATGGCCTGAAGGAATTCGCCCGCAAGAACCCTACCCGC  
TACAAGGTTCCGCGCACTTTCTACCACCTTTGAGGAGATGCCGCGGGATCAGATGGGCAAG  
ATTAGCGTCGTGAAGTGCAGGCGGAGTTGTTGAAGAAGCTCGGCAAG

>RXA02487-downstream  
TAGACGCCGATTTAAGAGGTCTGA

>RXA02490-upstream  
TCATAGCTACGCGCATGCCACATTCTAGATCGCCGAAGAAAGCAGCGGGACGTCTCTAT  
ATACTAAAGGGCACTAAAGCAACGCAGTTGAAGGGACACC

>RXA02490  
ATGTCAGCATACGAAACCAAGAATGGCTCCAGCACTACCCAGAGTGGACGCCACACTCG  
CTGGAATATGGCGACACCACCCTGCTGGACGTTTACGACAACAACCTGGCCATTAACGCA  
GACAAGCCAGCCACCTACTTTTTTCGGTCGTTCAAAACCTACGGTGAAGTGGACAAAGAA  
GTCCGCAAAACTGCCGCTGGCCTGCGCGCACTAGGTGTCCGCCCCGGCGATCACGTAGCG  
ATTATCCTCCCAACTGCCACAGCATCGCAGCTTTCTACGCAGTGCTGAAACTCGGC  
GCAGTAGTCATTGAGCACAACCCGCTCTACACCGCCACGAAGTGTCTGAACCCCTTCAAA  
GACCACGGTGGCGCGTTGCCATCGTCTGGGACAAAGCCTCCCCACCGTCTGAACAGCTA  
CGTGGACAGACCCAGTTGGAACCATCGTGTCTGGTCAACATGATCAACGCGATGCCACCA  
CTCCAGCGCCTAGCACTTCGGCTCCCAATCCCTGCACTGCGCAAGAGCCGCGAATCCCTC  
TCCGGCGCAGCCCCAACACCGTTTCTTTTGAACCCCTGACCAGCGCAGCAATGGGCGGC  
GACGGCGACGACGTAGTTTTCAGAACCCACCGTGACCAAGAATCCGTGCGGCTGATCCTC  
TACACCTCCGGCACCACCGGACGCCCCAAGGGTGCCAGCTCACCCACGGAACCTGTTT  
TCCAATCTCCTCCAAGGAAAGCACTGGGTTCCAGGTCTCGGAGACAAACCAGAACGCATG  
CTTGCAGCCCTACCAATGTTCCACGCATACGGT

>RXA02511-upstream  
CCATGCTTGCGCAAGCATGGGGCACCATTGATGGGGCACCAGGCACTGTTCGACCCAACGC  
TGACTTCAGCGATCCGTACCGCAGCACCGAAGGAGCACTG

>RXA02511  
ATGCTGGGACTTCATGGACGTAAGCCTGCGCAGGTTATTGTTGAGCCTGTTGCCAAATTG  
ATGATCAAGTTGAAGGTGACGCCTAATCAGCTCACCTTAGTCAGCGCTGGCCTACCGTT  
GGGGTGGCTTTGCTGCTGATTCTACGGGGCATTTGATTGGGGCGGCAGTTTTCAGGGC  
CTGTTTTCGGCTTTTCGACATGATTGATGGCACGGTTGCTCGCATGCAAGGTGGTGGCACC  
AAATTTGGTGCCACCTTGATGCCACGTGTGACCGCATCACTGATGGTGCATATTTGGT  
GCGATTACCTGGTGGCTGGTGTATTCTACGATGCACCACAGGCATTGGTCGCTGCCTCC  
TTGGTTTGTGTTGGTTGCCTCCAGGTGATCTCTTACGTGAAAGCCAGGGGAGAGGCCTCC  
GGATTACCATGGACGGCGGTCTCGTGGAACGCCCTGAGCGTCTGATTGTGAGCCTTGT  
GGTTTGGGGCTGACCGGAATGGGCGTTCCATATGCCATCGATGTGGCACTGTGGGCCCTT  
GCAGCTGGCAGTATTTACACTGTTGTGACGCGCTTGGTCATGGCTGGAAAGTCCCCATTG  
GCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGATTACAGCAACACCAAA

>RXA02511-downstream  
TAAAAATTAGCCGAGGGAGCATC

>RXA02512-upstream

GCTGGAAAGTCCCCATTGGCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGAT  
TACAGCAACACCAAATAAAAAATTAGCCGAGGGAGCATCGC

>RXA02512

ATGAAGCCGAAGGATTTCTGCACAGCGGAAAATTGGGCGGAGAATTTAAGCGCACTGGGC  
TATCTAGCTGGTTGGCGTTTTGTCCGGATGCTCCCTTTGCCTATTGCTCGCCGGGTGTTT  
GACCTTGGGGCGGATCTGGCGTCGAAAAGCGGAAAAGGCATGGGGCAGCTACGCGCTAAT  
CTGGCGCGGGTGGTTCGGTGCAGGAAAACGTTACGAGGCGCTGGTGAAGCAAGCAACGCGC  
AGCTATGCGCGGTATTGGCTGGAAGCGTTCCGGCTACCGGCGATCGCGCGAGATCCTGAG  
CTGCTTGCAGCGTTGCGTAAGGGAAGTGTGGCCTAGATTTGTTGGATGAATCTTTGGCT  
GCCGGCAAGGGCGTAGTTTTGACGCTCCACACAGCGGCAACTGGGATATGGCTGGCGCT  
TTTCTGATTAGCCATCATGGGCAATTCACCACCGTTGCAGAAAGGGTCAAGCCGGAACGC  
TTGTTTGAAGCGTTCGTGGAGTTTCGAGAAAGCCTTGATTTGAGGTGCTGCCTCTCACC  
GGTGGCGAGCGTCCGCCGTTTGAAAAGCTGAAAGAGCGCCTGACATCTGGAGGTATCGTG  
TGCCTTCTTGGGGAGCGTGACCTGCGGCATTCCGGCGTGGAGACCACTTTTTTGGTGAG  
AAGACCTCCATGCCAGCAGGACCTGCGCAGCTGGCCATTGAAACAGGTGCGGCGCTGCAC  
GTGGTGCATCCATGGTTCGATGACGACGGCTGGGGTCTCAGCGTATCCGATGCCGTGACC  
GTGGATAATTTATCCGACACGGTGCAGCGGATCGCACATCTTTTATGGCAAATATTACG  
GCGCACCCCGCTGATTGGCATATGCTCCAACCCCTGTGGTTGGTGATTGGATCCGGAG  
CGTCTCAAGCGCTCTAGGGAGCAGACAAATGTTCAAAACCGGTGGCATTACAGGAG

>RXA02527-upstream

ATTGGAGCAATCTTTTAATCAAGTTGGGAATTCCAGCGTTGATTGTGGTTGCCATGTGGT  
TTGCCCCGACCCCTGAAGCACTCACGGATCAAGCGTGGCGG

>RXA02527

ATGTTTGGCCTGTTTCATCGCGACGATTGTGGCGATTATTCTCAAGCCAATGCCAATGGGT  
GCCGTGACAATTATCGGCATGATCGCCGCGGTGTTGACTGGTTGGTGCCGTTGACGGCG  
TCTTCTGATGATCCCGGCGCGGTGTATGGCCTTATTGGTTTCAGTAACGGCACCATTGG  
CTGATTGTGATGGCGTTCCTGATTTTCGCGTGGATTTCATCAAGACGGGGCTTGGACGTGCA  
ATAGCGTTGTTCTTTGTGTCTAAAGTCGGCGGAAAAATGCTGGGTGTGACCTATGGTTTG  
GCGCTCGCTGATTGGTGTGGCTCCTGCGATTCCATCAGCAACTGCCCGAGGTGGTGGC  
ATTATGGCTCCGATTATGAAGTCGGTGGCATTGACTTATGATTCCACTCCTGGCCCAACT  
CGTCGACGGGCTGGCGCGTTCTTGGCGCTGAATGTGGGACAGGTAAATGCGATTACGTGC  
GCGATGTTTCTAACTGCAATGGCAGGAAACCCCTTGATCGCCTCTTTGGCTTCGCAGATG  
GATGTCAATATCACGTGGACAACTGGGCTGTGGGTGCGATTGTGCCTGGTCTGGTGGCG  
CTTATTGTGGTGCCGTGGGTGGTATACAAGATCTATCCACCTGAGTTGAAGGACACCCCT  
GAGGTCAAGAAAATGGCTTCTGATGAGCTCAAGCAATTGGGTGGGTTTACTTATGGTGAG  
AAGGTGCTGGCGGGAACCTTTGTTGTGTTGCTGCTGCTCTGGACAGGTGGCGATTGGTCT  
TTGGGAATCTCGGCAACTACCACCGCTTTCGTTGGCGTCATCATCTTGCTAGTGCTCAC  
GTGCTGACGTGGGAGGACATCATTCAAGAAAAGACTGCGTGGGACACCATGGTGTGGTTC  
GCGGTGCTATACATGATGGCAACAGCGTTATCGCAGTACGGATTTCATCGCATGGATCTCT  
GAGGTAATTGCTTCCAGTTTGGGTGGCATGAACTGGGTGCTTGTGTTGTGTTGGTG  
CTGATTTACTTCTTCAGTCACTATTTCTTTGCCCTCGGCAACAGCGCATATTTCTGCGATG  
TACTTGGCCTTCTGGGTGCTGCGATTGCGATTGGTGCACCCCGTTGATGGCGGCCCTG  
GTGTTGGCGTACACCTCCAATTTGTTCTCTTCACTCACTCAGTATTCTGGTGGTCTCTCG  
CCAACATTGTTTGGTTTGAATACATCACGGTGGGTGAGTGGTGGCGGACCTCGGCAATT  
GCTGGCGCGGTATCGATTACAATCTGGTTGGTTATCGGTGGTTTGTGGATGAATGTCATC  
GGACTCTGG

>RXA02527-downstream

TAATCGAAAATTAAAGGTAAGGG

>RXA02547

GCTGCGCGGCTGACCGTGGATGAGTATCCGGCGGCGAGGGAAGCGCTTGAATCTGCAGGT  
CAGAGGAATGTAGAGGACCGAACCCGTGCGGTTGATGAGTTCAAAGCGGCGGATCAAGAG  
CTGTCTTCTTTAGTAAAGGCAGCAGTAATTTAGTACCGTTTGGTGCAGGTGCGGGAA  
AATTTGTGTGAGGATTTGGGCGTGAGCCCGCGGATATGCCCTTTGCCGGTGAGCTGATT  
GATCCGAATAATGCGGAATGGGAACCCGTTGTGCAGCGCATTTTGGGTGGTTTGTGTCG  
GAAATGTTGGTTTCTCATGGGTGTTGCCACGGGTTCCGGATTGGGTAAATGCCAAACAT  
TTGGCAGCGCTGCTGAAATTCAACGGCGTGGTGACAACGGGGGAGTACAAAACCTCGCGT

TTTCCGGCGGATTCCCTGATCCGAAAAGTTGATGTTGTGGAGTCGCCGTTTCGCGATTGG  
GTAAATCAAGAATTAGGCAAGCGTTTAAATATTCGGTGCGTGCGCACTCCTGAGGAATTG  
TCGGCGCTGGGGCCACGCGATCAGGGCGTGACCATTTTGGGTGTGCGAAAATTTGCGCAG  
CAGACAGGCGATCCGACGACGCGTTGGGAAAAAGATGATCGCCGAAAGCTGGGGGATCGT  
TCCACATACCGTTTGGGTTCACCAATGATGCCAAGGTGAAACGCTTCGGGAAACCGTG  
AAAGCTGGCAAAGCAGTTGTGACGGCAGCTGATAATCGCATTGCTGCAAACCGCGTGAG  
CTGCGGGAACCTGAACGGCAGTATCAAGCTTCGCAAGAAATTTGAAAGTGTCGTGGGCT  
CAGATTGATGTGGAATCAGCCGACGCGCGATTGCTGAGCTGGACCGATTGCTGGAAGAG  
CTGAACAACACTCCAGAGGCCACCGAGCTTTCCGCGCGGCATGAGGCGGCGAAGCAGACG  
CTCGCGAGGGTTTCTGACTTGCTTGTGCGAGCTCAGAGTGAGGAAACCGTGGCGTCGATG  
AACCTGAAACGCGCCGAACTGAATTGAAACGGCTCGAAAGCCTGCCGTTGCGGAGGTT  
TCTGAAGAAATCGCGCGGGAAGTGGAGAACTATTTCTTGCCAACACCCGCCGGTTTAC  
GCCGCAACGTGGATGAGCAGACCATTTGCGCTGCGCGAGGATCTGGACAAACAAATCGAT  
GCCAATGAGGCGAAGCTTCGACGTTGTGAAAACCAAATGTTGGCATTTTGCGCAGCTAT  
ATTGAAACGTGGCCTGCGAACCAGCGCTGACTTACAAGCCGAACCTGAGTTTGTGGTGAG  
GCCATCAACCGCTCGGCGAGCTTCGACGCGATCGTTTGGCAGAATTCACGGCCAAATTC  
CTAGGGCTCATGAACGAGATGTCCACCCGAAACCTCGGCCAAATCTCGCGCGCTCTACGT  
GATGCGCGCCGGGAAATCGAGGAGCGCATCGAGCCGATCAACGCCCTCCTTGGCGCAGTCG  
GAATTCAACGAAGGTGCTTCTGACATCGACATCCGTGATCAAAGTGGTCCGATTGTG  
AGGGAATTCAGCAGAACTTGATGCCGCTACCAGCGGTGACCTGGGAACCAAGTACCGAG  
AAACAAGCCTTCGCGCGTTATGCGCTGATCGTGAAATCATTTCCAAACCTCGCCTCCAC  
GACTCCGCGCGACCGCGCTGGCGCAACACCGTTCTAGACACCCGCCCGCCAGTTTCGCTTC  
ATCGGCCTCGAGCGCGATTCCGACGGCGCAACCGTCAACACCTACGTGACTCCGCATCA  
CTTTAGGCGGACAAGCCAGAGCTGGTGTCTTCTGCTCGCGCTGCCTTGGCGCTAC  
CAGCTAGCCGAACCCGGCGCCATTATCCACCTACGCCACCGTCATTCTGGACGAAGCC  
TTCGACCGCGCCGACCCCGCTTACCCGCCAAACCATGAACGCTTCCACAGCTTCGGC  
TTCCACATGGTGCTCGCGACCCCGCTGAACTTATCCAAACCTCGGCGATTATGTCGGC  
TCCACCATCGTGGTCAGCTACACCGAAAAACCAAACGCCAGGGCGCAATTACAGGGCAAT  
TCCAGTTTCTCTAGGATCGAGAAA

>RXA02547-downstream  
TAACATGCCATTGTTTATCGACG

>RXA02561-upstream  
ATCTGCTCAATAACCTAACCTAAAGTCCATGCACGCCCTCGTCGCCCCAACCTCACCTCA  
GCGCACCCGTGTTCTCAGCGGCCTGATTTTCGCCCAAATC

>RXA02561  
ATGGTTGGTGCATCCAATGGCGTGACGCTATCGATGGGAAGTTTGCTGGCAGCACACTTG  
GCGGGAGCTTCGTGGGGAGGATCAGCCGCCACATTGACCACGATCGGCGCAGCTATCTTT  
TCGATTCCCCTTGCCCGCATGGTCTCCACATACGATCGCCGAACCTCACTCAGCACGGGC  
ATGTTGCTTGGTTGCGTGGGCGCACTACTGGCGATCCTCGGCGCACAAATTCGGCTTGTTT  
CCAGTAGTACTTTTGGCATTTTTGTTCCTCGGATCCATGTCGGCGGTTAACCTCCAAGCA  
CGTTTCGCCGCAACCGACGTGGCCAGTGAAGAAACCCGCGGCCGCGACCTCTCGATCGTT  
GTGTGGTCCACCACCATCGGCGCAATCGCCGACCAAATTTATTTGAACCAAGCGCCGCA  
TTCAGCGAAACCCCTGGGCCCTCGAACAACATGCCGCGCATACCTGCTGTGTTTATTTGGC  
CAGCTCATCGCCATCGCAGTCTGGCGATTACCCCTCCCCAAAGGCCCTCAAACCCGAAGCC  
ACCCCAAATGCACCAACAGAAAAGAAGCGCCTACCCCGAAAGCCCTCCAAGCCATCACA  
TCGGTTGCAACCGCACACTTCTCCATGGTTCGGTCTCATGTCCATGGCCGCCATCCACATG

>RXA02566  
ATCAGTTTGCACGTCGCCGGAATGTACGCACTCTCACCAGTGTTTCGGCCTGCTCACAGAC  
AAACTCGGCCGCAATGTACCATCTATTCCGGCTTCGCCATGCTCGCCACATCCGCAGCA  
TTTCTTATCATTTGGCCCGAACCACAGTGGGCCATGATCACATCCATGATCCTGCTTGGG  
CTCGGCTGGAACCTCTGCCCTCGTTCGTTCTTCAACATTGCTTGTGACGCGCACCCCATC  
CACCACCGCACCTACGCCAGGGGCGCAGCGACCTAACGATGAATCTTGGGGAGCTTCA  
GGCGGGTTGATCGCCGACCGTTAATTGCCATGGGCGGAATGCCCTTGTGGCAGGCGTC  
GTTCTTGCAAGTTGTGGCGCTTCAAACGGTGCTTAGTTTCAAGAACCCGTTCAATTGAAAAG  
ACTCCTGCTTCATGTTTT

>RXA02566-downstream

TAGCCTAGGAATTCACGCACGAC

>RXA02571-upstream

TGGACAGGCCCGGGCCGCGTACGGTGTGGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGC  
ATTGTCGTGGTTGTTGCCGCTTTTGGCAGTCGGGATGGC

>RXA02571

GTGGTGGCTCTAACTCAAATCGTCGGACCGTCCGGCTCCGGGCTCACGCGGGAATTGGAA  
AAACGCTACCGGGAACGCCCGAGCGGTGATGCTGACCGCCGACCCGCGCGCATATC  
ACCTACCTGCGCGCGACAGTCGCCGAGGAGCTGGCCTTTGGGCTGGAACAACGCGGCATC  
GTACCCGCGCAGATGTGGGAGCGCGTCCGAAACATCGGGCTCGGCCTCGAGAATCTGCTA  
GACCGCGCACCCGCGCAACTTTCCGGCGGGCAAACACGGCGGCTGGCGATCGGCACCGTC  
GCCATCTTAGAGGCGCAACGATGCTTCTCGACGACCCCTCTCCGGTCTTGATACCTCC  
TCGCGAGCCCAACTCATCACATGTTGGAATCATATGAGGGCGATGTCATCGTCGTGCG  
CACAAGCGGTGGCTCGACGCGCCGACTGTGTACTTAGGGGATTTGGAGGAGCTGTCCCTG  
CCTGCGCGGGTGGAAATTTCCGGTCCATCGCGAACGTTTTCAGCGATTACAGGAACCCGC  
GGACAACAACGCCGACGCTGGTGGCAATTCAACGAATCCCAACCACAGTTTCAGATCGGC  
CCCTGGATATTACTGTTTCTGCGAGTCAAGTGTGTGGTTGCAGGGTCCCAATGGTTCA  
GGGAAGTCCACACTCCTGCGTGGTCTTGCCAATGAACCCGGCACTGAATTGATGCTGCAA  
AACCCTAGCGATCAAGTCATTGACTCCACTGTTGCTAATTGGGTGCCAGGCAGTAACAGT  
GAAGAACATCCGCTGGATTTATCGCAACGCGAACTCCGCCTTGCCCAATGCGACGCAGCC  
CTGGGTAATAACCCGGAAGTTTGTCTTGCTGATGAACCCGACGTCGGCCTTGATGTCGGC  
GGTCGAAACGCCATCCACCAGCGCTTTGCGGATTTCTTAGGGAATGGGGGAGCGCTGATC  
CTGACCTGCCATGATGAAACCTTCGTGGCAGAGGTAGCTGAATACGCGATAGTGAAGGAA  
ATGGGGCTC

>RXA02571-downstream

TAGGTTTCTTTGGACCAAACCAC

>RXA02578-upstream

GGCAAAAATGAGGAACAGCAGCCCCGAATAATGAGGACCGTTGCAGATCGCTTCATAAA  
AACAGCCACACCTTTCCGCTAAACTCGCATGTTGAAATA

>RXA02578

ATGTCTACCCAATCATATGCACCCATCCGCCATCGCGGATTCATCAGCTCACTCGAGGGA  
CTACGCGCAATCGCCTCCCTGGGAGTCTTGGCGACCCACGTTGCATTCCAAACCTCCGTC  
GACCCCGCCAGCAACATCGGTGCAGTACTCGCGGTTTCGACTTTTTCGTGCGCGTCTTC  
TTCGCCCTCTCCGCCTTCGTTCTTTGGCGACGCCGCGCCGGGCAACCAGTGGGACTGTAC  
TACCTCAAACGCCTAGCCCGCATCATGCCCGCATACTGGGCAACGGTCATTGCAGTCCTG  
CTGTTTATTTCCACCGGCCCTGGTTAGCCAACCTGACGATGACCCAAATCTACTGGCCA  
GACGGGCTCATGACAGGCCTCACCCACCTTTGGTCCCTGTGCGTGGAAAGTGGCGTTTAC  
CTGGTGATGCCGCTTCTCGCGTGGGTGTTGGATAGGTTTGGTCGGCCGGTGGCGATCCTG  
TTGATTGTTGGTGGGGCAGTGTGAGTCTGGCGTGGCCGTGGATTCCCCTTGTGGAGCAT  
GCGTTGGACGAGGGGTGGGCGAACATGCAGATCTGGCCACCCGCTTACGCTTGCTGGTTT  
GCAGTCGGCATGATCGCCGAGAAATTGAAGGAGTTCGATTCCCACGGGTTCCGAGCTTT  
GTGTGGGTGGGTTTAGCTTTAGTGGTGGTTCGCTTGGATCGCGGGCCAAGAATGGTTCGGACCA  
CTAGGTTTAGTGCACCCAGCCCCCTGGGAATTCAACTTAAGAGTCTTCGCGGGCACACTT  
TTCGCTGTATTTCTGGTGGTTCCCTACGCGCTGGGTACGCCCTCTCGGCTTCTTGATTCC  
AGTTGGATGAAAACGCTCGGCACCTGGTTCGTATTCATCTTCTCTGGCACCTTCCCGTG  
CTGACGATTGTGTTCCCACTGCTCGGGTTGCCTTTATTTAGTGGAAATTTCTGTGGTG  
TTCATCGTGACGGTCTTGTGACGATCCCAAGTTGCCGCCATCAGCTACACCTTCATCGAA  
GAGCCCATCAGCGGTGGACCCGGCGGCCATTCAGGCTGGGGGTCTGTTAGGATTACCAT  
TTTTCTGGGGGTAGGTCTGGAAAA

>RXA02578-downstream

TGATGAATTGGCACACGTCAAG

>RXA02581

GTCCCTGTGCCGCTTTATGATCCAAACGAGCCAGGACACGCAGACCACCTCAACGCTGTT  
TTCGCAGACAGCGAGCCAGTTGTCTGTTCTGACCAACTCCAAGTCCGCAGGTGCCGTGCGC  
AAGCACTTCTCCAGCCTTCCAGCTGCAGAACGCCACGCATCCTCTCTGTAGATTCTTCTG



CCTGATTCTCTCGCGGATTCTTACGAGAACCCAATGCTGACCGAAGCCGGCCGCCGCTG  
GCTGCTCTGCGCCAGTCCGCGCCATTGATCTGACCGCATTCTGCAGTACACCTCCGGC  
TCCACCCGAACCCAGCTGGCGTTGTTCTGACCAACCGCTCCATCCTGACCAACGTCTTG  
CAGATCTTCAGCGCCGCACAGCTGAAAACCCCACTGCGCCTGGTTTCATGGCTGCCACTG  
CACCACGACATGGGCATTATCCTCGCGGCGTTTGTCACTATGCTTGGCCTGGACAACGAG  
TTCATGAACCCACGCGATTTCTGTCAGCAGCCTTCCCGCTGGATTAAGCAGCTCAACCGT  
CGCGAAAGCGACGTGGACGTTAACGTCTACACCGTGGTTCCTAACTTCGCCCTCGAGCTT  
GCAGCACGCTACGCAAAGCCAGCAGAGGGAGAGACCCCTGGATCTTTCCGCATTGGATGCC  
ATCATTATCGGTTCCGAGCCAGTCACAGAAAACGCTCTGACCACCTTCCGTGAAGCTTTC  
GAGCCTTACGGCCTGCCTGTTACAGCCCTGCGTCCTTCTACGGTCTTGCAGAAGCATCC  
CTGCTGGTCAACACCCACAGACCGAAAACCGCCCACTGATCTCTACTTCGACCGCGAG  
GCCTTGGCCGAAAACCGCGTTGAGCTTGTAGAAAAGGGCAATAACAAGGCTGTTGCTTTC  
GTCTCCAACGGCCAGGTTGCAGCCCCACAGCAGCTGGTCATCGTTGATTCCGAAACCGGA  
ACCGAGCTGGCAGACGGCCAGATCGGCGAAATCTGGACCCACGGCGAAAACACTGCTGCA  
GGTTACCTCGACCGCGAGGAAGACACCGCAGAAACCTTCCGCAACCGTCTGACCACCGC  
CTGGAAGAAAACCTCCCGCGCAGAAGGTGCTGCCGACGACAATACTGGATGGCCACCGGT  
GACCTCGGCGTCATCGTAGACAACGAGCTCTACATCACCGGTCGTCTGAAGGACCTCATC  
GTTGTGCGCAGGCCGAAACCACTACCCACAGGACATCGAGTACACCGTCCAGGCTGCTTCC  
GCACACATCCGTGCAGATTCCGTGCGAGCATTGCGAGTCCAGGCGATGACATTGAAAAG  
CTCATCATCTGGCAGAACGCGACACCACTGCAAACGAAGCCGACGATGCAGCTGCTGAA  
GAAGCAATCCGCTCCGCCGTTGGCACTGCACACGGTGTGTTCAGAAAGAGATCCGTATC  
CTCGCACCTGACGAGATCGCGCGTTCTCTCCCGAAAGATCGCACGCCGCGTCAACCAAG  
CGCAACTACATTCAGGAACAAGCTAAC

>RXA02581-downstream  
TAGTTCTTTGCAGACACCGCAGG

>RXA02582-upstream  
TGGATGTCTATTCTCCTCAGCCTCGTTTTGGTTGAGGCGGATAGTTTTAATATTTTTTTA  
AGTTTAAGTTGTAATCGAGCTGAAAGGCTGAGGCCCTCAAT

>RXA02582  
ATGGAACAGAGCCAATCGTCGGATCAGAAGATGACCGTTGAACAGGTTTCGCACCTGGCTC  
CGTGATTGGGTTGTCCGCACCACGGGTATTCCGGTGGAGGAAGTTACGGATGACAAGGCA  
ATGGAGACCTTTGGCCTTTCTCTCGCGATGTTGTTGTGTTGTCTGGTGAGCTGGAAAAC  
CTGCTGGACACCTCCTTGGATGCCACCATCGCTTATGAGTACCCAACGATCCGTAGTTTG  
GCGCAGCGCCTTGTGAGGGCGAGCCTCGTCGTGCACATACCCAGCGTGAATTGAATTTTC  
TCCGCGGTGAGCGATTCCCCAGGTTCCACGATATTGCGGTTGTGCGGTATGGCTGCGCGT  
TACCCAGGCGCTGAGAGCCTGGAGGATATGTGGAAGCTACTCGTCGAGGGCCGTGACGGT  
ATCTCGGATCTACCGATTGGCCGTTGGTCTGAGTATGCAGGCGATGAGGTTATGTCTCGG  
AAGATGGAAGAGTTTTCTACCATCGGTGGCTACCTGTCAGATATCTCTAGCTTTGATGCG  
GAGTTCTTTGGTCTGTCTCCGCTCGAGGCCGCCAACATGGATCCTCAGCAGCGTATTTTG  
CTGGAGCTAACGTGGGAGGCTTTGGAGTACGCTCGCATCGCACCAAAACACTTTGCGTGGC  
GAAGCCGTGGGCGTGTTCATAGGTTCTCCAACAACGATTACGGCATGATGATCGCTGCC  
GATCCAGCAGAAGCACATCCTTATGCGCTGACTGGTACTTCTAGTGCGATTGTGCGTAAC  
CGCATTAACCTACGCTTTTCGATTTCCGCGGTCTTCCGTCAACGTGGATACCGCATGTTCT  
TCTTCTCTGGTAGCGGTTACACAGGCTGTCCGTGCGCTGCGTAATGGCGAAGCGGATCAC  
GCTATCGCTGGTGGAGTGAACATTTTGGCATCTCCATTTGTCAAACTGCATTGCTGAG  
CTCGGTGTGATCAGCCCAACCGGCAAGATCCACGCATTCTCTGATGATGCCGATGGTTTC  
GTGCGTTCCGACGGCGCCGAGTCGTTGTGCTGAAGCGCGTGGATGACGCAATCCGCGAC  
GGCGACAAGATCATCGGTGTGATCAAGGGTCTGTCAGTGAACCTCCGATGGTCACTCCAAC  
GGACTGACCGCTCCAAACCCTGACGCACAGGTTGATGTGCTGCAGCGTGCATATGTTGAC  
GCTCAGGTTGATCCCACACCGTGGATTACGTTGAGGCTCACGGCACCGGCACCATCCTG  
GGTGACCCCATGGAAGCAACTGCCCTGGGTGCTGTTTTGGGCTATGGCCGTGACGCATCC  
ACCCCAACTCTTCTGGGCTCTGCAAAGTCCAACCTCGGCCACACTGAGTCAGCTGCGGGT  
ATTGCAGGTGTCAAGGTGCTGCTTGTGCTTGTGAGAACAAGACTCTGCCACCAACCGTG  
AACTTTGCAGGTCCAAACCGCTACATCGATTTCGATGCTGAGCGTTTGGAAAGTTGTGGAA  
GATCCACGTGAATGGCCGGAATACAACGGTCACGCAGTAGCTGGTGTGTCTGCGTTCCGG  
TTCGGTGGAACCAACGCGCACGTGGTGATCTCTGAGTACAACGCAGAAGACTACGAAACC  
CGTGCCCCGAAGGAGGCGTTGCTTCTGACCAGCAGGTTGCCCTGCCGGTGTCTGGTCAC  
CTGCCATCCAGGCGTCGACAAGCAGCTGCTGACTTGGCGGACTTCTTGGAGGGCCGCAAA

GATTGCGACCTAACCCAGTAGCCCGCGCTGGCAGGCCGCAATCATGGCCGCTCCCGC  
GCAGTCGTGCTTGAAGCACTATCGAGGAAGCCGTAAAGCGCCTGCGCCAGGTCGAGAA  
GGCAAGGTCAGCGTCGGTATCTCCGAGCTGATCCCCAGCGGCCAACGGTCCTGTGTTT  
GTGTACTCCGGTTTCGGATCCCAGCACCGCCTCATGATCAAGGAATTGTGCTCAATTTTCG  
CCACAGTTCCGCGAGCGCATCGAAGAGCTCGATGAAATGGTTAAGTTCGAGTCCGGCTGG  
TCCATCATGAAACTTGTGTTTGGATGATGAGCAAACTTACGACACCGAGACCGCGCAGGTT  
GTGATCACCAGCAATCCAGATCGCACTGACTGACCTGTTGGCAAGCTTCGGTGTAAAGCCA  
GCTGCCGTATGGGCATGTGATGGGTGAGATCGCTGCCGCTTACGCTGCCGGTGGACTC  
AGCGACCGGATACCATGCTCATTGCCAGCCACCGTTCCCGCCTAATGGGCGAGGGCGAG  
AAGTCCCTGGCTGAGGATCAGCTGGGTGCCATGGCTGTGGTGGAAATTCGCCGCTGCGGAC  
CTGGATAAGTTCATCGAAGAAAACCTGAGTACAAGGGCATTGAGCCTGCTGTTTATGCA  
GGCCAGGCATGACTACCGTGGGTGGACCTCGCGACGCCGTGGTTTTCAGTTTCGTAGAGAA  
CTGGAATCTGAAGACAAGTTTGCCCGCTGCTCAACGTCAAGGGCGCTGGCCACACCTCT  
GCTGTGGAACCACTTCTTGGTGAGCTCGCTGGCGAAATCGCTGGCATCGAGCCACTTCCG  
CTGCAGATCCCGTTGTTTTCAGCTCTGTGATCAGGGTGTACCTACCCAGTTGGAGCAGTG  
GTCCACGACGCCGATTACATGCTCCGCTGTACCCGCCAGTCCGTGTACTTCCAGGACTCC  
ACCGAAGCTGCATTGCTGTCAGGCCACAACACCTTGGTGGAAATTTCCCGAACCCAGTT  
GCACTCATGGGCATGATGAACACCGCGTTTACCGTGGGCAAGCCTGATGCACAGCTGCTG  
TTCAGCCTGAAGCGAAAAGTCCCAGAGGCAGAAATCCCTCCGCGACCTTCTGGCGAAGCTG  
TACGTCAACGGCGCAAACGTTGATTTCTCCGCGCTGTACGGCGAAGGTGAAACCATCGAT  
CCGCCACACATCACCTGGAAGCACAGCGCTTCTGGACTTCCGCACGCCCATCCTCTGGC  
GCATCCCTGGATCTGCCGGGCTTCCGCGTGAATCTGCCAAACAACACTGTGGCGTTTTCC  
ACCCGAGCTTCCCTCCGTCGACGCAAGTGGACGAGCGGACATGCTGCCACCAAGCGGCGAA  
ATCACCACCATCGTGACTCGCTCCTTGGGCGGTTTGGCCTGTCCGTATACAAGATTGAG  
GGAACCACAGCACTCTTGTGCGCGAAGGTTTTCGAGCCAACCCAGGATTGCGCGCAGCA  
TCTTCTTTCGACGGTCCAGGCTACGACGGATTCAACACCGATTACAGCGACCAAGCCAGAC  
CCTCGCTCCGACCTGCCCTTGGACATCGAAGCAGTCCGCTGGGACCCAGCGACCGAAACC  
GTCGAAGAGCGCATGCGCGCCATCGTCTCCGAAGCAATGGGCTACGACGTGGATGACCTC  
CCACGCGAACTCCCACTGATTGACCTCGGCCCTCGACTCCCTCATGGGCATGCGCATCAA  
AACCAGCATCGAAAATGACTTCCAGATCCCACCACTCCAGGTCCAAGCGCTCCGCGATGCA  
TCCGTCGCTGACGTGGTAATCATGGTGGAAAACATGGTTCGCTGGCCGCTCCTCTGAGACG  
CTTGTGCGACGCCACCCCGCAGGTGCCAGCTGAGGCAGCAGGGGAGGCTCAAGCTGCTGAG  
TCTTCTGCTTCGGGCGAGGACGTGCAGGGCGTTGGCGTTGCACCGCGAGATGCGTGGAA  
CGCATGGTCTTTGGTACTTGGGCAGGCCTGACTGGCGCTGCGGCAGCTGGCGTGACCAGC  
AAGTTGCCACAGATCGATGTCGATACTGCAACCGCAATTGCCGAGCGCCTCACCGAGCGT  
TCCGGAATTGAAATCAGCACTGAACAGGTGTTGGCTGCAGAAACCTCGAACCCTGTCT  
GACCTGGTGCGTGAAGGCCCTCGAACTGAAGTTTCAAGGCAACATTCGTGTGCTGCGTGGA  
CGTGCAAGAGGCTCCACCAAGCCTGCAGTGTTCATGTTCCACCCAGCTGGCGGTTCTTCC  
GTGGTCTACCAACCACTAATGCGTTCGTCTGCCTGAAGATGTCCCTGTCTATGGCGTTGAG  
CGTCTGGAAGGCGATCTCGCTGACCGCGCGGCAGCATATGTTGATGACATCAAGAAGTAC  
TCCGATGGCTTCCCAGTAGTTTTGGGTGGCTGGAGCTTCCGCGGTGCCGTTGCCTTCGAG  
GTTGCCACCAACTGGTTGGCTCCGATGTTGAGGTAGCTACCGTGGCGTTGCTGGATACT  
GTGCAGCCTTCAAACCCAGCACAGATAACCGCTGAGGAACTCGTGCACGCTGGACTCGC  
TACGCGGACTTCGCCAAGAAGACCTACGGCCTTGATTTTCGAGGTACCTTTTGAATCTTG  
GACACCATCGGTGAAGACGGAATGCTGTCCATGATGACCGACTTCCCTGGCCAAACCCGAC  
GCCTCCGAGCACGGATTGTCCGAGGTGCTGCTTGAACACCAGCGCGCTTCTTTTGTGGAC  
AACCAGCATCCTGGCTAACTTAATTTTGCAGACTGGGCAACGTTGAAGCCCCTGTATC  
CTGTTCCGCGCGGAACGCATGCATGATGGAGCTATCGAACTTGAACCAAACTATGCCAAG  
ATTGATCAAGATGGAGGATGGTCCGGAATTGTCAACGATTTGGAAATTGTTTTCAGCTGAAT  
GGTGACCACCTGGCAGTTGTGATGAACAGAAATCGGCACAGTCGGAGCTCATTTGAGT  
CGCCGATGATGAGATTTCTCGGAAGAAT

>RXA02582-downstream  
TAGTAACGGAGAGCTGACGGAAG

>RXA02583-upstream  
CAGTTGTCGATGAACCAGAAATCGGCACAGTCGGAGCTCATTTGAGTCGCCGATTGATG  
AGATTTCTCGGAAGAATTAGTAACGGAGAGCTGACGGAAG

>RXA02583

TTGAGTAACACCACTACTGCAGAGAAGCTAGCGGATCTGCGCGCACGCCTGGAGATTGCC  
AAAGACCCAGGTAGTGAACGCGCACGTAAAAAGCGCGACGAGGAAGGCCGAACCACCCCT  
CGTCAGCGTATTGATGCTCTGCTTGATGCCGGATCCTTTGTGGAGATCGGCGCACTAGGC  
CGTACCCCGGATGAACCCGATGCGCCTTACTCTGACGGTGTGGTGAATGTTATGGTGC  
ATCGATGGTCGCCCAGTGGCCATCTACGCCCATGACAAGACCGTTTACGGTGGTTCCGTG  
GGCATGACTTTCGGACGTAAAGTCAGCGAAGTCATGGACATGGCTATCCGCATTGGTTGC  
CCAGTTATCGGTATTCCAGGATTCCGGCGGAGCCCGCATTCCAGGATGCGGTGACCTCCTTG  
GCGATGTACTCAGAGATCGCGCGTCGTGACCTCCGCTGTCTGGCCGACGCCCTCAGATT  
TCCATCATGCTGGGTAAATCGGCAGGTGGCGCAGTGTATGCACCTGTGACCACTGACTTT  
GTTATCGGCGTTGATGGTGAACAGAAATGTATGTACCCGGCCAGCCGTGATCAAGGAA  
GTCACCGGCGAGCAGATCACTTCCGCAGACCTCGGTGGCGGTGCGCAGCAGATGCAAAAC  
GGCAACATTTCCTATTTGGCGTCTCTGAAGAAGAGGCCCTGAATATGGTCAAGGATTG  
CTCGACTTCCTGCTTTGACCTGCAATGATCCAGCCCTGTGTTTGCAGCACCAACGGAT  
GAAGAGATCGCCTACGACGAAGCTCTGAACTCGTTCATGCCTGACGACACTAACCAGGGC  
TACGACATGCATGACCTGCTGGACAAGCTTTTCGACGACGCCAACCTGCTGGAAATCCAA  
GAGGAGTACGCCCCAACCTGATCACTACCTTCGCCCCGCTTGATGGCAAGGCAGTCGGT  
GTGGTGGCCAACCAACCAATGGATAAGGCAGGCTGCATCGACGCTGACGCCGCCGACAAG  
GGCGCCCGCTTCATCCGTATCTGCGACGCCTACAACATCCCGATCATCTTCGTGCTGGAC  
ACCCCTGGCTACCTGCCTGGCGTGGACCAAGAGAAGGTCCGGTTTGATTACCGTGGCGCA  
AAGTAGCCTTCGAGTGGTGAATCGACCGTCCCTAAGATTTCCTTGATCGTGCAGCAAG  
GCTACGGCGGAGCATATGCCGTGATGGGTCCAAGAACCCTACCGGTGACCTCAACTTC  
GCATGGCCAACCGCACAGATCGCCGTGATGGGCGCAGCCGACGCTGTGCTGATGATCCAG  
GGCAAGCAGCTCGAAGCCGCCCCACCTGAGCAGCGTGAATACATGAAGAACTGTTTCATG  
GACTTCTACGATGAGAACATGACCAGCCCATATGTGGCCGCCGAGCGTGGTTACATCGAC  
GCCATGATCGAACCTGCAGAGACCGTTTGGTGCTTCGCCGAGCAGTCCGCCAGCTGGAA  
ACCAAGGCTGTGCGAGACCTCGACAAGAAGCACACGATCATGCCGATG

>RXA02583-downstream  
TAACGTCCAAAGAATTATCCAGA

>RXA02599-upstream  
GATCAAGCATCATACGATGTGCGAGATTGTGGCGGGCGTTGTTACAGGAGCAGTTGCAAC  
CGGCATTTGTTATGCACTCCTACTTGCGTAAAGGAGAATT

>RXA02599  
ATGGATCAGCTAATCCTCGACGCATTTATCGGCTTGAGAGTGACTTGGCTGAGTCCGGTG  
ATTATTTTGTTCACCCAGCTCACCGGGCCAACACTGATGTTTGTGTATGCGCTTGTGTGG  
GGCTTGTGCGCAAGAGCGCCACTGCCCCGATCGCGGTGGGGCTGGCTAATCTGATCAGT  
CATTTTCTCAAGAGGGCGTTTGAACGGCCTCGACCAAATACAGCAGAGCACTTGGTTGTA  
GAACTAACTTTTTCATTCCCTTCTGGTCATGCTGTGGGCGCTGCAGCATGTGCCGTGGCA  
GTGGGGTACTCCGTGAACCGGTGGTGGAACTCACGCTGTGGGTAATCGCGCTGCTTGTG  
GGGCTGTCTCGGTTGTATGTGCGGTGTGCATTGGCCAGCGATGTGCTTGCCGGCTGGGCC  
ATCGGTGCGTTGACTTCAGTGGTGGTGTACCAGCTGGAACCTCCTCCAGCGCCGC

>RXA02599-downstream  
TGAAACCACTGCTGAAAGTGGA

>RXA02618-upstream  
CGAAACCAGAAACACCCAGCGGCTCCTCGTCGAAAAGCGAATCTTTGAACTAGAAGCCCA  
GGCACGTTGGCTCGACCGAATTGAAGCATTGGAGCAGTAA

>RXA02618  
ATGACAAACACGCCTTTCCCCCTTGAACCTTCAAAACATCTCCTGCGCCTTCGGAGAAGGC  
CCACGCCACGTCTCCGCGCTCAACAACGTCTCGCTGGCAGTCAATCCCGGCGAACTCGTT  
GCCATCATGGGCCCCGTCCGGCTCAGGAAAATCCACCTTGCTCAACGTGCGCGGCTCCTG  
CAGCGCGCAACCTCTGGCCATGTGCTTATCGACGGTGCCAGCGCCTCAGACCTCAACGCC  
AAACGCGCAGCTGAAACCAGGCGTCGCCACATCGGAGTTATTTTCCAAAACCTACAACCTG  
GTCCCCACCCCTACCGTCGGAGAAAACATCGGTCTGCCCCTAGAACTCGACGGCAAAACC  
GACCGCCAGGCAGTAGCAATCGCACTCGCGGAAGTCGGCCTCAAGGGCTCTACGACCGCT  
TTTCCCGAGAGATCTCTG

>RXA02634-upstream  
CAACGCGAAGGCTTAGTTGTTTATTACCGGCTCACCTACCCGGAGGTGCGAGACTTTCTT  
AAGGTGAGCCGCTCACTATTAAAGAGGATGGCTGGCGAAG

>RXA02634  
ATGCGTGACCTTTTACCCTCTAGAGACGACTATCAGCTACTCCGCTTCTCCTGGAAGATG  
GACATTGCTGCTGGCGTCACCGTGGGCATTGTTGCCCTCCCCCTCGCTCTCGCCTTTGGT  
GTGAGTTCTGGAGTCGGAGCCGAGGCAGGATTAGTGAAGTGCATTATTGCTGGCCTGGTT  
GCAGCAATCTTCGGCGGTTCCAATGTGCAGGTTTCAGGACCAACAGGAGCGATGGTGGTT  
GTTCTCGCTCCAATCGTCGCCCAATATGGTGTGCGGTGCGGTGCGATTACTCAGCCTGATG  
GCTGGAGTTATCGTCCTTGTGCGCGGAGTGCCTCGATTAGGCCGAACGGTGAGTTTCATT  
CCGTGGCCGGTTCATCGAAGGATTACGGCAGGCATCGGTGTGATTATTTTCTGCAACAG  
GTGCCAGCTGCGTTTGGTTATTTCGGGCCATTTGCCACCAATGCGCTCCTCGCTGCGATT  
CACACTGTTTACACGCCACGAAGGACGCAATTCTACCTCTCTTAATTATTATCGTCACC  
GCTGCGATCATGATTGTGTTGGGAAAGATCGCCCCAAAGCTCCCTGCCAGCTTCATTGCC  
ATTTTGGTGGTGTCCATTGGCGTGGCTCTGCTCAAGCTTCCCGTTGAGTTGATCGGTGAG  
CTCCCCAATTCCCTTCCCTGCCCTCACCTGCCTGATGTGAACCTGGAGATGTTTACGAGT  
TTGCTGGGGCCAGCTTTTGTGCTGTCGCCGCGCTCGCTGCTATTGAGTCTCTCTTTCCGCT  
CGTGTGGCAGCCTCCATGGCCGATACGGGTCTTATAATGCTGACCGCGAATTGGTCCGT  
CAGGGGTTGGCGTTCGATAAGCGCTGGCTTTTTTGGCGGCATGCCGCAACTGGCGCAATC  
GCGCGTACGGCGGTCAATGTGCGCTCCGGCGGGCGTACCCGTATAGCGTCGATTATTCAC  
GCGCTTGTGCTGCTCGGCGTTGTGTATGTGGCGGCGAATATCGTTGCGGTCAATCCGCTC  
GCCGACTGTGCGGCGTGTCTATGGTCACCGCGAGCCGATGGTGTCCATTGAAGTGATC  
TCGCGCGTCAATGCGCTCCACTCGCTCTGATGCGATCGTTTTTGTATCACCGCGATCGTC  
ACCATCAGCGTCGACCTCGTCAATGCGGTGCGGCATCGGCATTGCGCTGCGACGTTCTTC  
ATGCTGCGACGCATGAGCATGAACGCCGGCGTCTTCCGGGAAACCTTGCCCGAACCGGCC  
ACGCTTAACGACGAAAAGATCGGCCTTTTCCGTATCGAGGGCGCATTGTTCTTTGGCGCA  
GCTGAACGTCTTTTCGCAGCAATCCTTGATTATGAGGACCTCGAAGTGGTGATCCTGCGC  
CTGTACACATCCAAATGATCGACGCCACCGGCGCCACCAGCTCACCGAGCTTGTCAT  
GCGCTGGAAAGAAAAATGTCACTGTATTAATTAAGGGCGTCCGGAAGAACACATTAC  
GTTCTCGGCGTCTCGGAGCGATCAGATCACTGCGGCATGAGAACCACCTCTTCGATGAC  
CTTGCCCCAGCGGTTGAACATGCCCCGAAACACGTTAAGATCGACAACAGT

>RXA02634-downstream  
TAAGGCTTCCGGGGCGATCTAAA

>RXA02638-upstream  
ATGAAGA

>RXA02638  
ATGGCGCGGAAGCGTCTTAACGCCGGCAGCCTCGTCGGTATCTTCCCTGAGGCGACGGTG  
TCACGGTCTTTGAAATCAAGGAACATAAACTGGCGCCGTCCGCATCGCCGACAGCGCT  
AACGTTCCGCTGCTGCCACTTATTATTTGGGGCGGCCAGCGCATCATCACCAGACATC  
GAGCGGACTTCGGCCGCTCCACATCCCGTATTATCATCAGCGTGGGTGAACCCGTCGAC  
GCCAGCGGCGATCCCGACGAAGCAACGGAACGCCTCTACGAGGCTATGAAAAAGCTTCTC  
GACGAAACCCGACCCGCTACGAACAAAAGTATGGCCCATTCGAAGGTGGAGAATTGTGG  
CGCCCGAAATCCCTCGGCGGCGGCCCAACGTTGGAGCAGGCGAAAATGTTGGAATC  
GCCGAACGGGAACGTGACAAGCAAAACGCGCGGCAAGGTGCGCAAGAAACGCACCACC  
TTTATAAGGAAAATCTTTAAAAAA

>RXA02638-downstream  
TGATTGCACTGGGTTTCAGCGCCC

>RXA02659  
TTCGGCAACGACCCAGACCTCCTCATGCGCTGGTGGTACGCCGGCGACGTCTGGACCGAC  
TCCCGCATGCACTGGAAGGGCAGCGAATCCTACGACCAGGTACAAAACCTCCTGGAAGAA  
GGCATCCGCGCTACCGACAAGGCAGAACAGCAAGACATCTGGAACCGCACCTTCGATGTC  
ATCTCCGACAATGTTCCCTCTACCCGCTGTTCCACCGCAAGGTCCCAACCGCATGGAAC  
TCCAACGCCCTCGTCGACTTCAAGCCAATCTCACTACCCGCTTGAACCTCTCAGGTGTT  
GCAACTACTGAA

>RXA02659-downstream  
TAACAACCCAGTGGCTTTCAAA

>RXA02676-upstream  
AACCATTGGGTATTAAAGAAATTTGTGGCTTAGATCTCAATTTCTGTATAGTTTGATCATA  
CTAATTCATCCACTTCCAAATTTTCACGAAGGATCACCCC

>RXA02676  
ATGGACACCTGGGAACAAACCCTTGGAAACAGGGCCACTGCTAGGCATTGCAGCCGGCGCC  
ATTGCCCTCATCTTGGTTCTCGTCATCGTTTTTAAACTCCATGCTTTTCTCACCTAATA  
CTGGTTTCAATTGTTACCGCACTTGCTGCCGGCATTCCCGTCACCGCAGTAGTGGACACT  
CTCCTTGACGGTTTTTGGTAAACACTCGCCTCGGTCGCCCTATTGGTAGGCCTGGGTGCC  
ATGCTTGGTCGATTGGTTGAAACATCCGGTGGCGCAAAATCTCTAGCCGACACTATGGTG  
CGAATCTTCGGTGAAAAACGAGCAGCTTTTCGCACTCGGTGTCGCATCGCTGATCATGGGA  
TTCCCTATCTTCTTCGATGCTGGCCTCGTGGTCATGCTCCAGTGATCTTCGCAGTAGCT  
CGACGCCTCAACGGCTCCGTCCTTACTTTTGGTATCCCTGCAGCTGGCGCCTTCTCTGTC  
ATGCACGTGTTCTGTCACCTCACCCAGGCCAATTGCAGCCTCTGAATTTCTTCGGCGCA  
CAAGTTGGATACGTACTAATCGCTGGCATCATCGTTGCACTACCCACCTGGTATTTAACC  
GGTTACCTGCTAGGTAAGTTCTTAGGCCGAAAGTTCCCCCTTCCCGTACCCGATCTACTC  
AGTGGTGGAGCACAGGAAGATGATCAGCCTCAGAACCAGCTAACGCAGTGTGATCATT  
GTCAATTTTGCTCATTCTCATGCTCCTTATTTTGGCAATACCGGAACATCAATGGCAGTT  
TCCGCCGGCCTCCTAGATGCAGAATCCACCATGGTGAATTTCTAGGATTCCTCGGCGAA  
ACACCAGTGGCACTGCTCATTACCTTGATCATTGCCCTGTTCTTCTAGGCAACCGACGT  
GGCATTAATGGTTCTGCTCTAGAGAAAACCATCGAAGGCGCACTCGGCCAATCTGTTCA  
GTCGTATTAATCACTGGCGCCGGTGGCATGTTCCGGTGGAGTGCTACGCACGTCTGGAATT  
GGAGGAGCGCTTGCACTCCATGGCAGATCTAGGACTTCCAGTTATCGCAGGTTGTTTC  
ATCGTGGCAGCCGTCCTTCGTGTCGCGCAGGGTTCTGCCACCGTTGCGCTAACACCGCC  
GCAGCACTCATGGCACCTGCTGTTGCCGCTGCTGACTTTAACGAATTCCAGCTTGCTGCC  
ATCGTTATTTCCACTGCCGCTGGTTCTGTTATTGCCAGCCACGTCAACGACTCCGGATTCT  
TGGCTCGTTGGTCGACTCATGAACGCCGACGTACCCACCACGCTAAAACTTGGACCGTA  
AACCAAACCTGCATTGCGATTGTGGGATTGTGATGGCCTATGCAATGTTCCGGATTGGCA  
TCGCTTGCA

>RXA02676-downstream  
TAGTCCGCTGACCCCATGATTC

>RXA02677-upstream  
TTAGTGCAGTGATTTATTTCCGTTACGCTGCCGGGCTGGTGGTTTGGAGGGATACTAG  
AGTCGATAGCAGGTATATAAAGGCCAGGAGAGATGGGTTT

>RXA02677  
ATGAAAGTCATCGCGCACCGAGGTTTATCGTCTCGCTTTCCCGAATTAACAGAGTCTGCG  
TTTCGGGCGGCTCTAGAGCTACCGATTATGGAATTGAACTGATGTCCGGCTGACTAAA  
TGTGGCGAAGTGGTTAACGTCCATGACCCATTGTGGATCGCGTGTGCAATGGTCGCGGT  
CGGGTGTGCGGTTTGGACTTGGAAATCCTTGCTGAGCTTGAATTTGGAACCAAAGAAACC  
CCAGAAAAAGTGCTTACTTTAAACAATCTATTAGATATTTTGGAGATTATCCAGATAAG  
CACCTTTATATAGAAACCAAGCACCCAATGCGCTACGCGGTGATGCTGGAAGAAGAAATC  
ACAAAAATCTTAAATATCGTGGGCTGACGGAAGACCCACGCATCCACATCATTCTTTT  
GCACTTCCCGCGATGTATCGCATGGCTCGCCTTGCTCCACAGCTTGATCGCATTATCTG  
CGCAGGTGCTGGGAGCGTTGGGGTAATCCGCGCGATGTGCGCTGCGGTGTACCCACCGGT  
TTGGGGTTGTGCTGGAGCGGGCGAAGATGGATCCAAGGATGATTGGGGCGAAAGGGTTA  
CCCACCTATCTTTTACCGTCGATAAGCAAAAAGACATGCTGTGGGCGCGCAACAGGGC  
GTCGACATGCTCGCCACCAATTATCCGGACCGTGCGGCGGAGCTTTTGAACGCACATCCC  
AAGCCCGCCATGTACGCTAATGCGCATGGCAAAGAAGAC

>RXA02677-downstream  
TAAGAAGAATGAACAGCTGCCGG

>RXA02691-upstream  
CTTAGGGCTTATCTGTTTTCCAGCCTTGCTTTTTACTAGGCGCTCCTGTCCCGCTTCAGT  
CACCAAACACACCCCTGGTTATGACCAGATCGGCTAAA

>RXA02691

ATGAACACCATGCGCTGACCAACCGCTCAACCAGGACGGATTCCCTACCGCATCCAAAGGG  
GTGGAACCCGACAACCTCCCCGACCGCGTTCTCGTGACGGCCTTAAACCAAAGCATCAG  
CAGCTTCGTGAAATTTTGGAGGAAATCTGCACCAACCGCTTCAGCCTGGGGACATGCTG  
CCTGGTGAGCGCATCCTGGAAGAAAAGTATGGCGTCAGCCGAATTACGGTTCGTGCGGGCG  
ATTGGTGATCTGGTCGCGTCCGGCAGGTTGAAGCGAGCTCGCGGCAAAGGTACCTTCGTG  
GCCCCACTCGCCGTTGATTTCCCGCCTGCATTTGGCCTCGTTTTCCGCAGAGATGGCCGCC  
CAGAAGCTATCGGCTACCAGCAGGATTTTGTAGTTCTTCCCGCGGTCCCGCCCCAGATGAT  
ATTGCTGATTTCTTTGGTACCGATCGCGCGGCCCCAGCACATCACGTTGCGCCGCTGCGC  
TTTGGAATGGTCGACCCATATGCCATTGACAACGGTTGGTACAACCTCCGAATTCGCACCT  
GACCTGCTGGAAAATGATGTGTACAACCTCCGTGTACTCCATCCTGGACCGCGTCTATGGC  
GTCCCCGTCAACCGAGCCGAGCAAACGGTCACCGCCGTAGCAGCCGACGAAGACACCGCA  
CGGCTTCTGGACGTACCCCCGGCGCCCCACTCCTTCGTATCCTTCGACAGTCACTTTCT  
GGCGATAAGCCCGTGAATGGTGCGTTTTCCTTGTACCGAACCGACCGATATTCTTTAAAA  
ACATTGGTTACACGCTCCGAAGATCTC

>RXA02691-downstream

TGACGTGAACCCATTTTGGTGGC

>RXA02718-upstream

TCCACCAAAATTCAGCCCGCATCCCCCTATTCGATTGAAGGACGTCTCCTTGAGCAGTTT  
CGATGCCCATGACCTTGACCTCGACAAATTTCCGGAGGTC

>RXA02718

GTGCGAGATCGTTTGACGCAGTTCCTCGATGCTCAAGAGCTAACAATTGCTGATATCGGC  
GCTCCTGTCACAGATGCTGTGGCCCATCTTCGCAGTTTCGTGCTCAATGGAGGAAAGCGA  
ATCCGTCTCTTTATGCGTGGGCTGGTTTCTGGCGGCGCAAGGCCATAAGAATTCTTCT  
GAAAAACTTGAGTCCGTCTTGACGCCGCGAGCGAGTCTCGAATTCATCCAGGCTTGTGCC  
TTGATTCATGACGATATTATCGATTCTTCTGATACCCGGCGCGGAGCCCCACAGTTTAC  
CGGGCTGTGGAAGCTGATCACCGCGCAATAATTTGAAGGCGATCCCGAGCACCTTGGC  
GTTTCAGTCTCGATTTTGGCTGGCGATATGGCATTTGGTGTGGGCAGAAGACATGCTGCAG  
GATTCCGGTTTGAGTGCAGAGGCATTGGCCCCGACGAGGGATGCTTGGCGTGGCATGCGT  
ACTGAGGTTATTGGCGGCCAGCTGCTTGATATTTATCTAGAGTCGCACGCCAACGAGTCG  
GTGGAGCTTGGGATTCTGTCAACCGCTTCAAAACGGCCGCTTACACGATTGCGCGCCCA  
TTGCACCTGGGCGCCTCCATTGCTGGCGGTTTCGCCGAGCTTATCGACGCGCTCCTCCAC  
TACGGCCACGACATCGGCATTGCATTCCAGTTGAGGGATGATCTGCTTGGTGTGTTGGG  
GATCCCGCTATCACCGGCAAACAGCTGGAGACGATATCCGTGAAGGCAAGCGCACTGTT  
CTTCTTGCGCTCGCTCTACAACGCGCTGATAAGCAATCTCCTGAAGCTGCAACGGCCATT  
CGCGCAGGTGTTGGAAGGTGACTTCACCAGAAGATATTGCTGTCAATACAGAGCATATT  
CGAGCTACTGGTGCTGAAGAAGAAGTTGAGCAGCGAATTTCCAGCTGACTGAATCCGGT  
TTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACTG  
GCTATCCGCTCAACCGAACGTCGGATG

>RXA02718-downstream

TAGTAGACGCGTATGACACTTTT

>RXA02749-upstream

CAACCTAGACTTCGGTAAGAAGTAACTTTGCTTTAGTTGGTTCGGCGCATCACTTTCCCTA  
AGCGATGCGCCGATTACTTGTTTTTGTACAAATTTAACT

>RXA02749

ATGTCACCCATCCTAAAAGTGCGGGACCTCGTCAAACGCTATGGCGACACCGTTGCGGTT  
GACGGTTTAAATTTTGTATGTTTCAAGGGGAAATTTTTCCTTTCTAGGGGAGAACGGC  
GCAGGAAAAACAACCACGATTTTCATGCCTGATTGGCATTGATCAAGCCACCTCTGGGGAG  
ATCGAACTGCAGGGTGGCCAAGTAGATTCTGAAAACTTGGAGTGGTGTTCACAATCC  
GTCTTAGACCTTTGCTGAGTGCCAAAGAAAACCTTGGAAACACGCGGACAGCTGTACCCA  
GGGGTGGGGAAGCAGCGGGTTGCACAGCTCATTGAGCAAATCGGGATGGAAGGGTTTGGC  
GACCGCCGATACGGAGTGTTGTGCGGGCGGTGAAAAACGTCGCACCGACATCGCACGAGCT  
TTACTGCACAGCCAGACATTCTTTTCTTGATGAACCCACAGCAGGCCTCGACCCCA  
TCACGACGCCAAGTTTGGGACACCATCAATTCCTGCGTAACGATGTGGGCCTCACTGTC

TTTTTGACCACTCACTACATGGAAGAAACAGAACTGGCTGATTCTAATCATTGAC  
CGTGGCAAAGAGGTGCGATCAGGAACCCCGATGGAAGTGCAGCGCCCGTTACACCACAACA  
GAATTGACTCTTAGAACAACGACCCTACTCATTCCGGTAAAGAGTTGGCCCACTTGAGC  
CCAGAAATCGACGGTGACCGACTGCGGATCAAGTTGGAAAATGGGCTCGAAGCTGCGCGC  
CTGGCAACAGAACTAGATGGGGTTCTCGACGTAGAGATCCGCCACGGTTCCATGGACGAT  
GTATTTCTAGCAGTTACAGCTGAACGGAAACGATCA

>RXA02749-downstream  
TGATTACAGTTCTGACACGCAGA

>RXA02762-upstream  
TTCCAGTCGGCGATCCTCTTCGCCCCCTACGTTATCTTGACTCTGGTTGTGGTCTTCGTG  
GGATCCATGCAGACCTTCCTCAACGGTAGCTACCTGGGTT

>RXA02762  
ATGCTCTCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTT  
TTCCTCTGGATCGCAAACGCGTTCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTA  
GGACTAACCGGAACCTTCTTCATGTTGCGCGGAATCGGTGTGGTTGCCTTGATCTTCATC  
TACACCCAGGTTCTTGAAACTCGTGGACGTACCTTGGAGGAGATTGATGAGGATGTTACT  
TCCGGTGTCAATTTCAACAAGGACATCCGAAAAGGAAAGGTGCAC

>RXA02762-downstream  
TAAAAACCCAGACACTGCATAGA

>RXA02767-upstream  
GGGAAAACGTTTCTTCGCGCCCGCCACAGAATCATAAAAATTTTCTGAGGTTGTCATGGGTA  
CCAGTCTAAGCCCTGGCCTTACGCCAGTAAGGTGTTACCC

>RXA02767  
ATGCGCGAACTAGCACTCAACATGGCCGGCGTCACCGTGCGGCGCGGCGAGAAATTGCTT  
CTCGACGATATCTCCCTCTCAATTCCGCAAGGGTTCGCACTGGGCGGTACTTGGTCCAAAT  
GGCGCCGGTAAAAACCATGCTGAAGATCGCAGCCACCTTGCTGTACCCATCGGAAGGC  
ACCGTGACATCCTGGGGCATCGCTTTGGTGGGTGGATACTCGTGAGCTGCGGAAAACA  
ATCGGCCTGGTGGACCCGAAGCAAAGATTTACCAACCTGCCGGCCACGAAATTGTGCTG  
TCGGGGTTAACCGCTCCAACGGGTTGTTGCCACGGTGGTTCGGCTTCGGCTTCGGAGTTG  
GAGCGGTGCGCTTTGATGTTGGAGTTGGTGGGCATGACAGCGCGTGCCGATCGTTACTGG  
GCCGATATGAGCCAGGGCGAAAAAGCCCGCACCTGATTGCTCGTGCGCTGATTATCTCA  
CCGACCTACTGCTGCTTGATGAACCCACACCGGCTTGACCTGCCCGGACGTGAAACT  
TTGCTCAGTGTGATTGATGGTTTGGCAGCCGCTCTTCCTGGTCTGACGACAGTGATGATC  
ACCCACCACGTGGAAGAGATCGCCGCTCCACGACAGATATCCTCATGATCAAGGACGCC  
CGCATACTGGCTTCGGGGACTGTTTCAGAAGTGATGACTCCTGAAAATTTGGGCGCGCTG  
TATGACATGTCGGTGTGCTTGAAACTGTGCGCAGCCGGTGGTTCGCGTTCGATGCTCTG  
CAT

>RXA02767-downstream  
TAAAAGGGGCTAGTTTACACAA

>RXA02792-upstream  
AGAACAAAGTGCTGCCATACTCATGAACTTTGCCGAACCCCAACCCCGCTGGCCGTG  
ATGGCCTAGAAAAATCATCGACTTTGTGGAAACCCACCC

>RXA02792  
ATGATCGAGGCCACACACCTACGCCACAGTTTTGGCGACAACATCGTCATCGATGACGTC  
ACCTCCATCTACCTGCACACGGCACCGTCAGCTTGGTCGGCCCCAACGGCAGTGGCAAA  
ACCACCTGCTGCGTGCATATACGGAGCACTGCAACCAAATGAAGGGCACATCCACGTA  
GATGGCGTTCCACTAATAAGCTTGCAACCGCAAAGACATCGCAAAAACCATGGCCGTAGTC  
ATCCAAGAACATGACTCCGACCTCCCCATGACCGTCGCTGACCTGGTCTTACTAGGCAGA  
CTCCCCACCAAAGATGTTTGGCGGCAACTCTCAAGCTGATCAGTTACTCGTTAAGGAA  
GCACTCACCCGAGTCGGCGCCATTACCTGGCCGACCGACAATTCGGCGCACTTTCAGGC  
GGTGAACGCCAACGCGTCTCATCGCACGAGCACTCGTACAAAACGCCACACACATTCTG  
CTCGACGAACCCACCAACCACTCGACATCCGCTACCAGCACGAAGTCCTTACCTCGTC

CGCGAACTCAGCTCAAGTTCCATCATCGTCCTCCACGACCTCAACCTCGCAGGTGCCTAC  
AGCGACCACATCATCCTCCTTGACCAAGGACGTGTGGTTACTCAAGGAACGCCCTCAGAG  
GTATTGACCCCAGAGCATTTGGAACCTGTGTATGGCGTTCGTGTTGAGCGCTTTGACCTA  
GGCGATGAAGTCCACCTTCGGTTCAAGCGTCAC

>RXA02792-downstream  
TAGGAGTTTTGTTGAGGAGGTGG

>RXA02794-upstream  
TGAACCTCAGGTGCCAGTTGCGGTGCGGCCGCTGCCTTACTGTTCCGAGTGGGCGCTGGAT  
TTGGCGATTACGCCCTCCAAGCAGCGCGTTTCTCGGCGCA

>RXA02794  
ATGGCAGCTTCCGGATTGATCTTCTTCGTGGCGCGCGCAGCGGGGCGCATCTCCTCGACC  
CGCTTGTTGATGTCCGGCGTAGCGATCGGATACATGCTCTCTGCGGCAACAAGCTTTCTC  
ATCTTCTCCTCCGACTCCGCCGAAGGCAGCCGCTCCGTGTTGTTCTGGCTGCTTGGATCC  
TTAGGACTTGCCGCATGGAATGGGCCGATGGCGATCATCTTCTCATCGTGGGCATTGCC  
CTGGCGTTGCTCATGGTGTGGGTCCGCAATTGGATGCCCTAAACTCCGGCGATGAAACC  
GCACTTACCTTGGGAGTATCCCTGATCGCCTCCGCATTCTCCTCCTGGTGATCACCTGC  
CTGCTGGTGGGATCCATGGTTGCCATGGCCGGCAGCATCGGATTCATCGGCCTTGTCTATC  
CCCCACCTGGCCAGGCGTTTTGTTAGTGGAAAACACCGACTCATGCTGCCTGTATCCGCG  
TTGATGGGCGCAATTTTGTCTCATCTGGGCTGATATCGCCGCCCGCACCTGCTTGGCGCC  
CAAGAGATTCCCATCGGCATCATCACCGCACTCATCGGAGCACCTTCCTCCTGATTCTG  
GTTCCGCCGGATGCACACCTAC

>RXA02794-downstream  
TGATTTTAAAGGAATTATGCGTA

>RXA02809  
GCAGCACTAACCAACGCCCTTTCTTACCTCTCCGCAGAGTGGAAACAACAAGGCTGCAGGC  
ATCGTCTCCTACGGCTCCGCAATGGGCGTTCGCGCAGCTGAGCACCTCCGCGGCATCCTT  
TCCGAGCTTCAGATCGCACACGTTCAAAAGACCGGCTGCTGAGCATCTTCACCGACTTC  
GAATACCCTAACTTCAAGCCTTCCGAGCAGGCGCATCTCCTCTGTGGACGCTATGCTTGAG  
CAGCTTGTGTCTGGACCAAGGCAATGTCCACC

>RXA02811-upstream  
CATAATCACTCTTTCCAGATAGCGGAATCCCTTTGATTGTAACCTGGCTCACCTCGATT  
TGTGTTTATGACATCACACGCACCAGAATCGGGAGGACTT

>RXA02811  
GTGACAGAGTCAACTCTCGGAGCATCGAATAGCTCCCAAACAATTGAAAATAAAGGCCTC  
ACCATCTTGGGCATCAGCGGCCGACGCTTGGCTGCGGTGCTCATTGGCTGGTTTTTTGTC  
ATTTTCGACGGCTACGACCTCATTGTGTACGGCACCCTCCAATCGGCCCTGGCTAAGGAG  
TGGAACCTAAGCTCTGCAACGCTGGGCACCATCGGCTCCACCGCTTCTTTGGCATGGCG  
ATCGGCGCTGTGTTTATTGGTTCGACTGTCAGACCGCTGGGCCGAAAAGCAGCGGTGATT  
GGATCCGTGCTGATTCTCTCTGTCTTACCATGCTGTGTGCATTTGCTCCAAACCCATGG  
GTGTTCCGGCGCTTTCCGTTTCATC

>RXA02836-upstream  
CCATCACTCGGCTTACCGTCTACGGTGCTGCCCGCAGGACAGAGCGCCCCCAAAGCTC  
GCTTCAGACGGGATCCACCCCTCGAGATGGACGTCACCG

>RXA02836  
ATGACAATCGATGAAGGCCGTCGCCAGTTCGAGGTCAATGTATTTCGGCGCGATGGCCCTC  
ACCCGACTCGTCTGCCCCACATGCAGAAACAAAAGTGGGGGACGATCGTGAACATCACA  
TCGATGGGCGGGAAGATCTACACGCCTCTCGGCGGCTGGTATCACGGCACCAAGTTCGCC  
CTCGAGGCCCTCTCGGACGCCCTCCGCCTGGAGGTCGCCCATTCGGCATCGACGTTGTT  
GTCATCGAACCAGGGCGGCATCGCCACCGAGTGGGGAGGAATCGCTGCCGACAATCTCGAC  
GCAGTG

>RXA02850



GAAGAGCTTGGCGGAGCAACCACCCACATGGTGACCGCTGGTAACTCCCACTACACCGCT  
GCGACCGATGAGGAAGCACTGGATTGGGTACAGGACCTGGTGTCTTCTCCCATCCAAC  
AATCGCTCCTACGCACCGATGGAAGACTTCGACGAGGAAGAAGGCGGCGTTGAAGAAAAC  
ATCACCGCTGACGATCTGAAGCTCGACGAGATCATCCCAGATTCCGCGACCGTTCTTAC  
GACGTCCGCGATGTCATNGAATGCCTCACCGACGATGGCGAATACCTGGAAATCCAGGCA  
GNCCGCGCAGAAAACGTTGTTATTGCATTCGGCCGCATCGAAGGCCAGTCCGTTGGCTTT  
GTTGCCAACCAGCCAACCCAGTTCGCTGGCTGCCTGGACATCGACTCCTCTGAGAAGGCA  
GCTCGCTTCGTCCGCACCTGCGACGCGTTCAACATCCCAATCGTCATGCTTGTGGACGTC  
CCCGGCTTCCTC

>RXA02851

CCTCGCCAGAAGGCCGACATCATGATCGGTTCCATCCAGGAAAACATCAACGATGTGGAT  
CTGGAATTGGACACCATCATCCCGGATTCCCCGAACCAGCCTTATGACATGAAGGAAGTT  
ATTTCCCGCATCGTNGACGACGCCGAGTTCTTCGAGATCCAGGAAGACTACGCAGAGAAC  
ATCCTGTGTGGCTTCGCTCGCGTTGAGGNCCGTTNTGTTGGCATCGTGGCTAACCAGCCA  
ACCCAGTTCGCTGGCTGNTTGGATATTAAGGCATCTGAGAAGGCTGCCCGTTTCATCCGC  
ACCTGCGATGCCTTCAACATCCCAATCCTTGAGTTCGTGGACGTTCCAGGCTTCCTGCCT  
GGCACCACCCAGGAATTCGACGGCATCATCCGCCGCGGCGCAAAGCTGCTTTACGCTTAC  
GCTGAAGCAACCGTCGGCAAGATCACCGTCATACCCGCAAGTCTACGGCGGAGCGTAC  
TGCGTGATGGGTTCCAAGGATATGGGCGCTGGCCTGGTA

>RXA02865-upstream

GAGCGGGTTGCTATCGGCCGAAAGTTTAGGGTTTTGTTCAATCTGTTGGTTAGTATTGC  
TTGGGTAAACAAGTCATAACAATTTTCATTAAGGGTCGTT

>RXA02865

TTGTCGCGCACAGGTGTTTCGAAAAAACCAAAGCTCACCGCTCCTGTTGTCATCATCGGC  
ACCTTCGTCTTGTGATCATCGCCTTCACCGCTTCCCTCATGCTGGGTCCCGTGACGGTT  
CCATTGAATGAGCTTGCAACCAACCCCGTTGTCACCGATATCCGTGCACCACGCATTATC  
ATCGCAGCATTTGGTGGGTGCGGCGCTGGCTGTCTCCGGTGCGATCATGCAGACGGTGTTT  
CACAACCCGTTGGCGGATCCCGGCATTGTGGGTGTGTCTCCGGTGCGCTGTTGCAGCT  
GTCTTGGCGATTGTACCGGTGCGAGTTTCTTTGGCCAATGGACCGTTCTTTTGGCGCC  
TTCGTGGGCGCATTGGTACGGTGGCTGTGGTATATTTGATCGCTAGTTCCCGCGCGATG  
GATGGCCGTGGCGCAGATCCGGCCACGTTGGTACTGGTCCGGCATGGCTATCACTGCCTTT  
TTGGGTGCTGTTATTTCCAGCGCCACTGCGAACGCACCACAAGATTCTGAGCTTCGATCC  
GTGACGTTTTGGCTCAACGGCGATCTGGTATCTCGGACGTGGGAACATGTGGGCGTTGCA  
ATAATCCCCATTATCGTTGGGTTGATTCTAGCTATCGGCGGTTCCCGCGATCTGAACCTG  
TTGCTGCTGGGTGATTCCACAGCGCAAAACATCTGGACTCAACGTCAACCGCGCACGCATC  
ATTTTGCTAGCACTTGCGGCACTGCTCACCGCCACAGCTGTTGCGGTCTCCGGCACCAT  
ACGTTTGTGGATTGGTAGTACCCACCTGGTGCGCATTTGTTTGGTGCCGATCACCGA  
GCGTTACTCCCGCGCCGCGGATTTTGGGCGCCACGTTTGTATCGTTTCCGACACTGTT  
GCCCCGATGATCTTCTCCCCATCGTCTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGC  
TCACCAATTTTCTTTTATTACTGCTCAGCATGCGCAAGCGACGCGGATTGGGGCTG

>RXA02865-downstream

TAAAAACTCATGCCTCAATTAGT

>RXA02900-upstream

TATGTCCTTTGGCTCCGGTACCCTGGCAGGAGTACCTGGGCTGTTTTTCTAAATGGCCT  
GACGTTTTCAAGATTGAATTTAAGGAAAGCATCGTAGTTC

>RXA02900

ATGAGTAACCCTGCCGCGAGCACACCTGCCAACAAATTCGGACGATGTTGCGAAGGAGAAT  
TGGGACTCTTCTTTTACGCCGAAGACTGACATTGACTCTTCCCAGCCTGTCAATAACTCG  
ACTGGTGAAGCCGCTGCGCGCGCAGTGAACCTGTACAAGGCGTATGGCCAGGGTGATACC  
ACTGTCACCGCGTTGGATCACGTCAACGTGGAGTTTGAGAAGAACAAGTTCACTGCCATC  
ATGGGTCTTCTGGCTCGGGTAAGTCCACGTTGATGCACTGCATGGCTGGTCTGGATGCT  
GCGACTGGTGGTTCGGCATTCAATTGGTGATACGGATCTGTCGCGGTTGAAGGACAAAGAG  
ATGACCTCTTTGCGTCGTGATCGTTTGGGATTCATTTTCCAGTCGTTCAACTTGGTTCT  
ACTCTGACGGCGTCGGAGAACATTACGCTGCCTACCGATATCGCGGGCCGCAAGATTGAT  
CAGTCGTGGTTCGATGAGATTACCTCTCGTCTGGGCTGACTGAGCGCCTTAAGCACCGT

CCTGCAGAGCTCTCTGGTGGTCAGCAGCAGCGTGTGGCGTGTGCTCGTGCGTTGGTGTCT  
CGTCCGGAGATCATTTTCGGCGACGAGCCAACCGGTAACCTGGATTCTGAACCTCTTAGG  
GAAGTGCTGGATATCCTGCGCACCGCAGTTGATCAGGATGATCAGACCGTTGTGATCGTT  
ACCCACGATGCCAAGGCGGCGTCCTATGCAGATCGTGTCAATTTCTTGGCGGACGGTCGT  
ATCGTGAACAGTTGTTTGATCCCACCATCGAGGAAATCTTGGCCACGATGAACGGAATT  
GAGGATATTGCC

>RXA02900-downstream  
TAATGAATTCCGGTTCACAATG

>RXN00024-upstream  
TTAAGACATCAACATATGGCTTGTGCTACTGAAAGATTTTCTTCTGAAATTCTGTAGAA  
ACGCTCCTATGCTCGGGCAGTAAGTTGTGAGCATAGGAA

>RXN00024  
ATGGAGCACGGCGTGACCGTTATTAAAGGCACTGAATTTGATGTTTTCCCACTAAACCTC  
GGTGGAATACCTTTGGCTGGACCTCGAATAGGGAACAGACCTTCGCGTTTTGGATGCA  
TTCGTGGCAGCGGGAGGAACTTTGTTGACACCGCCGATTCTTATTCTGCATGGGTTGAA  
GGCAATGAGGGTGGCGAGTCGGAGCGGGAGCTCGGCGCGTGGATTAAGGAACGTGGCGCA  
GACAAGCTGATCATTGCTACCAAGTCTGGTGCGTTGGAGCCTGTTGCTGGTCGTTCCCGT  
GAGGCAACTTTCAAGGCTGTGAGGGTTCCCTGGAGCGTTTGGGCGTGAATCGATCGAT  
ATTTTTTACTACCACTACGACGATGAGGCAGTCAGCATTGATGAGCAGGTTGCTATCGCT  
AATGATCTGATTGCACAGGGCAAGATTAAGCACCTCGCATTGTCTAACTACAGCGCGGAG  
CGTTTAGCTGAGTCTTTGAGAAGTCTGTAGGCACTCCAGCGCAGCCGTTGCTCTGCAA  
CCGCACTACAACCTGGTGTGCGAGGAAGGATTATGAGGAGAACGTGCAGCCACTCGCCGAG  
AAGCATGGCGTTGCAGTCTTCCCTTATTTTCGCGCTTGCCGCGGGTCTTTTGACCGGAAAG  
TACACCTCCAAGGAGGATATTTCCGGTAAAGCGCGTGCGGGGCAGTTGGATCGTTACGCC  
AGCGATGAGGCGTTTGCCGTGGTGACAGAGTTGCGTGCTGTTGCCGATGAGTTGGGTGTT  
GCGCCAACGACTGTGGCGCTTGCGTGGTTGGTTGCGCATGGTGTGACCGCACCGATTGCG  
TCCGTGTCCAAGGTAGAGCAGTTGAAGGATTTGATGGCTGTGAAGGATGTGGAGCTGAGC  
GCTGAGCAGCTTGCACGTTTGATAAGGTTTCGGAGCCTTTTCGCT

>RXN00024-downstream  
TAAGCTCTCCTCAAAAGTAAGTG

>RXN00092-upstream  
CGAAACCAGAAACACCCAGCGCTCCTCGTCGAAAAGCGAATCTTTGAACTAGAAGCCCA  
GGCAGCTTGCGCTCGACCGAATTGAAGCATTGGAGCAGTAA

>RXN00092  
ATGACAAACACGCCTTTCCCCCTTGAACCTTCAAAACATCTCCTGCGCCTTCGGAGAAGGC  
CCACGCCACGTCTCCGCGCTCAACAACGTCTCGCTGGCAGTCAATCCCGGCGAACTCGTT  
GCCATCATGGGCCCCGTCCGGCTCAGGAAAATCCACCTTGCTCAACGTGCGCGGCCTCCTG  
CAGCGCGCAACCTCTGGCCATGTGCTTATCGACGGTGCCAGCGCCTCAGACCTCAACGCC  
AAACGCGCAGCTGAAACCAGGCGTCGCCACATCGGAGTTATTTTCCAAAACCTACAACCTG  
GTCCCCACCTCACCCTCGGAGAAAACGTGCGTCTGCCCTAGAACTCGACGGCAAAACC  
GACCGCCAGGCAGTAGCAATCGCACTCGCGGAAGTCGGCCTCGAAGGCTTCGACGACCGC  
TTCCCCGAAGAGATCTCCGGCGGCCAAGCCCAGCGCGTCGCCATCGCGAGAGCCCTCATC  
GGCCCCGAAAAATCTTGCTTGCCGACGAACCCACCGGCGCCCTCGACACCTCCACCGGC  
GACGCAGTCTCCGCGTCTCCGCCAAAGAATCGATTCCGGTGCCGAGGCCTCCTTGTC  
ACCCACGAACCCCGCTTCGCCGCGTGGGCAGACCGAACAATCATGCTTAGGGATGGTGAA  
ATCCAG

>RXN00092-downstream  
TGACCACACTTCTAGCAGCAACC

>RXN00099-upstream  
CTCTGGTGAAGAGGATGTTGACTCGGGAGATTCTTCCACTGATTCACTGATTAAGTGGTA  
CCGCGCAAATAGGTAGTCGCTTGCTTATAGGGTCAGGGGC

>RXN00099

GTGAAGAATCCTCGCCTCATAGCACTGGCCGCTATCATCCTGACCTCGTTCAATCTGCGA  
ACAGCTATTACTGCTTTAGCTCCGCTGGTTTCTGAGATTCCGGGATGATTTAGGGGTTAGT  
GCTTCTCTTATTGGTGTGTTGGGCATGATCCCGACTGCTATGTTCCGCGATGCTGCGTTT  
GCGCTTCCGTCGTTGAAGAGGAAGTTCACTACTTCCCAACTGTTGATGTTTGCCATGCTG  
TTGACTGCTGCGGGTCAGATTATTCTGTGCTGCTGGACCTGCTTCGCTGTTGATGGTCGGT  
ACTGTGTTCCGCGATGTTTGCAGATCGGAGTTACCAATGTGTTGCTTCCGATTGCTGTTAGG  
GAGTATTTTCCGCGTCACGTGCGTGGAATGTCGACAACCTTATCTGGTGTGCTTCCAGATT  
GTTTCCAGGCACTTGTCTCCGACGCTTCCCGTGCCGATTTCTCAGTGGGCTACACATGTGGGG  
TTGACCGGTTGGAGGGTGTGCTGCTGCGTTTCGTGGGCGCTGCTGGGGTTGGTTGCGGCGATT  
TCGTGGATTCCGCTGTTGAGTTTGCAGGGTGCCAGGGTTGTTGCGGCGCCGTCGAAGGTT  
TCTCTTCTGTGTGGAAGTCTTCCGTTGGTGTGGGGCTCGGGTTGATGTTTGGGTTTACT  
TCGTTTGCAGCTATATCCTCATGGGTTTATGCCGAGATGGTAGGTGATCCTCAGCTC  
GGTCCGGTGTGTTAGGCTGGTGGTCAATTTGGGATTGCCGCTGAACATTCTGGGACCG  
TGGTTGGTGACGCGTTTCACTAACTGCTTCCCGATGGTTGTTATCGCCAGTGTCATGTTT  
CTCATCGGTAATGGTGGGTTTGTGTTGGCTCCGGATGTTGCGCCGTGGTTGTGGGCGACG  
TTGTCTGGTCTTGGTCCCTTGCCTTCCCGATGGCGTTGACGCTCATTAATATTCGTGCT  
GAACTAGTGCTGGTGTCTTGTGCTTGGTTCCTTCCGGCAGGGTTTGGGTTATACGATT  
GCGTGTTCGGTCCCTTGTGACTGGTTTCATTGTGCTGATGCGACAGGCAGCTTCCGAACA  
ATCTTTGTGCTTTTGTGCGGTTGCAACACTCTTCGTTATTAGAGGCGGTTACTTTGCGACA  
AGGCAGGTTTACGTCGAAAAGCTTTTAAATCGC

>RXN00099-downstream  
TAGGATGGCGCTATGCCGCAAAG

>RXN00113-upstream  
TCTGCGCATCCCACTCGAGGAGCTGGCAAACGGCCGCACCATCGATGTTGAGGCACGCAC  
CGACTCCATCGAAGAGTCCGCATCCGGCCGTATCGTTACC

>RXN00113  
GTGCGCATCGTGCTCACCACCGAAGGCGAAGTAGCAGCCAAGCTGGTTACCCGCTTCGCA  
ATTCTGTTGACGCATCACCACCAACGAAATGGCTGCACCAGCAGATTCTACGGCGCACGC  
GACGAAGTTGTGAGGCAACCCCTCGTTTCTTTCATCCGCCAGGCAACTGTTTCTGCACCT  
GCAGACATGACCCATTTCGCCATGGTTTCTGGTGTGCTACAACCCAATTACACCTCTGAC  
AACGCTGCAAAGCTTGTGTCCTGGACGAGCTCTTGTCCACGGCATGTGGCTGTCCGCT  
ACCGCACAGCACCTCGCTGGTCTTGGCTCTGAGGTCATTGGTTGGACCTACTCCATGTAC  
GGCATGGTTCAACTCAACGACGTTGTTGACATCACCGTCGAGCGTGTGGCCGCGCAGGT  
CTGAAGCCTGCATACGAGGTCACCTGCCGCTTGTATGGCAACGTTGTCTCCCGCGGACAG  
GCATGTCTCAAGGCTCCTTCCACCGCTTATGTTTACCCAAGCCAGGGCATCCAGGCTAAG  
GGCATGGGCCAAGGCGATCGCACCGCAAGCGCAGAGGCTCGCGCTGTGTGGGAGCGTGCA  
GATGCACACACCCGCGCAAACCTGGGCTTCTCCATCCAGCAGGTCATTGATGAAAACCA  
ACTGAGCTGAAGGTCGGGGACACCACTTCGTGCACCCAGCTGGGGTTTTGAACCTCACC  
CAGTTCACGCAGGTCGCGCTCGCCGTGGTTGCCTACGCTCAGACCGAGCGCCTCAAGGCT  
GCAAACGCAATTGTGACGCGCTCCCTCTACGCAAGGCCACTCCCTCGGCGAGTACACCGCA  
CTGGCATCCTTGGGCAACATCTTCGAACTCGAAGGCGTCATCGACGTTGTGTTCTCCCGC  
GGTCCGCAATGCACTCCCTGGTTCCACGTGATGAGAAGGGCCGTTCCAACCTACGGTCTT  
GCCGCTTCCGTCGAACATGATCAACGTTGCAGCCACCGAGGTGGAGAAGTGGGTTGAC  
CGTGTGCTGAAGAATCCGGCGAATTCTTGCAGATCGTTAACTACAACGTTGATGGCCAG  
CAGTACGCAGTCGAGGTACCTTGGCTGGCCTGAAGGCCCTCAAGGCTTCTGCATCTGCA  
AACCACGCTGCTTACGTGAACATTCCAGGCATTGACGTGCCATTCCACTCCAGCGTCTTG  
CGCCAGGCGTTTCTGCTTTTCGAGAGAAGCTGGACGAGCTGCTGCCAGAGACCATCGAC  
ATTGATGCTCTTCGCGGCGCTACATCCCGAACCTGGTTGCTCGTCTTTCGAGCTCACC  
CAGAGCTTCGTGGATGCCATCCTTGCTGTGTTCCATCCGAGCGCCTCAAGGGCATCAAG  
GTGGAGGACACCGACGAGAACACCTGGCACGTCTGCTCCTCATCGAGCTGCTGTCTTGG  
CAGTTCGATCCCTGTGCGTTGGATCGAAACCCAGGCTCTGATCATCGATACCGTCGAT  
CAGATCATCGAGGTGGCTTGGCAGCATCGCAACCTGACCAACCTGGCACTGCGCACC  
ATGGATGTCATTGGCAAGTCCCGCCAGTATTCAACGTGGAGCGCGACAGGACACCGTT  
ATGCTCAACGATGTTCCGCCAGGCACCTGTTGCTGAGGTTGAAGAAGAAGCAGTTGAGGAA  
GCACCTGCAGCAGCGCAGCTCCAGCAGCTGAGGCACCAAGTTGCTGCAGCTCCAGTAGCC  
GCAGCCGCACCTGCACCTGTTGGAAACGCACCTGAAGTGAAGTTCAACGCTGCCAATGCC  
ATCATGGTTCTTCTGCTGTCCAGAACAAGATCAACATTGATCAGATCACCGCAGCGGAT  
ACCTCTGAGACCCTGACCAACGGTGTGTCTCACGCCGTAACCAGATGCTCATGGACATG

TCCACCGAGCTGTCCGTCCCAACCATCGACGGCGCAGCTGACGCTGACGTAGCTACCCCTG  
CAGGGACGTGTTGTACCGCAGCTCCTGGCTACAAGCCTTTTCGGACCAGTTCTTTCCGAG  
ACCGTTTCGTGCACGTCTTCGCGCACTGACCGGTGCAGCAGGTCTGAAGACCTCCTACATC  
GGCGATCGCGTGACCGGCACCTGGGGACTTCCAGAAAGCTGGACCGCACACGTTGAGGTT  
GAATTGCTGTGGGACCCGCGAAGGCGAGTCCGTCCGCGGCGGCAACCTGGGTAGCCTG  
CCTGCTAACGCATCCAGCAAGGGCGACGTTCGATGCGCTTATCGACGCAGCCGTGCAGAAT  
GTTGCTGCAGCCAACGGCACAGCGTCTCCATGTCCTCCGGCGGTGCAGCTTCAGGTGGC  
GGAGTTGTTGATTCCGCGACACTTGATGCCATCCACCGTCACTGGTGAAGAAGGC  
GTCCTGGCAAACGTTGCTCGCGGCATCCTGTCTCAGCTTGGTCTCGACACCAAGGACGAG  
GTTGAAGGCGCAGAGATCGACACCGAAGTCTACGACGCTGTGCAAGCAGAACTGGGCACC  
GGCTGGCTGAAGCTTGTACCCCCAGTGTCTCCGCTGATCGTGCGATCTTGTTTCGACGAC  
CGTTGGGCATCTGCACGTGAAGATCTGGCACGCCCTTGCCAACGGCGAGGATATTGCCGTC  
GAGCGCTTTGCTGGAACGGGGGAGACCGTTCGTCAGCAAGCTGCATGGTGGGCTGAGCAC  
GTTGAAGACACCGCTCTCGCTGCAACCCCTGAAGCAGGTTTCCGAGGTGGCTGCGAAGCCA  
GCCAACGAGCCACACATCGACGATGTTGCGCTGGTTACCGGTGCGGCTCCTGAGTCGATC  
GCCGGTGCAGTTGCGGCTCGCCTGTGTCCCAGGGCGCGACCGTCATTCTCACCGCATCG  
AACGTCTCCAGGGCGGTAAGGAATACGCACGCAAGCTCTACGCTGCGAACGCAACCCCT  
AACGCAAAGCTGTGGATTGTTCTGCGAACATGTCTCCTACCGCGATGTTGATGCAGTC  
ATCGATTGGATCGGCAACGAGCAGCGCGTACCGTTCGGCAGCACCGTACCGTGACCAAG  
CCAGCTCTGACCCCAACCCCTTGCGTACCCATTTCGAGCTCCATCCGTATCCGGTACCTTG  
GCGGATGCAGGCCCACAGGCTGAAAACAGGCACGCCCTGCTCCTCTGGTCCGTGGAGCGC  
ACCATCGCAGGACTTGCAGATCTTGATCCCGCGGTGTCGATGGACGCGTCCACGTTGTA  
CTCCAGGTTCCCGAACCAGCGGAATGTTCCGGTGGCGACGGCGCTTACGGCGAAGTCAAG  
GCTGCTTTCGACGCCATCCTTGCCAAGTGGGGCTCCGAGACCGGCTGGCCACAGTTTGTCT  
TCCCTCGCACAGGCACGCATCGGCTGGGTGCGAGGCACCGGCTCATGGGTGCGAACGAC  
GTGCTCATCCCTGCCGCTGAAAAGCTGGGCATCCACGTCTACACCCCTGAAGAGATCTCT  
TCCGAACTGCTGGGTCTTGATCCCGCAGAACTCCGCGAAAAGGCTCTGGAAGCACCGATC  
GATTACGACCTGACCGGTGGACTTTCCGGTGGCGTATCCATCGCAGCACTGGCAGCATCC  
CTCGAGTCCGACGCGAGTAGAGACCACCTCTGCAGCAGAAGACACCATCAAGGCGCTTCCA  
TCACCTAAGCACCCAGAGCAGCCAGTGGGCACGCCAGTTGGAGAGGTCAAGACCGATCTC  
GAAGACATGGTTGTATGGTTGGCGTGGCGAAGTCTCCTCATGGGGCTCCGGACGTACC  
CGCTTCGAAGCTGAGTACGGCATCCAGCGCGACGGCTCCGTTGACCTCACCGCAGCAGGC  
GTCCTTGAGCTTGATGGATGATGGGTCTGATCTCCTGGAGCGAAGATCCAAAGCCAGCC  
TGGTACGACGCTGACGGCACCGAAGTGCTGAAAGAAGAGATCTACGAGCGCTTCCGCGAC  
GAAGTCATCGCACGATGCGGTGTTTCGTGAGCTTGTGACGACGCATTCTCGTTCGACGGC  
GGCTCCCTCGACGCAGCTGAAGTCTTCTCGACCGCGACATCTCCTTCTCCGTAACCTCT  
GCTGAAGAAGCACAGGCCTACGTGATGCAGATGCTTCCGTGACCGTTGAAGAAGCAGAC  
GGCGAATGGATCGTGACCAAGAAGGGCTCCACCTCCTTCGTGCCACGCAAGGCAACC  
CTGACCCGCTCCGTAGCAGGCCAGCTGCCAACCGACTTCGACCCTGCCAAGTGGGGTATC  
CCAGCCTCCATGATCGATGCACTCGACAACATCGCAGCGTGGAACCTGGTCACTGCAGTC  
GACGCCTTCTGTCTCCGGCTTCAGCCCAGCAGAACTCCTGCAGTCCATCCACCCAGCT  
GACGTGTCTCCACCCAGGGCACCGGTATCGGTGGCATGCAGTCCCTACGCAAGCTGTTTC  
GTCAACCGCTTCTCGGCCAGGATCGTCCATCCGACATCCTCCAGGAGACCCCTGCCAAAC  
GTTGTGGCTGCACACACCATGCAGTCTACGTCCGTGGCTACGGCCAGATGATCCACCCA  
GTGGCAGCATGTGCAACCGCAGCTGTCTCCGTGGAAGAAGGCGTGGACAAGATCCGCGCT  
AACCAAGGCAGATTTTCGTTGTCGCCGGTGGTATCGATGACATCCAGGTTGAATCCCTGACC  
GGCTTCGGTGACATGAACGCCACCGCAGACACCCAGGCAATGCTGGACAAGGGCATCGAC  
CCACGCTTCATCTCCGCGCAAACGATCGACGTGCGCGAGGCTTCTCGAAGCAGCAGGT  
GGCGGTACCGTCTCTTGGCACGTGCATCCGTTGCTGCTGAACTGGGACTGCCAGTTCTC  
GCAGTTGTTGCACACGCACAGTCTACGCCGATGGTGCTCACACCTCCATCCAGCACC  
GGACTTGGCGCACTGGGTGCAGCACGTGGTGGCAAGAAGTCCGTAAGTCTGCTCGCGAACTG  
AACAAATTGGGTCTGACCCAGATGACGTTTCGCGTGGTCTCGAAGCACGACACCTCCACC  
AACGCCAACGATCCAAACGAGTCCGAGCTGCACAACCTGCTGTGGAAGACCATTTGACGC  
GAAGCCGACAACCCGATGTTTCGCTCGCTCCGAGAACTCCCTTACCGGACACTCAAAGGCG  
GGTGCAGCACTCTTCAGATCGGTGGACTTGTCTCCATCCTGGAAACCGGCAAGCTGCCA  
CAGAACGCATCCCTTGACTGCGTTGACCCAGAGATGGAAGCAAAGGGCGAGAAGTTCGTC  
TGGCTGCGCAAGCCACTGGATCTCGGCGCAGGCTCCATTAAGGCCGGCGTACTTACCTCA  
CTGGGCTTCGGCCACGTGGCTGCAGTCGTGCTGGCAACCAGCGGCATCTTCGAGCAG  
GCAATGCGCAACGCAGGCCTCGACGTGGAAGCATGGCGTGCACGCGCAACCCAGCGCCTG  
CGCACCGGTGCAAACCGCCTAGAAGCTGGCATGGTTGGCCGAGCACCATTGTTTCGAGCAG  
GTCGACGGAGCTCGCCTGCCAGAGCATGGCGCTACCAAGCAGAGATCAACTTGCTTATC

GACGCTGACGCTCGCCTCGGTGCTGACGGCATCTACCAGGGC

>RXN00113-downstream  
TAAACGTTAGATAGCTAAGAAAG

>RXN00164-upstream  
CTGCTTTGCGGAGGTTATGAAATGAGTGGGGAGACGTCGAAAAGCATGCGCTTTCCGTT  
GGCCAGCCTGCCGCAAGTGC GGCGCGAGGTGGCCCCGGCAG

>RXN00164  
GTGGGTTCGTATTCCGCGGGCGAAGTGGTGGTTTTTAGGCGCGCTGGTGTGCTGAGTGCG  
GGCGCTTATGCGTCGGTGCTGGTGCCGCAGGTGCTGGGGCGGATTGTGGATCTGGTGTCC  
GATGGCGCGCAGATGCGTGATTTTGTGAGCTCAGTGTGATTCTCATTGCGGTGGCAATT  
GCCGGCGCGGTGCTCAGTGCGTGCGGGTTCTATGTGGTGTGCGGATTCTGAGAAGATT  
ATCGCCAATTTGAGGGAAGATATGGTGGGCACCGCGCTTGGGTGCCCCACGCACCAGGTG  
GAAGATGCGGGCTCTGGCGATTGGTGAGCCGCTCCACCGATGATGTCTCCGAGCTATCC  
GCAGCGGTGACAGAGACCGTCCCGATTTTAAGTTCCCTCACTGTTTACCATTGCCGCGACG  
ATCATTGCGCTGTTTTCTTTGGACTGGCAATTTGTGCTCATTCCTGTGCTGGTGGCGCCG  
GTGTACTACTTCGCGTCCAAGCACTATTTGAGCAAGGCGCCGGATCGGTATGCGGCAGAA  
CGCGCGGCGATGGCGGAGCGTGCGCGAAAGGTACTTGAGGCTATTCGCGGGCGTGCAACT  
GTGCGGGCGTATTCCATGGAAGATGCCATGCATAATCAGATTGATCAGGCGTCGTGGTCT  
GTGGTGGTCAAGGGTATTTCGTGCGCGCACCAACCATGTTGATTTTGAACATGTGGATGCTG  
TTTGCGGAATTCCTCATGCTCGCGGTGCGGTTGGTGATCGGCTACAAGCTGGTCATTGAT  
AATGCGCTGACGATCGGCGCGGTTACCGGTGCCGTGCTGATGATTATTCGTCTGCGTGGC  
CCGATGAATATGTTTCATGCGCGTGCTCGACACCATTCAATCCGGCTATGCGTCGCTGGCG  
CGCATCGTGGGAGTTGTTGCGGATCCGCGCATTCCTGTGCCGACAGCGGTGTGAAAGCA  
CCTCAGGGCAAAGTGGAAATGCGCAACGTCAGCTTTAGCTATGGCGATTTCCTGGGCGGTG  
AAAGACATCGACATCACGATCAATTCGGGCGAAACTGTCGCGCTCGTGGGCGCATCTGGC  
GCAGGTAAGACGACGCGTCCCGCCTTGCTGGCGGGCTTGCGGGTGCCAGATCAAGGGCAA  
GTGCTTGTGCGACGACTTCCCGCTCTCTGACCTCTGACCGCGAGCGTATCGCCCGCTTG  
GCCATGGTCAGCCAGGAGGTTTCATGTTTTCTCCGGCACGCTGCGCCAGGATCTCACCTTG  
GCTAAACCAGATGCCCTCCGATGAGGAATTAGCGCATGCTCTTGGGCAAGTTAATGCCCTT  
GACTGGTTGGAGAGTCTTCCAGAAGGACTGGACACGGTCGTTGGTGCGCGAGGAATCCAG  
CTAGAACCAGTGGTGGCTCAGCAGTTGGCGTTGGCCCCGGGTGTTGTTGCTCAATCCGGCG  
ATCGTCATCATGGATGAAGCCACGGCAGAAGCAGGATCGGCGGGTGCCAGCGCACTGGAA  
GAGGCTGCAGATGCAGTGAGCAAGAACCGTTCCGCATTGGTGGTGCGCACCGGTTGGAT  
CAGGCATCGCGGCTGATCAGATTCTGGTGATGGATAAGGGGAGGTTGTGGAATCCGGT  
ACTCACCAGGAGTTATTGGATCACGGGGGTATTTATCAGCGTCTGTGGACTGCGTGGAGT  
GTCGGAAGA

>RXN00164-downstream  
TAGTTGACTGTTCAATGCGTTGA

>RXN00193  
AAAGCTTTCTNCCAACGCGAAGGTTTCATCTCAGCCTTCGGTTTTACCGTCCTCGTGGTC  
ATCGTCTCCGTGATCACAGTCAACATCTTCGCCCTTCCTCTTGGCGTGGTTGCTGACCCGC  
AAACTCCGCGGTACCAACTTTTTCCGCACAGTCTTCTTTATGCCGAACCTTATCGGCGGC  
ATTGTGCTGGGTTATACCTGGCAGACCATGATCAACGCCGTGCTTTCGCACTATGCCACG  
ACTATTAGCGCGGACTGGAAATTCGGCTACGCCGGCCTCATCATGCTACTTAAGTGGCAG  
CTCATCGGCTACATGATGATCATTTTACATCGCCGGCCTGCAAAACGTCCCACCAGAGCTC  
ATTGAGGCTGCCGAACCTCGACGGCGTCAACAAGTGGGAGATGCTGCGGCACGTCACTATT  
CCGATGGTCATGCCATCCATCACCATCTGCCTCTTTTGTGACTTTGTGCAACTCCTTTAAG  
CTCTTCGACCAGAACCTGGCGCTGACCAACGGCGCTCCTGGCGGGCAAACCTGAGATGGTG  
GCGCTCAACATCATCAACACGCTGTTTAACCGTATGAATGTCGAGGGCGTCGGT

>RXN00201-upstream  
ACGTCGCGGACTTCAAGTAGTCGGCGATGAAAAAGTCCGTTTACTAAACCCCGATCTGTG  
TTACGCCATCGCGCGGCTCGGGCACACCGATACCTGGGCA

>RXN00201

GTGGCAGATTGCGGATTACCCATCCCAGAACACGTAGAGATCATCGATTTGGCACTCGTG  
TTTGGGATCCCCACCTTTGAACAAGTACTGAATGCTCTCAAGCCGGAAGTAGTTGTGGAA  
GGCGGGTGATTGCCGAAGGGGCACCCCAACGTATCCGCGAAATGGTGGATACGGATGTG  
GAAGTATGTGCG

>RXN00243-upstream

CACTGCGCCAGATTTTTGATGCCGACACTGTGGCAGGTGTGCGCGCTGAGTACGAAAAAT  
TTAACAAAGCAGCCCATGATGGAAATGAAGAGGAACAGAA

>RXN00243

GTGACCAGCGAACAAAGCTTTAGATCCTATCCACCCAGGTCAGTTCCGTCTTTCTCGGATT  
CAGTTGATCAACTGGGGAACCTTCCACGGAACGGTGGACATTCCTGTGACCAGGGAAGGA  
ATCTTAGTTACCGGTGGTTTCGGGATCAGGAAAAATCCACGCTGATTGATGCGATCACGGCG  
GTATTGCTTCCGCAAGGAAAGCTGAGGTTTAACTCTGCCGCACAGGCTAATACTCCGCGG  
AATAAGGGACGCAGTTTGGTTACCTATATCCGTGGCGCTTGGCGTGCGCAGGAGGATCCG  
CTGCAGGATCAGATTGTCTCCACGTACCTACGTCCCCGCGCAACCTATTCTGCTGGTTGGA  
TTGACTTATTCCAACGGTGAAGGCGTCGAGCACACCTTGGTGGCTATTTTCTATCTGAAA  
TCGGGACACAATTTAACCTCCGATATTTCTTCATATTATGGTGTGTTTCCCGTTGATCAA  
GACATCAATGCGCTGCTGGATTTCCTGAAAGAGGGCATCGATAAACGCCAGATCAGAGCT  
GCTTTCAAGGAAGCCATCTTTAGCGAGCAGCATTCTGTATTCTCCGGCAGGTTTAGAAGC  
CGTTTGGGGATCTCCAGTGAGGAAGCTTTGCTGTTGTTGCACCGCGCGCAGTCGGCGAAA  
GATCTTCAAAGCTTGGATGATCTATTTTCGGGATTACATGCTGGTGGAAACCGGATACGTTT  
AGCATTGCCAAAACGCGGTGGAACAATTCCAAGACCTTGAAGGTGCTTATGAGCAGGTC  
GAAGATATTAAACGGCAGATCCACACCCTGGATCCTTTGGTGCAGCTGAAGAATCGGCGA  
GAGAAAGCGCAACAGTCCAAAGATCATGCCAATGCACTGAAGAAGGCGCTGCCGACTGTC  
GGGAATCGCATTAAGAAGGAAGAGCAAGAACCGCTGGTTCGACAATTTACTGTGAGCAA  
ACGCAGCGAAGTCAAGGTGGAGTCCGCCAAAATTGAGACAGATCGTGCCCGCGAAA

>RXN00243-downstream

TGAAAAACCTCGCGCACGACAAC

>RXN00297-upstream

AACAAGGCACCGGAAAACAAGCAACGCACCTTGCAGAGGTGGTCTTAAGCATCTTGGAGC  
AAAACAACATGGCACAATAACGATCATGCAACAGGTGCTC

>RXN00297

ATGGGTTTTCACGGTGGTGTTCATCGTCATCGGAATAGGTGGATTCTCGGTAGAAGAGAC  
ACCTTGGGCACACATGCCAGAAACCTTTGAGCCTGTTTGTCTATTACGTGGCCACCCCA  
GCGTTGTTGTTTGATCGGGTCACCAAGTCAGATACCTCGACGATTTTCTCTCTGAACCTT  
GTGGTCATTGCACTCTCTGCGTTGATCGTAGGTTTCTGTGTTTTCTACTCATGCGGTTT  
GTGATCAAAAAGAACTGCCGAGTATCGGTGATCGGCATGCTAGCTGCGTCTACGCCAAC  
GCCGGTAACCTGGGTATCCCTTTGGCAGCCTATATTTGGATGATTTACCGTGGTGGATT  
CCCGTGATTTTGTTCAGGTGGCGTTTACGCCACCGATCACCATGACCATCATGGAGATG  
CTGACCAACAAGAAATCCACCAACTTGGTGCGCAACCTCCTGGTCACGCCACTAACCAAC  
ACCATGGTGTCTCGCAGCGATTGCCGGTATTGCTGTGTCTTTGACTTCGATGAGCGTGCCC  
GTGGTGATTGCTCAGCCAGTGGAATGTTGGCGAATGCTTCAGTGCCACTGGCTTTGGTG  
GTGTTCCGACTGTCTTGTCCAAGAGCAAGATCCTGGAAAAGGGGCAGGTATCCAGGCGC  
GATGTGTTTACGGCGGCACTGTTCAAGAATGTTCTGCACCCAATTGTTGCGGGACTTTTA  
GCCTTAGCCTTTGGTATGGAAGGTACTGCCTTGTGTCGGCGGTGATTCTCGGTGCACTG  
CCAACAGCGCAGAATGTCTACACCTACGCGTTGCGATTTAGAACAGCTGAATCGATGGCG  
AGAGACACAGGGGTGGTCACCACTACTTTCCTTCCCGTATTGGTGGCGGTCTCCATT  
ATCTTTGGATCT

>RXN00297-downstream

TAGGGTTAGCATTAGTGTCATG

>RXN00298-upstream

TTTAGACAAGTTCTGGTTAAAATTCTTCATGAAGGTGAGAATCTGGGAATTTCTCGGTAC  
TCTTTCAGATTTCGTAGTTATCCACTGATTGGAAGAATGAG

>RXN00298

ATGAGCTCAAATATAGCTATCACGACCGAGCCTGAAGGGAAAAATAAAAAGGGTCTCAAA  
TCAGACCCGTTTCATTTTTTCCATTTCTGTGCGTTTTATCGTGGTGTGTCATCGCCACA  
ATTGCGCTAGGCGAGAAAGCTCGAACAACCTTTTCCGCGATTGCCGGCTGGCTCTTAGAA  
AATTTAGGGTGGATGTATATCGGGGGTGTCTCCTTGGTTTTTCATTTCTCATGGGTATC  
TTTGCGTCCCGGTATGGCCGGGTAAAACCTTGGTGATGACGATGATGACCCCGAGCACACC  
CTAATCGTGTGGTTCTGTATGCTTTTTGCTGGCGGTGTCGGTGCAGTCTTAATGTTTTGG  
GGTGTGCGGAACCGATTAAACCACGCGTTCAACGTGCCAATGGCTAATGAAGAATCCATG  
AGTGAAGCCGCAATTGTGCAAGGCTTTTGTCTATACTTTCTATCACTTCGGTATTCACATG  
TGGGTAATCATGGCACTCCCAGGATTATCATTGGGATACTTTATTTACAAACGTAAGCTA  
CCTCCCCGTCTATCCTCTGTGTTTTCTCCGATCTTGGGTAAGCACATTTATTCACACCC  
GGCAAGCTCATCGATGTACTGGCCATCGTAGGCACCACGTTTGGTATTGCTGTGTGAGTA  
GGTCTTGGTGTGCTGCAAATCAATGCAGGTATGAACAACTATGGAGCACCCCGCAAGTA  
TCGTGGGTTTCAGCTTTTGATCATCTTGATCATCACCGCGGTTGCATGTATTTCCGTTGCT  
TCCGGTTTGGATAAGGGCATTAAGTTACTGTCCAACATTAATATTGCAATGGCCGTTGCG  
TTGATGTTCTTCATCTTGTTCACTGGTCCAACCTCACATTGCTGCGCTTTCTCGTAGAA  
TCCTTCGGAATCTATGCATCCTGGATGCCTAATCTGATGTTTTGGACTGACTCTTTCCAA  
GATAACCCAGGCTGGCAGGGCAAATGGACGGTGTCTATTGGGCATGGACTATTTGTTGG  
TCGCCATATGTGCGCATGTTTCGTGGCGCGTATTTTCGCGTGGACGTACCGTCCGTGAATTT  
ATCGGTGGGGTTCTAGCTCTGCCAGCGATCTTTGGCGTAGTTTGGTCTCTATCTTTGGT  
CGTGACGGCATCGAAGTGGAAGTGAAGTAAACCCAGGTTTCTTGACCCAGCCAAGTGTGTT  
GAAGGTGACGTGCCAGCAGCGCTTTTAAATGTGCTGCAAGAGTATCCGCTGACTGGAATT  
GTCTCCGCGTTTGCATTTGTAATTATTGTGATTTTCTTTATCACCTCCATCGATTCCGCA  
GCGCTAGTTAACGATATGTTTCGCTACCGGTGCAGAAAATCAAACACCGACTAGTTACCGC  
GTGATGTGGGCTTGACCATTTGGGGCGGTGCGAGGTTCCCTGCTGATCATTTCCCATCC  
TCTGGTATTGCCACGCTGCAAGAAGTGTTATCATCGTGGCTTTCCCATTTCTCCTCGTG  
CAATTTGTGATGATGTTTTCTTTGCTTAAAGGCATGAGTGAAGATGCTGCTGCGGTTTCGT  
CGTGTGCAGACTCGTCAGTGGGAAAAGACTGATACACCAGAAAACTTGAAGAGCATTCG  
TCCCAACCAGCCCCGGGCTATGATGACGAGGGCAACCCCTTGCCAATGCCTGCCCTCGAA  
CATGATGAGGACGGTAACATTGTTATCCCAGGCAACGTAGTCATTGAAGGTGATCTTGGG  
GTAGTTGGTGATGTGGTCGACGATCCTGAGGAAGCCCAAGAGATGGGGTCTCGTTTTAAG  
ATCGTCGAGCAAACCTCGGCCCCAGTCCAGGGACGAATACGATATT

>RXN00298-downstream

TAAACGATTGCTTTTCGACGCAC

>RXN00349-upstream

TGTGTACATCACAAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT  
GTGATTGGACTCTTTTTCTTTGCAAAATGTTTTCCAGCGG

>RXN00349

ATGTTGAGTTTTGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCA  
CCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTG  
ATGAATTTGGCTGCGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTGAC  
ACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGAT  
ATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTC  
AACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAACTGTCTGAGGTTGAC  
CGTTTGATCCGTTCCATTACGGCTGGTGGCAGCCCGCCTGAGGTTGCCGAGAAAATCCTG  
GACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGCA  
ATGATGGGTGGTGTGTTGCTGTGCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCT  
TTTATTACCGCGTTACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCT  
ACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTAT  
TCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATT  
GTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCT  
CCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCT  
GGCGTGGGTTTGGGCATTACGCTTTCTGAAATCTTGATGTGATGTTGCCTGCCATGGAG  
TCCGCTGCAGCACCTAATTATTCGTCTACATTTCGCCCGCATTATCGCTGGTGGCGTCACC  
GCAGCGGCCTTCGAGTGGGTTGTTACGCGAGTGGTCCCTCGGTGATTATTGCGGGGCTT  
ACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTAGGCCCGCTCTCT

GCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCAATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTGCGTAATAAAAGG

>RXN00349-downstream  
TAAAAATCAACCTGCTTAGGCGT

>RXN00368-upstream  
TTCTTCCAAAACGCAATGAAGTAGTTTTCTATGCAGTTATCTCCTTCAAATACGTGACGCAGCGCTTTCACATCTCTGCGTTGACGTCTTTGTCTTTC

>RXN00368  
ATGCGTCTGGGTGTGTGGCTGATTGTGCGGGGTTGTTTATCACTCCGTTGGCGCTGGTG GTGGGCTTGGCGTTGGGAGGCAATCAGTTTCTGCTCTGTGGGATTCCGGATTGGGCAAA GCCCTATGGAATTCGCCCTATACAACAGTGCTTTCTGCGGTGGGCGCGACCATTATCGGC ACGATCATGGCTCTCACGCTGGACCGAAGTATGTTTTCGGGCGCACCGCGTTGCGGTTA TTTTTGTTATCCCCGCTGTTGATCCCTCCGTTTATTGGGGCTATTGCGTGGTTGCAGCTG TTCGGGAAGAACCAGGGCATCAACCGGTTTTTCGGCACGGAAGTGTGGGATATTTACGGC GCTGATGGTGTGACATTTTGTGATTGTGCACTCCTATCCCACTGTGTACATCATTGTT TCGGCAGCTCTGAGGCAACTTCTAGTAGATTGGAGCAAGCTGCACGGATCGCGGGGGCG GATACTTTTACGGTGTGCGCACCATCACACTCCCACTGCTCAAACCTGCATTGTTGTGCG GCGTTTACTCTTACCACAGTGGCGAACCTCGCCGACTTTGGCATTCAGCTCTGTTGGGA TCGCCAGCGCGTTTTGAAACCTTAGCCACCATGATTTATCGCTTCATGGAATCCGGCACC GTGAGCAATCCATTGCAGGTGGTATCCACCATTTGGCATCGTGTGTTGTTTCTGGGAATC GCAGCAGTAACCGCGGATTATCTGGTGTCTTTGTACGCGGCATCAAAGTTGCAAGACGCA GGAACACCGCATCGCTTTACTCTCAACAAATCACGAATCCCAGTCAGCGTGATCACGTGG ATCATCGCGTTGATCATCACCGCCGCCCGCTGCTGGGTCTGGCATAACAGAGCATTACTG CCTGCCCCAGGTGTGCCGTTCAACCTAGACAACATCACGCTCAACAACTTTGAAGCAGCA CTGAGCAATCCACGAGTAATCGAAGGATTGAGCAACTCCCTCATGTTATCCCTGGGTGCA GCCCTAATCTGTGGGGTGTGCGGATGGCTGATCGGAGTGCTCATCACCCGAACCCAGCAT TTCGCCAACGTACCGTTGACACTCACTGTGCTGCTTCCACCGCACTGCCGGGCATGATC ATCGGCGTCGGCTGGCTCATTTTGGGCAGATACACCGGAATTTACAACACACCTTGGGTG ATTTTGGGTGCATATGTGTGTGCTTTTACCGCGCTGGTTGTCCAAGCTGTACGCGGACCA CTCAGTCAAGCACCCGAAGCAATCGAAGAAGCCGCACGAATCAGCGGCGCAGGCAGATTA CGATCCATCATGGACACCACCGGAGCGATGGCAATTCCCGCAGCTTTCCGCCGGCGCAGTG CTGGTTGCCGTAACGTGCGGTTGAGAGTTAACCGTGTCATTTTGCTCATCGCGCCGGGC ACCACACCTTGGGTGTGCAAGGTGTTCAATTTGCAGCAGGCGGGAAATTACAATCAGGCA TCGGCGTTGTGCTTGATGTTTGCATTATCGGTATCGTGGCGCTCGCGTTGACGGTGC GCAGCCAGAAGGAGTTT

>RXN00368-downstream  
TAGGTGTCATCGATCAAATTGCG

>RXN00378-upstream  
ACCGTGAGCCTTATACCTGTGAGGACATTAAAGTGACACCTCTTTTTCTATCTTTTACAA CCCAAGAAGGTTTATCGTGAGCACACCGGATTCTTCTCTCG

>RXN00378  
GTGGACAAGGCCGTAAACACTGCTATCTCTGACGCCAAAACAGCGGCGCTCAAGGCAGGT GTTGATTGAACCGAGCCACCGCCTCAGAAGAAGAGGAAGATTTAAGCTCAAGCATTAAAG GTTTCTTTGGCCTTTGAGCTCGAGGGGTAAAGCAATGCACCATCGTTGATGGTGGTGGAA AAAGCCCTAGAGAAGATCCCCGGTGTATCCGCGGATCTGATTTACCCTTCACAACTGCA TGGATTACAGCAACTGATCGGGTACATCCCGAAACCTCATTTGAGGTGTTTGAGCAGTTT GGCATCAAAGCACACCTTTCTAATTTCATCGCTGCTGCGCAGGCATCAACAGCTCAGCGCG GAAGTAAATAGGGAAGCACGCTTTCATCGTTTACCGCTCCCGAATGGATGCCAAGCGAATC TCGCCTCGTGTGCGAAGGCATAACCGACAAGAAATGGTACATGCGGTACGCGCTCGTGAA AGTGGTTGGATTAAACGCAGGAATCACACCCTCGCAGCATGAAGACCCAATGTGGGGC



GATGTGCTGTTACCGCCCGCGCACTGATTACACCTAAGCGTTTGTGGGTGTCGTTGCCG  
 TTTGCGCTCATCGTATTGGCGTTATCGTTGAATCCTTCGTGGCAGTTTGATTATTGGCAG  
 TGGTTGTCCGCTGTGTTGGCTATTCTGTGGTGGTGTGGGGTGCCTGGCCGTTTACCGC  
 GCTGCAGCAGGCGGTATTCTGTCGAGGAATTTCCGCTCTTGATGCGACCAGCTCAATCGCT  
 ATTGCTGCTGCATACGCGTGGTCTATCGCCATGCTGTTGTTTGAACCCAGGAGGTAAA  
 TCCTGGCGGTATATCCGTCCTGGTTTCGCTTTTGACCACGGCACGTTGACCCAAAACGAG  
 ATTTATTTTGATGTGGCCTGCGGAATCACCGTGTGCTTCTTGCCGGACGGCTGCTGACA  
 AGGCGTCGAAGCCAATCCAGTTTGTAGCGGAACCTGGTCGCCTCCAAATCGATCCACAG  
 CGCATTGTCACTGTGGTGCCTAAACACCGATTGAAGCGCGTAGTCCAGGAACCTGAACATT  
 CCAGTGCAGGAAGTCCGTGTCAATGACGATGTGAAAGTTCCACCTAATACCACGATCCCT  
 GTGGATGGCACTGTATCGGTGGCGGTTTCGCGGATCGCAGCTAGCATCATCATGGGACAA  
 GACCAGCGTGATGTAAAAGTAAATGACAAAGTTTCGCCGGCAGCCTCAACCTCGAATCC  
 GAAATCAAGGTTTCGTGTTATTTCGCACTGGTCACCGCACCCGCATCGCCGCGGTACATAGG  
 TGGGTAAAGAAGCGACGTTGAAGGAAAACGCCACAATAGGGCAGCGATCCGTTTCGGCC  
 GGTAACCTTGTGCCCATCACGTTACCCCTTGCTGTGGTGGACTTCTGTCTGTGGGCACTG  
 ATCTCTGGAACATCAACGCTGCATTTACCACTACCTTGGCTGTCCTTGCGTGCCTGGCT  
 CCGGTGGCCTTAGCGTTGTCTGCTCCACTTGCCACGAGGAATTCCATCGAAGCTGCAGCA  
 CGACACGGTATTTTGGTCCGCTCTGGTGAAATTTTCCGAGTTCTCGATGATGTGGATACT  
 GCCGTATTTAATCGTGTGGGCACACTAACCGATGGCGAAATGACAGTGGAAACCGTCACA  
 GCAGACAAAGGCGAGGACCCAGAACTAGTGTGCGTGTGCGCGGGCGTTGGCCATGGAA  
 TCCCACCAAGCGATTTCCTCAAGCACTGGTGAAAGCATCCCGTGAAGCTCGTGATACCGGC  
 GCCGGTGGTGAAGATGTCCACACTGGATTGAAGTAGGCAACGTGGAAATCACCGAAGCC  
 GGCTCATTTCAAGCAACCATCGAGCTGCCACTGATCAAACCATCTGGCGAAAAAATCATG  
 CGCACACAGAAGCACTCCTGTGGCGACACGATCCATGACAGAAGTCCGTGAGCACTTA  
 AGCCCCGACTAGTGGCAGCAGCAACCTCAGGTGGCGCACCACTGATCGTGCATGGAAA  
 GGCAAGACCGCGGAGTTATCACTCTAAGTGACCACGTGAGATCAGATTCTCCGATGCG  
 ATTATTGCGATTGAAGAACAAGGCATCGAGACCATGATGCTTTCACGTGATACTTACCCG  
 GTGGCAGCTCGATACGCAGACAGCTTAGGCATCACCCACGTCTTGGCCGGCATCGCGCCG  
 GGCAAGAAAGCCAGGTGCTCCGTGCACTCCACACCCGCGGATCCACTGTGCGGATGATC  
 GGCGATGAATCAGTAATGGACTGTTTGAAGTGCCTGACGTGGGTGTACTGATGGGCGTC  
 GATCGTCCCTCAGATCTGCGTGATGATTCCGATGACCCGGCAGCTGACGTTGTGGTCATG  
 CGCGAAGAGGTCATGAGCGTGCCGACGCTGTTTAAACTGGCTCGACGCTACGCCAAGTTG  
 GTCAATGGCAATATTGCTCTGGCCTGGATCTATAACGGTGTGCCATGGTGCTTGCACTG  
 TCTGGCTTGCTGCATCCAATGGCTGCGACCGTGGCTATGCTGGCGTCTTCGCTGCTTATT  
 GAATGGCGCTCGGGCAGGGCGCGCAAGTAC

>RXN00378-downstream  
 TAACCAGCAATTCCCAAGCCAA

>RXN00410-upstream  
 GTGTTGATGCGTTAGTCCACCCACGCAGCTACGCCCCAAAGGAATAATCTTGAACCCCTGC  
 CACAGATAACGCTCCGCCGGTCTTTTCAGCCCAAGATCTC

>RXN00410  
 ATGATGATCTATGGAAAAGGATCAACAGAAGTTCGGGCTCTCGATGGCATTCTGTACAG  
 ATTCACTCCGACAAATGGACCTCCATCATGGGGCAATCAGGCTCTGGCAAAACAACCTCTG  
 TTGCAGTGCCTTTCCGGATTGGCGCAGCCAACTCAGGCAGAGTGACACTGAACAAAAAC  
 AACATCACGTTGAGCTCCCTGTCAGAAAATAAGCGTGCCAAGCTGCGTGCACGCACATC  
 AGCATGGTGTTCAGGATTTCAACTTGGTGCCTATTTTGTGCGTGAAGGACAATATTTTG  
 CTGCCGTTGCGTCTTGCGCATCGCAGGGTGGATAAGCAGTGGTTTGAACACATCACCAGT  
 GTGTTGAAGATTGATAATCGTATGCGCCATTTGCCCTGGGGAGCTGTCTGGCGGTGAGCAA  
 CAACGCGCCGATTGCCCGGGCGTTGATGTCTAGGCCGATATTGTCTATTGCGGATGAG  
 CCAACAGGAAGTTTGGATTCCGTCACCGAGCGATGCACTGTTGAATTTGTTCCGCGAGCAT  
 GTTGATGATTTTGGGCAGTCACTTGTGTTTGTACCCACGATAAAGATGCTGCTCACCGT  
 GGTGACGTGTTGATCACAATGCGTGATGGCAAGATCATCGATACGGCAGATTTGCGGGTG  
 GGGCGT

>RXN00410-downstream  
 TAATGTTTCAGGCTTGCTTTTCGCT

>RXN00411-upstream  
 CATTGTGGCAAAATGACTGTTTCGACTCACCGGCAACACCGCTGCGATTGAAGAGTTCTATC  
 AAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCG

>RXN00411  
 ATGAACGAGATGATCCTCGCAGCTGACTGGAACCGGCTAGGACCCACCTTCCAAACAGCC  
 ATCATTGACACCCGTGTTGATGGTCATCATCACCATGGTGGTGGCTGGCTTACTGGGTCTT  
 GTCGTGCGCCTGCTGCTTTACACCACCCGCGCTGGTGAATCTTGAAGAACAAGGTCATC  
 TACACCATTTTGAATGTGCTGGTGAACCTTGTTCGACCCATCCCATTATTATTTTGATC  
 GCCGCCATCAAGCCACTAACGGTCGCCGTCATGGGCACCTCCATCGGCCGAGATGCCGGC  
 ATCTTCGTCATGGTTGTGCGCAGCGATTTTCTCTGTGGCTCGAATCGTGGAGCAAACTTG  
 GTCTCCATTGATCCTGGTGTATCGAGGCAGCTCGCTCCATGGGTGCGTCCCCGATGCGC  
 ATCATCGCCACCGTGATCATTCCAGAAGCACTTGGACCATTGGTTCTGGGTTACACCTTC  
 CTGTTTCATCGCGATCGTTCGATATGTCCGCAATGGTCGGCTACATCGGTGGCGGTGGTCTT  
 GGTGACTTCGCCATTGTTTACGGCTACCGCGCTTCGACAACGAAGTTATGTACGTTGCC  
 GTCCTGGTTATCGTCATCATCGTGCAGGCAGCCAGCTTCTGGGCAATTGGCTGTCCAAG  
 AAGATCATGCGCCG

>RXN00411-downstream  
 TAAACCTCTGCATAGAAAAACC

>RXN00412-upstream  
 CTTTTGACGAACACCACGTCGCGTACGCTTCCTCGGGGCGTTAAACTATTTGTCTTCCAG  
 CTTTTGTCCCCGACTTTTGTACGAATCGAGGACACCGTC

>RXN00412  
 GTGTACACACCGCGTCCACACCGACGCCAGAGGAATACTCCGCGCAGCAACCCAGCACC  
 CAGGGCACTCGCGTTGAGTTCCGCGGCATAACCAAAGTCTTTAGCAACAATAAATCTGCT  
 AAAACCACCGCGCTTGATAATGTCACTCTCACCGTAGAACCCGGTGAGGTAATCGGCATC  
 ATCGGTTACTCTGGCGCCGGCAAGTCCACTCTTGTCCGCCTCATCAATGGCCTTGACTCC  
 CCCACGAGCGGTTTCGTTGCTGCTCAACGGCACCGACATCGTCGGAATGCCCGAGTCTAAG  
 CTGCGTAAACTGCGCAGTAATATCGGCATGATTTTCCAGCAGTTCAACCTGTTCCAGTCG  
 CGTACTGCGGCTGGAAATGTGGAGTACCCGCTGGAAGTTGCCAAGATGGACAAGGCAGCT  
 CGTAAAGCTCGCGTGCAAGAAATGCTCGAGTTTCGTCGGCCTGGGCGACAAAGGCAAAAAC  
 TACCCCGAGCAGCTGTGCGGCGGCCAGAAGCAGCGCGTCGGCATTGCCCGTGCACTGGCC  
 ACCAATCCAACGCTTTTGCTTGCCGACGAAGCCACCTCCGCTTTGGACCCAGAAACCACC  
 CATGAAGTTCTGGAGCTGCTGCGCAAGGTAAACCGCGAACTGGGCATCACCATCGTTGTG  
 ATCACCCACGAAATGGAAGTTGTGCGTTCCATCGCAGACAAGGTTGCTGTGATGGAATCC  
 GGCAAGTTGTGGAATACGGCAGCGTCTACGAGGTGTTCTCCAATCCACAAACACAGGTT  
 GCTCAAAAGTTTCGTGGCCACCGCGCTGCGTAACACCCAGACCAAGTGGAAATCGGAAGAT  
 CTGCTTAGCCATGAGGGACGCTCTGTTACCATTTGATCTGACTGAAACGTCGCGCTTCTTT  
 GCAGCAACCGCTCGTGCTGCCGAACAAGGTGCTTTTGTCAACATCGTTACGGTGGCGTG  
 ACCACCTTGCAACGCCAATCATTGGCAAAATGACTGTTGACTCACCGGCAACACCGCT  
 GCGATTGAAGAGTTCTATCAAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCGA

>RXN00412-downstream  
 TGAACGAGATGATCCTCGCAGCT

>RXN00419-upstream  
 GCTGGTTGAAGACTCGAAATGAGATCGACCCAACCGGAGTCTTTGCATCTGACATGTCCC  
 GCCGACTTGAGCTTTCTTAAGAAAGGGCTTGAACATAACA

>RXN00419  
 ATGCTTAACGCAGTGGGCAAAGCCCAAAACATTCTCCTTCTTGGTGGAACTCTGAGATC  
 GGTATTTCCATTGTCTCCGCTTCTCAAGCAGGGTCCATCCCATGTGACCTTGGCAGCG  
 CGTAAAGATTCCCCACGCGTGGACGCAGCAGTCGCAGAGATCAAAGCAGCTGGCGCTGCT  
 TCCGTTGCTGTTGTTGATTTTCGATGCGCTCGACACCGAATCCCACCTGCAGCCATCGAC  
 GCAGCCTTTGAAAACGGCGACGTTGACGTAGCAATCGTGGCTTTCGGCATCCTCGGCGAC  
 AACGAAGCACAGTGGCGCGACCAAGCACTAGCAGTGGAAGCAACCACCGTGAACCTACACC

GCCGGCGTTTCCGTAGGTGTAAGTGGTGGGCCAGAAATTTGAGCAGCAGGGCCACGGCACC  
ATCGTGGCATTGTCTCTGTGGCAGGCCAGCGAGTCCGCCGCTCCAATTTGTCTACGGC  
TCCGCCAAGGCAGGTTTTCGACGGTTTCTACACCCAGCTCGGCCAAGCCCTGCGTGGATCC  
GGTGCCAACGTATTGGTGGTTCGCCCAGGCCAGGTACGCACCAAGATGTCCGCAGATGGT  
GGCGAAGCCCCACTGACCGTCAACCGCGAAGACGTGGCAGATGCTGTTTATGATGCAGTG  
GTGAACAAGAAGGACATCATCTTTGTCCACCCACTGTTCCAGTACGTCTCTTTTGCCTTC  
CAATTCATTCGCGGAGCAATCTTCCGCAAGCTGCCGTTTC

>RXN00419-downstream  
TAACGGAAGTTACGGAAGTTACG

>RXN00432-upstream  
AGCTAATCTGCCTTGCTTTACACCTCCGGGCTATAACAATCCAGTGCCAGTGGCTAGGGA  
TTTACTAAAAATCGGGTAACACGCGCGTAGTATTTTTCGC

>RXN00432  
ATGGAATTATTGGAGACCTTCATCACTGATGTCATTAATGACAATTTGTGGATGATCTTG  
CCCTTCTTGCTCGTTGCTGCTGGCCTCTATTTCCGGTGGGCGTACGTTGCTGGTTCAGATT  
CGGATGATTCCGGAGATGTTCAAAGCGGTGCTCGAGAAGCCTGCGAAGGATGGGGAGTTC  
GCGGACAAGCAGGACATTTCCGGCTTTTAAGGCGTTCACGATTTCTGCGGCGTCCGAGTT  
GGTACGGCGAATGTTGCGGGTGTGCGCTGGCGATCACTCTGGGTGGACCGGGTGCAGTG  
TTCTGGATGTGGATCATTGCGCTGGTGGCGGTGCGACATCGTTCATTGAGTCGACTCTT  
GGACAGTTGTGGAAGGTGAAGGACGGCGACAGCTATCGCGGTGGCCCTGCGTACTACATG  
ACGCTTGGTTTGAATGCTCGGTGGCTTGCGGTGTTTTCCGGTGTGCGCATCACGTTGACC  
TTTGGTTTTGTGTACAACGCTTTGCAGTCCAACCGGTTGTTGAGGCGATTACGGTATCA  
CTCGGCACCCCTTCTACCACTGCAAAGGCTTTTGTGGCTTGGGCATGGCTGGATTGTCT  
GCGCTGGTTATTTTTGGCGGCGTGCAGCGTATCGCAAACGTGACGCAGTGGATGGTTCCG  
TTCATGGCGGGTGCCTACATCATTGTGGGTGTGGTGGTGATTGTGATTAACATTACAGCAG  
GTTCCGACCATGATCAACGACATCATTGCTGGTGCTTTTGGTTTTCCGTCCGGTTGCTACT  
GCGTCCGTGTGGGGCGCGTTCTGGTTGGCGTTTATGAACGGTATGCGCCGTGGACTGTTTC  
TCCAATGAGGCTGGTGAGGGTTCTGTCCCGAACGCTGCTGCTACCGCGACTGTGTCTCAC  
CCTGTGAAGCAGGGTTTGGTTTCAGACTCTGGGCGTATATTTCCGACACCCTGCTCGTTTGT  
AGCATTACCGCTTTTGTCTCTGCTGTCTGGAGTGGAGTACGCGACCGGCGATATTACAG  
TCTTCTTCTTTGACTCAGTCCGCGCTGGCTAGCGTTGTTGGTGGTTGGGGAACCCACTTC  
ATTACCGTAGTGATGTTCTTCTTCCGCTGTTTCTTCCGTGCTGGGTAACTACTACTTGGCA  
CAGGCGAATATTACGACTTTCACCGATTGCAAGACTGTCATGACTGTTTTCCGACTCTTG  
GTGCTGCTCAGCGTGTCTCTGGCGCGGTGCTTCGGTGCCGTTGATCTGGGCTTTGGGT  
GATACTTTTCGCTGGCATCATGGTGCTCATTAACTGGCGGCGATCATTCCGCTGGGTGGC  
GTTGCAAGTGAAGTTGCTTAAGAATTACACCATTCAGAAGAAGGCTGGTCTGGATCCTGTG  
TTCCACCGCGACATGATGCCAGAGGTTCTGAATATTGCGTGCTGGAACGGCAAAGATGCA  
GCTACATCCAATATCACGAAGCGATGGAAGTGATCAAGAAGAGC

>RXN00432-downstream  
TAGTCATCGAAGGAACAGTGGTA

>RXN00443-upstream  
TAAACAAGGAGCGTTTAATTTCCACCCAATCCCACTGAAAGTTTCCACCCACAGTTAT  
GCTGATTAAAGTACTGAACCTACCGTAGGAAAGGCACTCAG

>RXN00443  
GTGAACAAAAGTATCCGTGAGCTCTCTACAGTTTCATCACTATTTCCGGCGGGTATCTCA  
CTCGTAGCGTGCTCTTCTTCAGACACCGCAAGCACTACCACCCAGAATGCCTCTGCTACC  
GAAGCAGCTGGGGTTTCCGGAACCGCTAGCGTTTTCGCTGCGGCGTCTTTGACCAACGTT  
GCTGAGGATCTCGCGGCTGCGTTCAACGAAGACAATCCTGATGCAAAGTTGGAGTTTAAAC  
TTCGCTGGTTCTTCCGCGCTGGTTCCGCGATCAGCGAAGGCGCACCATCTGATCTGTTC  
ATTTCTGCGGACATCGCCAACATGGACGATGCGCTGGCACTTCCAGAATTTGCCGGCGCA  
ACCTCGAAGGTCATCGCTACCAACAAGCTGGTGCTGGTCACCGCAGACGGCAACCCCGGC  
GAAATTTTCAGAGCTTGCCGACGTCAAGGACTCCCTCGTTGCTATCTGCGCCCCTGAAGTT  
CCATGTGGAACCATCACCCACGAGGCTTTGGACTACGCGAGACATCGAGTTGAACACCAGC  
TCTGAGGAAGCCAATGTTGCTGATGTCGCCACGAAGATTTCCACCGGTGCAGTTGATGCG  
GGCTTTGTTTACCAAACCGACGCTCAGTCTTTGGCTAAAACCTCAGGACAACACTGTCATT

GAAGTCTGAAGGTATCGACGCCAACGAATACCCAATGGCATTGACCACCACCGGTGAAGAC  
AACGAGGTAGCGAAGGCTTTTCGCAGAGTTCTCTCAGCAGCGATCGTGCCAAGGAGATCCTT  
GCCAGCTATGGTTTTTGGCACAAAC

>RXN00443-downstream  
TAAAAAGGCTCGTCGAAGCGAGA

>RXN00444-upstream  
TACCCAATGGCATTGACCACCACCGGTGAAGACAACGAGGTAGCGAAGGCTTTTCGCAGAG  
TTCTCTCAGCAGCGATCGTGCCAAGGAGATCCTTGCCAGCT

>RXN00444  
ATGGTTTTTGGCACAAACTAAAAAGGCTCGTCGAAGCGAGAATCATATCCTCCCAGGGTGG  
TTGCTCATCCCAGCCACCCCTGGCCATGCTGCTGATCATTGGACCTATTTTTGCTTTGCTG  
TTGCAGATCCCCCTGGGATCGGTCTTGGGAGTTGCTTACCGCGCCGGAATCTTTAGGAACC  
GCACGGTTATCTATCGGAACCTGCTCTGTTTTCTACCGCGCTATGCGCAATTGTGGGTTTC  
CCGCTAGCGTTGGCGCTGCATTTATATGAGCGTTTCGCACCCAGGGTGACATCAGTTTTG  
ACGGTGCTGGTTTTATGCGCCTTTGGTGTTGTCGCCGGTGGTGCTGGTTTTGGCGCTGACT  
TTTCTGTGGGGCAGGCGTGGTTTTTTAGGTTCTTGGCTTGATCAGGTTGGATTGCCGATT  
GCATTTACCACCACGGCTGTGGTGTTTTGCCAGGTGTTTGTAGCGTTGCCATTTTTTCATT  
TCCACTGTGACTACTGCACTGCGTGGCATTCCAAAACAGTTTGAGGAAATCGCAGCTACT  
GAAGGCGCAACCCGCTGGGAGATCATGCACAAGATGATCATTCCGCTGGCGATGCCTGGA  
ATTTTCACCGGTATGATTTTGGGATTTCGCCAGGGCCTTGGGCGAGTATGGTGCGACACTG  
ACTTTTGCTGGAAATATTGCAGGTGTTACCCGCACCATTCGGTTGCATATTGAGCTTGGT  
TTGAGTTCCAATGACATGGATAAAGCCTTGGGAGCGGTGATTATGCTTTTGGCTGTCTAT  
GTCTCATCATTGGAGCCATCGGAGCGTTACGATTGTTTTCCAAGGTGAGAAAGGTT

>RXN00444-downstream  
TAATTGATGTCTCGTTCGCCGGA

>RXN00449-upstream  
TCGTTGGCTTACATGGTCATTGATGACCGGGCTGAATATGTGAGAAAATCCATCCCTTCT  
TTAAGCAAGGGAGTGAATTACAGAAAAGGATTGTTTCAGCA

>RXN00449  
ATGAGCACACCTGACATTAAAGAAGGCTCGGCAGAATCACCGGGCGAAGTAATGGTCGTT  
GGAGACAGGCGAGAGTGGCGTCGACAAGCAACCGGCATCATTGCCGGCCTCGTCTTAGCC  
GCCCTGGTCTATCTTCTTCCCCTCGAACTCCGTGGAAACCGTCATGCAATCCAGTGGC  
GTCGATCCAGAAAATGAATACACCAACAACGCGATGCGTCTTACTGCTGCAGTCACAATC  
TTGATGGCAGTGTGGTGGATGACAGAAGCAATCCCACTAGCAGCAACCGCACTTATCCCG  
TTGGTTGCATTCCCTGCTTTCCAGGTTGTGGACTTTGGGAAGGCAACAGCTCCGTATGCC  
AACCTACGAGCTTCCCTCTTCTTGGGCGGCTTTCTTATGGCACTTGGCCTGCAGAAATGG  
AACCTACACCGACGTATGGCTCTAGCGGTGCTGCTAGCTGTTGGTACTAAGCCAAAGCAA  
TTGGTCTTGGGTTTTATGGTGGCAACTGGATTTTGTCCATGTGGGTGTCTAACACTGCA  
ACGGCCGTGGTTATGTTACCGATCGGTATGTCGGTACTGGCACTGACCGCTGAGACTGTG  
GGCGGAATGAAAAACCAAAAGAAATTCGCCACTGGACTCATGCTGTCCATTGCTTATTCT  
GCTTCCATCGGTTCACTCGGCACCTTAATTGGCACGCCACCCAATGCCTTGCTTGCTGCG  
TATATGCTCTGAATCGCATGATATCCACATCGGATTTGGTCAGTGGATGATTCTTGGTGTA  
CCAATTGCTGTCGCTTTCACCATCATCGCGTGGCTTGTGTTGACCACCGTGTTCAAGCCA  
GAAATGAAAGAAATCCCTGGCGGACGTGAACGTGATCAAACGTGAAATCGCTGAAATGGGG  
CCGTGGACTGCACCTCAGGTACAGTGGGTGTTATTTTTGCGGCAGCTGCACTGGCTTGG  
GTCTTCATTCCATTAACCTCTAGATTGGACCGGTTCCCAGCTCTCTATCAATGACTCCCTC  
ATTGGCATCGCTGCCGGCCTGCTGATGTTTATCGTTCCCGCTAACTTTAAAACCGGCGAA  
CGCATCTTGTATGGCGTACTGCAGGCGAATTCATGGGATGTTCTCTTGGTTTTGGT  
GGCGGGCTTTCACTTTCTGCGATGTTTACCAGCACGGGACTTTCCCTATGGATCGGTGAA  
CTAGCTAAGGGACTTGATGCCCTTCCAATCTTCATTCTCATCTTCGCCATTGCTGTCTGT  
GTGTTGTTTCTGACCGAGTTACCTCCAACACCGCAACAGCGGCAACCTTCTGCCAATC  
ATGGGTGGCGTCGCCGTAGGTATCGGACTGACCGCAGGTGGCGAGCAGAATGTTCTGCTG  
CTGACCATCCCAGTCGCACTGTCCGCAACCTGTGCGTTTCATGCTTCCAGTGGCAACGCCT  
CCAAACGCGATTGCATTCCGGCTCCGGCTACATTAAGATCGGCGAAATGGTCAAGGGTGGT  
CTGTGGCTGAACATCATCGCAGTCATCCTCATTACGATTTTACCTACTTCGTAGCGATC

CCACTCTTTGGCATCATGCTT

>RXN00449-downstream  
TAAAAGTTAACAGGCCCGCAGTC

>RXN00456-upstream  
CTACCAACCCGAGATCGTCACAGCGGTGCTAACGGATCATGCCTAGCTTATGGCGTGC  
TCGTCGCAGACTTTTGTCTATTGCCCTAGGTGTACTTGGT

>RXN00456  
GTGCTGCAGGCACTGCTGGCGATCATGGTGTCTGTTGAGCGTAGCCGCCATACTTGAGGGA  
AACCGAGCACTTGTGGATTGCTGCTTACCACGTTGGGTTTGGGGTGGCGCAGTGG  
ATTCAAAAAGTAGTGGCAGAAGATCTAGGCCAGCATTATGTGCATGAGGTGCGTCGTGAA  
TTGGTGGGTGCTGCGCTGGTGCCTGGAATACGGCCTCGTTGGGCGTGAAGTGTACCCGA  
GCCAGCAATGATCTACCGCGGTGCGCAATTGGGTGGCTTTGGGCATTGTTCCGATGGTC  
ACCGGGCTGCCGTTGATTGCGATTGTGCTGGTGGCGTTGTTTATCCAAGATCTCCGCACA  
GGCGTGGCTGTTACTGTGCCACTGCTCATGTGTGTAGCCGTGCTGCCGGTGGTGGCGCGG  
TGGACTTTGAAAAGAGCACGTGAACACGCAAAAAACGTGGACGCATGGCTGCGCGGATC  
GCAGATTCTGTCTGCTGGGATTTACTGCACGCAACAGGAGCAATAGACCGTGAGCTC  
AATGCAGTCACCCGAGATTCCGACCGAGTGGTGATAGCTGCTGTAAGACGTTCCCTGGGCC  
ACCGGTTTTAGCCGCGCATTGATGGCCATGGCAGCCTCGCTTGGCACTGTGAGCATTGTG  
ATTTCTGGCCACCTGGAAGTAAGTGAGGTTGCGGGAATAATGATGCTTCTTGGCGTTCTT  
GCCACTCCAGTTGCAGAACTTGGCCGCGTGGTGAATATCGCCAAAATTATAAAGCCGCG  
ACACGCATCCTGATTCCACTTCTGCAACGAGGCTCAGAATTTAAACACTCCCAACAAAAA  
CTACCCGGGTTGCAAGCAACAGAAGGAATCCCCGGTGTCTATGTCAAAGGTATTTCCGCC  
CTTCTGGAGAACGGATCTACCTCCACGGCTCTGCAGATGCGACGAGAAAATGGGTCAAC  
TCGTTGTCTGCAATGGAGGAAGGCACAGATGTAATAGTCAACGGTCAAAGGCTTTTCGAG  
CTTCCTTTTGAACAACGACGCGCCCTCATCGGAATCGCCTCAGCACACCACCACTTAAGC  
CGTGGTTTCAATCGCGCCTGGTTGGTTTGGCGAGTGCCGGATGCCACCGTGGAAGAAAT  
GAGCAAGCACTGGAACAAGTTGGTCTGAACAACACCGGGAACAACGCTTGAAAAACGGC  
GGACACCCCTGGAGTACTTCGAGATCAACAACTGAAAATTGCCAGCGCCACCCTTCGA  
ACCCACCGCTTTTGGTACTTGAAGGCATACCCCTGAAAACCTCCTCAACTATCCCGGA  
GTGATCATCTCCACCGTTTCAAGGAGAACCCATCCGAAACATGGCGGCAAGTGAACATC

>RXN00456-downstream  
TAATCTAGAAACATGGCAGGACG

>RXN00466-upstream  
TTTAAAGCGCACTAAGAGCTCGTCAATTCTTTAAACAAGCTGAGAATGTGAATAATAG  
GATAGGTTAACCTGATTGATGATGAAAACGGAGATTTGTC

>RXN00466  
GTGCAATCCCGCTGTCCAAAATCCTGCGCAGTAGCGTCGTAGGCGTTGCTGTCTTAGCC  
CTGTTAGCTGGGTGTTCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGGA  
AACTCCGCTTTTCTGTTTCGATTGAACACGAGTTTCGGAACCACCACAATCGATGATGTA  
CCCGAAAGAGTTGTACCCCTTGGCGTTACCGACGCCGATATTGTCTCGCATTTGGGGACC  
GTCCAGTAGGCAACACCGGATACAAATTCTTCGAAAACGGATTGGGACCGTGGACTGAT  
GAGTTAGTGGAAGGCAAAGAATTAACACTGCTTGAAGTCTGATTCCACACCAGATCTTGAA  
CAAGTAGCAGCCCTGGAGCCAGACCTGATTATTGGAGTCTCTGCGGGGTTTGACGACGTT  
GTATACGAGCAACTATCTGATATCGCACCGGTGGTTCGCGGTCAGCGGGAACAGCTGCA  
TACGCAGTAGCTCGCGAGGAAGCTACCAACCTTGTTCGCGTGCAGTGGGGCAATCAGAA  
AAAGGACAAGAGCTCAATGAGGAAACAGATGCTCTGATCCAAGCTGCGCGTGATGAAAAAT  
CCTTCTTTTACGGTAAACAGGAACCGTCATCTTGCCATACCAGGGTAAATACGGTGCC  
TACCTGCCAGGCGATGCACGGGGACAATTCTTCGATTCACTTGGCATTTTCGTGCCGGAA  
GCAGTTCTTTTCGCGAGACACCGGCGACAGCTTCTTTGTGATGTCCCCGCTGAAAGCGTC  
AAAGACGTAGACGGTGATGTTCTCCTCGTGCTTTCCAACGACGAAAATCTGGATATCACA  
GCAGAGAATCCACTGTTTGAACACTCAACGTTGTGCAAAAAGACGCAGTAATTGTGGCA  
ACAACCGAAGAACGCGGGGCGATTACCTACAACCTCAGTGCTGTCTGTCTCTTTTGGCTT  
GAACATCTCGCACACGATTTGCTGAGGCTTTGAAG

>RXN00466-downstream

TAAAACTCAACTACTCGAGCACA

>RXN00477-upstream

TGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACTCTCTACACTCGCTAGAGCCACGA  
TGAAAGGTCTATCTATGAGCATCTACAGAAAGAATTCGTG

>RXN00477

ATGAAGGTCTCGACTAAAACTCCACGCTCCTCAGGTACCGCCGTAGTCATAGGCGCAGGT  
GTTGCTGGTTTAGCCACTTCTGCACTTTTAGCACGTGATGGCTGGCAAGTAAGTGTGTTG  
GAAAAAATACTGATGTCGGTGGCCGAGCTGGATCGCTTGAAATATCAGGCTTTCCTGGC  
TTTCGATGGGATACCGGACCTTCTTGGTACCTCATGCCCAGGCTTTGACCATTCTTC  
GCACTTTTTGGTGCATGTACTTCTGATTATCTCGATTTGGTAGAATTAACGCCTGGTTAT  
CGAGTTTTTCTGGCACACATGACGCTGTGATGTCCCCACTGGGCGTGAAGAAGCAATT  
GCGCTATTGCAATCCATCGAACC CGCGCGGGTGCAAACTAGGAAATTATCTTGATAGC  
GCGGCAGACGCTATGACATTGCCATTGATAGATTCCCTTTATAATAATTTCTCCACGTTA  
GGCCCGCTGCTTACCGGGATGTACTGACCCGAGCTGGCCGACTGTTTTCTCTACTGACC  
CGTTCTTTACAAAAGTACGTAAATAGTCAATTCAGTAGCCCCGGTGTGCGCCAGATCCTA  
ACCTATCCAGCAGTCTTCTGTCTTCCCGACCCACTACTACCCCATCGATGTACCACTTG  
ATGAGTCATACCGATTTGGTGCAGGGAGTGAAATACCTATAGGTGGTTTTACTGCAGTG  
GTTAACGCTCTGCATCAGTTAGCGCTGGAAAACGGGGTTGAGTTTCAACTCGATTCTGAG  
GTCATTTCCATCAACACTGCTTCATCGAGGGGCAACACAAGCGCCACAGGTGTGAGCTTG  
CTTCACAACAGAAAAGTGCAAAATCTAGATGCGGATCTTGTGGTTTCAGCAGGCGACCTA  
CACCATACAGAAAATAATCTGCTTCCCGGGAACCTCGAACCTATCCGAACGATATTGG  
TCCAATCGCAATCCTGGAATTGGAGCGGTATTAATCCTCCTGGGCGTAAAAGGAGAGTTA  
CCCCAGCTCGACCATCACAACTTTTCTTCAGTGAAGATTGGACAGATGATTTTGCTGTA  
GTTTTCGACGGGCTCAACTTACCCGCCCCCACAATGCATCAAATTCATTTATGTCTCC  
AAGCCTTCAACGTCCGAAGACGGCGTTGCACCTGCTGGATACGAAAACCTTTTTGTTTTA  
ATTCCGACCAAGGCCTCTAGCAGCATCGGCCACGGTGATGCGTATATGCAGTCGGCTTCA  
GCATCCGTGGAAACAATCGCGTCACATGCAATCAATCAAATTGCTACGCAAGCCGGCATC  
CCTGACCTCACTGACCGAATTGTGGTCAAACGCACCATTTGGCCCTGCGGATTTTGAGCAC  
CGCTACCATTTCATGGGTAGGCAGTGCGCTGGGTCCAGCACATACCCTCAGACAGTCCGCT  
TTCTTAAGAGGGCGCAATAGCTCCCGCAAGGTCAATAACCTCTTCTATTCCGGTGCCACC  
ACCGTCCCGGGTGTAGGAATACCCATGTGTTAATTTCTGCCGAGAATATTATTAAGCGT  
TTACATGCCGATACAGTGCAGGACCACTGCCCCGAACCATTGCCGCCTAAAACGACACCA  
TCTCAAAAGACCTCATACGATCAT

>RXN00477-downstream

TAAATTTTGATCCCTATCATCGA

>RXN00523-upstream

TGGTGACTCGTCCGAGTGAAATTGCCGTGGGCATCATCATGCCGATCATTTGGTGCGCCAC  
TGTTTATTTGGATTATTCGTGCTCAGAAAGTCAAAGAGCT

>RXN00523

ATGAGCCTTAGCCATCAACTCAAGCGCCAGCGCGCATCGCGCAACTCCCGCAGGTGGCTG  
ATTGTTGCGGCATTGGGCGTCTGACGCTTGGTATTTTGGCTTTTCTTTGATGTGGGGC  
GAGGTGTTTTATGGCCCTGCTCAGGTGCTGAAAGTGTTGTCTGGACAGCAGGTTCCTGGC  
GCGAGTTATTCCGTTGGCGTGTGCGTTTGCCGCGCGCGGTGATGGGTTTGACTGCGGGT  
TTGGCGTTTGGCGCGGCGGGCGTGATTTTTTTCAGACGCTGTTGCGTAATCAGTTGGCGTCG  
CCGATATTATCGGCATTTCTTCTGGCGCGTCCGCGCGGGCGTAATTTGCATTGTGTTT  
TTCGGGATGTGCGAGTCTGAGTGTGCGCGATTTCTTTGTGTGCGTCTTGGCTGTGGCG  
TTGTTGATTTATCTGGTGGCGTATCGCGGTGGTTTTTCGGCCACGCGTCTGATTCTTACC  
GGCATTGGTATTGCTGCGATGCTGAATTCATTAGTGTCGTATTCGCTGTCCAAGGCTGAT  
TCTTGGGATCTGCCGACCGCGACGCGCTGGCTTACCGGCTCGCTCAATGGTGCGACGTGG  
GATCGTGCGATGCCGCTGATTGTCAACACTGTGGTACTCATTCCGCTGCTGGTGGCTAAT  
GCGCGCAATGTGGATCTTATGCGTTTGGGCAATGATTCCGCGGTGGGTTTGGGCGTTGCT  
ACTAATCGCACGCGCGTCATTGCGATTATTGCCGCTGTTGCGCTCATCGCCGTTGCTACC  
GCTGCATGCGGCCCGATCGCATTCGTGGCGTTTGTGTCTGGCCCCATTGCCGCGCGCATT  
TTAGGCTCCGGCGGATCGCTCATCATCCCCCTCCGCACTCATCGGCGGGTTGATCGTGCTC  
ATCGCCGACCTAATTGGCCAATACTTCCTCGGCACCCGCTACCCCGTCCGAGTTGTACCC

GGCGCATTGCGCGCCCCATTCTTATCTATTTACTCATTTCGTTCCAACCGCGCGGGAGTA  
ACCCTG

>RXN00523-downstream  
TGACCACCAACCATCAACTATCC

>RXN00525-upstream  
CCATCGTGTTTATTACTACAACCCTGAGCTTGCTGATGAATCTGATCGGGTGGTCACCA  
TGGTTGACGGGCGCATCATTGGGTCTGAGGTGAAACACTC

>RXN00525  
ATGAGCCTTGCAGAATCAATTCTTTTGGCGCTCACCAGCCTGAGAAGCAACAAGATGCGT  
GCATTGTTGACGCTGTTAGGAGTCATCATTGGTATCGCATCAGTCATCGGAATTTTGACC  
ATTGGTAAAGCCCTGCAGGATCAAACCTTTGAATAGTTTGGAAGCTTGGGCGCGAATGAT  
CTGTGCGGCGCAGGTGGAGGAACGCCCCGACGAAGATTCCCCCGAACCCGATATGTTGCT  
TTTTCTGGGGCTGCAAACCTCTAGTGGCAATCTGATTCCGGAAGAAACAGTTGATACGCTG  
CGCGATCGTTTTTCGAGGCAGCATCACGGGAATCAGCGTTGGCGGAATGGGTACGCAAGGC  
ACTCTCATCGGCGACACCGCAGATCTTAAATCCGATCTCCTCGGCGTCAACGAGGATTAT  
ATGTGGATGAATGGCGTCGAAATGAACTACGGCCGCGCCATCACGCAAGACGATGTTGCC  
GCTCAGCGCCCCGTTGCGGTTCATCGCCCCAGACACCTTTAATACGCTTTTCGACGCAAAC  
CCCAACCTCGCTCTGGGGTCCGAAGTAGCTTTTGAACCTCAACGGTCAAGAGACATTTTTCG  
CGGGTTATCGGTGTGTATAAAGAAGCCGAGCAGGTGGACTTGTGGGAAGCAATCCAACC  
GTCCACACCTACACCCCATATACGGTGGCCAATGACATCACCCACACGGAAGATGGATTG  
AACAGTTAAGTATCCGTGCAGCTCAGGGCGTAGACCAGGATTCACTTAAGGGTTCAGTG  
CAAACCTACTTCGACGCGCTGTACGCCAACAATGACTCGCACCACGTTGCCATGTTGGAC  
TTCCGTAAACAGATCGAAGAGTTCAACACCATTCTCGGCGCAATGAGTTTGGGTATCTCA  
GCCATCGGCGGAATTTCTTGCTGTGCGGTGGCATCGGAGTGATGAACATTATGTTGGTG  
TCTGTACCGAGCGAACCCGCGAAATCGGTGTCCGAAAAGCCCTCGGCGCTCGTCGACGT  
GACATTGCGCTGCAATTCGTGCTTGAAGCCATGATCATTGTTTCATCGGTGGCATCCTC  
GGCGTGCTTTTGGGCGGCATTTTGGGATTGATCATGTCCAGCGCTATTGGCTACATTTCC  
TTGCCACCACTGAGTGGAATCGTGATCGCCTTGGTATTTTCCATGGCTATCGGCCTGTTT  
TTCGGCTACTACCCCGCCAACAAGGCAGCAAAGCTCGATCCAATTGACGCCTTGCGTTAT  
GAG

>RXN00525-downstream  
TAAAAGCCTCGTTTTTAAGGTAG

>RXN00559-upstream  
CCCTTCAATCCAGTCTTTGACGGCCAATACGGCTTGCCGGGTTTCCAGCGGATCAATCCT  
CATGAAGCATCAGCCTAGTACGAACCGTTAAAGTGTCAT

>RXN00559  
ATGTCTGATAATCCGCATGAGAATCCCCGTGAGAATCCACACCGCTCCCCAGAAGTCGTC  
CTTCGTTTCATGGCTGCCCCCTACTGACGTTTTGATGGCTGGTAGCCATGGCGTTGGCGGT  
GGCCGAGTCCTGGAATGGATCGATAAGGCTGCTTATGCTTGTGCTACCCAGTGGTCTGGA  
ACCTACTGTGTCACTGCTTATGTTGGTCACATTCATTCATTCGCCCCTATTCCCTCTGGC  
CACATGGTTCGAGGTGCGTTCCCGCATTGCGATGACTGGCCGTTCCCTCCATGCACATCGTG  
AATGAGGTGCTTTCTGCGGATCCTCGCGATGGCAACTACACCCGTGCGTGTGACTGCTTG  
GTTATTTTCGTGGCGAAGGACACCGCAACTGGTCGCGCTACCCAGTTCTTTCATTTACC  
CCTAAGAATGAAGAAGAGCAGCGCTGTTGGAAGCTGCTAACTCCCGCATCGGGCTGCGC  
AAGGCTATTGAAGCGGAGATGGAAGAGCAGACGTACAACGGACCTTCTGAGGCCCCCTCGT  
TTGATTACCCGCTTCTTGGCTAAGCCAACAGATATCAACTGGGGTGGCAAGGTCCACGGT  
GGCACTGCCATGGAATGGATCGATGAGGCGGGTGCTGCGTGCACCATGGAGTGGTCTGGT  
AACCACACCGTTGCGGTTTATGCTGGTGGTATCCGCTTCTACCAGCCCATTGAGATCGGT  
GACCTCATTGAGGTGGACGCGCCGATGATGCTACCGATAAGCGTTCCATGCAGATGTCC  
ATCCACGTCCGTGCGGTTGATGCTACCGTGGCCGTGCTGAGCTAGAAACCGCTATTAC  
GCAACGGTGACCTACTTAGGAATTGATGTGACGAGAGCCTTTGCCTGCACCACAGTTT  
GTGCCTCGTACCCCTGAGGATATCCAGTTGGCTGAGCATGAAACATCCTGAGGGATCTG  
CGTGCTGATTACACCCCAATGCCGCTGTTCCAGCGCAGGGTTCCACTGCAGATCGAC

>RXN00559-downstream  
TAGTTAGACCCGAAAAAGCCCCC

>RXN00563  
TTCTACAAGGATCTCTACGCACGTTCCGCACGCGGCACGGCAGCACTGTGGATCGTGGCG  
GCTAACTTGAGTCTCTACTCAGACATCGACGCCATCATCAACTGGGTGCGATCCGAGCAG  
ACCACCACCGTCAACGGCGCATCCAAGCTGGTCAAGCCAGCTTTGGTCCCTACCTTGCTG  
TTCCCATTCGCGGCACCTCGCGTGTCCGGATCCATGGCAGATGCAGGCCACAGGCAGAA  
TCCCAGATGCGACTTCTGCTCTGGTCTGTTGAGCGCCTCATCGCAGGTCTTGCGCCATTG  
GGCTCTCCATCAACGTGGGTCAACGCCTGCACGTGGTCATCCCAGGTTACCAAACCGT  
GGACGCTTCGGTGGCGATGGTGCATACGGTGAATCCAAGGCAGCTCTCGACGCCGTGGTT  
ACCCGTTGGAACGCAGAGCAAGCTGCATGGGGAGCACACACCTCCCTCGTGCACGCTCAC  
ATCGGTTGGGTTTCGCGGCACCGGCCTCATGGGCGGCAACGATCCTTTGGTCAAGGCAGCT  
GAAGAAGCAGGCGTGGAACCTACTCCACCCAAGAAATTGCAGAGAACTGCTGTCCCAG  
GCAACTTCCACTGTTTCGCGAGCAGGCAGCATCCGCGCCAATCACCGTCGACTTCACTGGC  
GGACTTGGTGAATCTGATCTGAACCTGGCGGAAATGGCACGTGCAGAAGCAGCTAAGGCA  
GCTAACGCACCAGTGGTTGAGGCTCCACGCACAGTGGCAGCACTGCCAACTCCTTACCGA  
CCAGTGGTTCAAACCACCCCTGATTTTCGAGGTCAAGTCACCCAAAACCTTGACGAGATG  
GTCGTCATCGTTGGCGCCGGCGAGCTCGGCCCACTGGGTTCTGCACGTACGCGTTTCGAC  
GCCGAACCTCAACGTTCCCTCTCCGCCCGGGTGTATCGAATTGCATGGACGATGGGA  
CTTATCCACTGGGATGAAGATCCAAAGCCAGGCTGGTACGACGACTCCGACGACGCAGTG  
GCCGAAGAAGACATCTTCGACCGCTACCACGACGAAGTCATGGCACGCGTTGGTGTCCGC  
AAGTACAATGACATGCCCTGAGTACGGCATGATCGACAACCTTTGCACCAGAGCTGACCACC  
GTCTACTTCGACGAGACCTCACCTTCAACGTGGGATCCCGCGAAGAGGCACTGACCTAC  
GTCGACTCCGAGCCAGAACTCACCTTTGCTTCTTTCGACGAAGCAGCAGGGGAGTGGAAG  
GTCACTCGCAAGGCAGGCTCCGCAATCCGCGTACCTCGCCGATGGCGATGACCCGCTTC  
GTTGGTGGACAGGTTCTTAAGGACTTCGACCCAGCTGTGTGGGGCATTCAGCTGACATG  
GTGGACAACCTGGACACCGTTCGCGCTGTGGAACATTGTCTGTACTGTGACGCGCTTCCTG  
TCCGCTGGATTACCCACGAGAGCTGCTTGGCTTCCGTTACCCAGCACGCGTGTCTCT  
ACCCAAGGCACCGGCATGGGCGGCATGGAATCCCTCCGTGGCATCTACGTCGACCGCAT  
CTGGCAGAGCCACGCGCCAACGACGTTCTGCAGGAAGCACTGCCAACGTTGTTGCAGCT  
CACGTCATGCGTACGTCGGTGGCTACGGACAGATGATCCACCCAGTCGAGCTTGT  
GCAACCGCAGCTGTTTCTGTGGAAGAAGCATGGACAAGATCCGCATCGGCAAGTCCGAC  
TTCGTTGTGCGCAGGTGGCTTCGATGCCCTGTCCGTTGAAGGCATCACCGGCTTCGGCGAC  
ATGGCAGCAACCGCCGACTCCGCAGAGATGGAAGGCAAGGGAATTGAGCACCGCTTCTTC  
TCCCGCGCCAACGACCGGCGCCGCGGTGGATTATCGAATCCGAAGGTGGCGGAACCGTC  
CTTCTGGCAGCGGATCACTCGCAGCTGACCTGGGCCCTCCAGTACTCGGTGTATCGGA  
TTCGCAGAGTCTTTGAGATGGTGGCCACACCTCCATCCCAGCCCCAGGCCTCGGTGCC  
CTTGGTGTGCTCGCGATGGTGTGGAATCTCGCCTTGCACTAGCACTGCGTTCCGTCGGT  
GTCTCTGTGATGAGATCTCCATTATCTCCAAGCACGACACCTCCACCAACGCAATGAT  
CCAAACGAGTCCGACCTGCAGAGCGCATCCGATCCGCTATCGGTGCTGCAGACGGCAAC  
CCGATGTACGTGATTTCCCAGAAGTCACTCACCGGACACGCCAAGGGTGGTGCAGCAGCA  
TTCCAGATGATCGGTCTCACCCAGGTCTCCGATCCGGACTGGTGCCAGCCAACCGCGCA  
CTCGACTGCGTTGACCCAGTACTGTCCAAGCATTCACCTCGTCTGGCTGCGCAAGCCA  
CTAGACCTTCGTGCGAAGGCACCAAAGGCAGGTCTTGTTACCTCCCTTGGCTTCGGACAC  
GTCTCCGCTCTGGTTGCGATTGTTACCCAGACGCGCTTCTATGAGGCAGTTCTGTGGCA  
CGTGGTGTGAGGCAGCTGACGTATGGCGCGCATCCGCGATCGCTCGCGAAGAAGCAGGC  
CTTCGTACCATCGTCGCCGGTATGCACGGTGGCGTACTGTACGAACGCCAGTCGAGCGC  
AACCTCGGTGTCCACGGAGACGCAAGTAAGGAAGTTGAAGCTGCAGTCTCTGGATTCC  
CGCGCCCGCCTAGTTGACGGTGTCTCCGCGCCGAAGGC

>RXN00563-downstream  
TAGTTGGTTATTGCGTTGAGCCC

>RXN00570  
ACGAGACCTCGGCCCCAAGAAATTGGCAACGGGCTTGTGCGCACTGATTTTCTCCGCATCC  
GGACCCATCGCAGTGATCTCTGGCTGCTGCTGCAGCGGGAAACCTTTGCGCTGATCAAACA  
TCTTCATGGATCTTCGGAGCATTTTAGGCAACGGACTGCTCAGCTGTGGCTTACCTAT  
ATGTACCGCAGCCCGCAGGCATACTTCTGGACGATTCGCGAACCCTCATCGTGGGCGAC  
TCACTTACCCACTTAAGTTTCGCTGAAGTTATCGGCGCATACCTTGTTACCGGCGTTGTG  
GTGTTTGCCTCGGATGGACCGGTCTCATCGGACGGATCATGGCGGTACTGCCACCAACC





>RXN00661-upstream  
 CGGATGCAAGAGAACCGTGGTTTCGCTGATTTTGGCGAACCCGGAATTAAGGCCCCGAG  
 GATTACATGCTTTTAAATCCTTTGAAAAGGGGACAAGATC

>RXN00661  
 ATGAATCCTATAACCGAATTATTAGACGCAACACTATGGATCGGCGGAGTTCCGATTCTG  
 TGGCGCGAAATCATCGGCAACGTTTTTCGGATTATTTAGCGCGTGGGCAGGAATGCGACGC  
 ATCGTGTGGGCATGGCCCATCGGCATCATAGGCAACGCGCTGCTGTTACAGTATTTATG  
 GCGGCCCTTTTCCACACTCCACAAAACCTCGATCTCTACGGCCAAGCGGGTCGCCAGATC  
 ATGTTTCATCATCGTCAGTGGTTATGGCTGGTACCAATGGTCGGCCGCAAACGTCGCGCA  
 CTCACCCAGAAAATGCAGTAGCAGTGGTTCTCGCTGGGCAAGCACCAGAAAGACGCGCC  
 GGCAATTGTGATTGCGGCGGTTGTGGGAACACTCAGCTTTGCCTGGATTTTCCAAGCACTC  
 GGCTCCTGGGGGCCATGGGCCGACGCGTGGATTTTCGTCGGCTCAATCCTGGCTACCTAC  
 GGAATGGCTCGCGGATGGACAGAGTTCTGGCTGATCTGGATCGCCGTCGACATAGTTGGC  
 GTTCTCTACTTTTGAAGTGTGGCTACTACCCATCCGCGGTGCTTTACCTGGTGTACGGT  
 GCGTTTGTGAGCTGGGGATTTGTGCTGTGGCTGCGGGTGCAAAAAGCAGACAAGGCTCGT  
 GCGCTGGAAGCTCAGGAGTCTGTGACAGTC

>RXN00661-downstream  
 TGAAAAGCGTTTACTAAATAGAA

>RXN00733-upstream  
 ACGGCGAGGTTGTCGGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACC  
 GTGAAATTGTTGAATCCCAAGAGACTGCGCAGGCGCAATC

>RXN00733  
 ATGAGTAATACTGCAGGCCCCCGCGGGCGTTCCCATCAGGCAGACGCCGCGCCGAATCAA  
 AAGGCACAGAAATTCGGACCATCTGCCAAAAGGCTTTTCGGAATTCAGGCCATGACCGT  
 AACACCTTAATTTTTGTTATCTTCTAGCCGTCCTGAGCGTTGGACTTACCGTCTTGGGC  
 CCATGGTTGCTGGGTAAAGCCACCAACGTGGTGTGGAAGGATTCCTATCTAAGCGCATG  
 CCGGCTGGTGCCTCAAAGGAAGATATCATCGCGCAGTTGCAGGCTGCAGGTAAACATAAT  
 CAGGCTTCCATGATGGAAGACATGAACCTTGTTCAGGCTCAGGCATTGATTTTGAAAAA  
 TTAGCCATGATCCTCGGACTGGTGATCGGTGCTTATCTCATCGGTAGCCTGTTGTGCTTG  
 TTCCAGGCGCGGATGCTCAACCGCATCGTGCAAAGTGCCATGCACCGGCTGCGCATGGAG  
 GTGGAGGAAAAAATCCACCGCTACCGCTGAGCTATTTGATTTCCATCAAACGTGGTGAT  
 CTGCTTAGCCGTGTGACCAACGATGTGGATAATATCGGTCAATCCCTGCAACAAACCTTG  
 TCACAGGCGATCACTTCCCTACTGACCGTCATCGGTGTGTTGGTGATGATGTTTATCATC  
 TCCCCACTGCTCGCACTCGTGGCGCTGGTATCCATTCCGGTCACCATCGTGGTCACTGTG  
 GTGGTTGCGAGCCGTTCCCAGAACTCTTTGCGGAACAGTGGAAGCAGACCGGTATTTTG  
 AATGCGCGCCTGGAGGAAACCTACTCTGGCCACGCCGTGGTTAAGGTTTTCGGACACCAA  
 AAGGATGTTCAAGAAGCATTTCAGGAAGAAAATCAAGCTTGTGTA

>RXN00733-downstream  
 TAAGGCCAGCTTTGGTGCCAGT

>RXN00784-upstream  
 GTCACATCAGTTATCGCGCGGAATAGTTAGCGGGCGCATGTGGTTGGGATATATGAATAA  
 ATCTATTCCAACACGCGTAAACGAGGACGTTTAAAGCT

>RXN00784  
 ATGTCTATTGAATTCCTCCGCAACAGCAAAAATGAAAATCGAAGTGTGGAGCGACATCATG  
 TGCCCCCTTCTGCTACATCGGCAAAAAGCGCCTCGACGACGCCCTAAGTACCTTTGACCAG  
 GCCGGACGCATCGAAGTGAATACAAGAGCTTCGAACTCATGCCAGGCCTAGAAACCCAC  
 CCACTGCGTTCCGACGTTGAATACCTCGCCGACGCCAAGGGCATGAGCCTCGAGCAGGCC  
 CGCCAAATGAACGGCCAAGTCCAAGCAATGGCACAAGCCACCGGACTTGAAATGAATCCT  
 GACGAAACCATCGCGGCCAACACCATCAACGCGCACCGCCTTACCCACTTCGCGAAAGCC  
 CACGGCAAGCAACAAGAAGTGGCGCAGGAACCTTCAAGGCTCACTTCGTAGACGGCAAG  
 AACGTTGATGACCTCGATGTGCTGGTCTCCATTGCTGCAGAGGTTGGTCTCGATGCCAGT  
 GCAGCCCGCAAGCTCTCAATCCGACGTGTACACCAACGAAGTCCAACAAGACGTCCAC  
 GAAGCCCGCCAACCTCGGCGTCCAAGGTGTGCCCTTCTTTGTATTGACCGCAAATACGCC

ATCAACGGCGCCCAACAAGAAGAAGTATTACCGGCACCGTAGAAAAAGCCTTCGAAGAG  
TGGGCAGCCGAAAACCCAGTCAGCCCATTTGAGGTCATTGACGGCCAAAGCTGCTCCGTC  
GACGGCACCTGCAAC

>RXN00784-downstream  
TAACTTTTGGGACCTATGTGCGT

>RXN00792-upstream  
CACCTTTGGTGCTGAGCCAGGCCACCCAGGCCTTTGAGGTTGGCGCAGATGCCTTAAACG  
GCGGCCACGTGGCTGCCAATACACGATCGGATCCTTGTC

>RXN00792  
ATGAGCCAAGAAATTTTGAGCCATTTTGCACCCGCATTAGAGCGCATTCGAAGCGGCGCC  
GTCGAGCGCGAACAGCAGCGCGCCTTGCCAGTGGAAGAGATTAAAGAGCTGGTAGAGCTA  
GGTTTTACTGGGCTTCGAGTGCCCGAAGAAGTAGGCGGTGCGGGCGCTTCCCTGGAAAGC  
GTAGTTGAGTTACTGATCGAGATCGCGGGCGCCGATTCCAATATCGCCCAAGCCCTGCGC  
GGACATTTTGCTTCGTGGAAGTACTCCTGGAAGCGCCGGAGAGCGAATTCGCGACCCAT  
TGGCTGCGCGAAGTCGCCACCGGAAGACTTGTGGGCAACGCCGAAAGTGAGAAACGCGGC  
GTTTACGGCGATCCGCGAGACCTTCATCGATGAGGTGGAGACTGAAAACGGACCGATTTTC  
GTGCTCAACGGCACTAAGTTTTATACCACCGGCACCTATTTTGCGGACTACACCTGGACC  
ACCGCGCTGCTGCGCAACCTTAACGGCCAAGAACTTTGGTCAGTTTGCCGGTTCGATCTG  
CAGCGCCCGGGCGTGGATGTTGCTGATGATTGGAGCGGGTTGGGCAAAAGCTCACCGCC  
TCTGGAACGACCACGTTTTAAAGACCTGGAGGTGGATCCGCGGTGGATCATTCCACGCACT  
GATGCGCCACGCTGGTGTGGACGTATCTGCAGCTGAGCCTGCTGACCGTGCTGGTTGGC  
AGTGCCGCGAGCAGCTGTCGATGAGGTGGTTGCCCGCGCCAATCCTCCACCAGAAATGCG  
TGAACCCCTGGCGTCGAGCGCCGAGCGATCCGGCCGCAACCATAGCGATCGGCGACGCA  
CGCAGCCGAGTCACCGTTATTCGTGGAGCGCTTCTCGACGCCACCCGCCACGTTTCCAAC  
GCCGCCACGATCGTAACCCCGAAGCCTTCAACGAGGCGGACGCTATTGTTGCAGCGCTC  
TGGCCCATCGTCTCCGGACAAGCTTTGGTGGTGACATCCAACGTTTTCGATGCGGTGGGT  
GCATCTGCAGTGCTTGGTGAGCATTCCATTGATCGCCACTGGCGCAATGTGCGTACCGTG  
TCCTCAAACAACCCGGTGTTTCTGGCCAAGAATGCAGTGGGGGAGTATGCCCTAACGGC  
ACTCCTGTGGGTACCAACATTGGTAAAGCACTGAGCCGTCCGGTGAGCCTAAGCAGC

>RXN00792-downstream  
TAGACGTGTGATTTTCGCTGGTTT

>RXN00819-upstream  
GATGAGGTTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCT  
AGCACTGAGCGCGGATCTCAAGCAGAAAAGGTTCGTGCAAC

>RXN00819  
ATGCGTGATCCCATTCGAAGGTGCTGTTATTCCTTCTGATCTTTTGGTTTCGCAGAAGTT  
CTCACCGAAGCCGAACGCGCAGTTCTTCTGGAACCCGAGGGTGCTTGAGGAAGAGGTG  
AAGCCTTATATTAATGAGGCCTGGGATAAGGCAGTCTTCCCGATGAGATCGTGACGCC  
CTCCAAGATCTGCAATTGCTTGATCCGCCTGCACTTCGGGAAGCAGGGGAGTCGGTTTCA  
GACATTTTCACTGGTTTCCGCAATTTTGAAGTCCGCGCTGTGACATCAATGTTGGTACC  
TATTACAACGCATCTGCTGGTCTCTTCCGAACGGCCTGCATGGTTGGTGGCTCCCGGAG  
CAGGCGCAGCGATTGGATGCGCAGATCAAATCTGGTGAGGTCAAGGGCGTTTTTGCATG  
ACGGAACCTGATCATGGCTCTGATATCGCAGGTGGTCTGGCAACCACGGCCACTAAGGAC  
GCAGACACCGGCGAGTGATTATCAATGGTGAAAACGGTGGATCGGTGGTGCTTCCACT  
GCTGATTTGATCGCTACCTTCGCCAGGGATACAGCCGATAACCAGGTGAAATGCTTCCTC  
GTGGCACCTCAGGCAGAGGGCGTGTCCATGGAGATTATTGATCGCAAAGCCTCACTGCGC  
ATCATGCAAAATGCACACATTACCTATAACAATGTCCGGGTGTCTGGGGATGCGCGGCTG  
CACAACATCAATCTTTCAAGGATGTTTCCGAATGCCTGCGCCGTATGCGTCCGATGTG  
GCGTGGATGGCGGTTCGGTGCGCAGGAGGTGCCTATGAAGCAGCCGTGAAGTATGTGCGC  
AGCAGGGAACAGTTTGGCCGTCCGATCGCGGGGTTCAGTTGATTACAGGAAAAGCTCGCG  
CTCATGCTGGGCAATCTCACGGCGTCGCTGGGCATGATGGTCAAACCTACCGATCAGCAG  
CAGGCGGGAATTTTCAAAGAGGAAAACCTCCGCGCTGGCGAAAATGTTTACCTCGCTCAA  
CTTCGGGAGACCGCTAGTTGGGCGCGGGAAAATCTGCGGAGGCAACGGCATCATTTTGGAC  
AACGATGTTGCCGGTTCCATGCCGATGCAGAAGCCGTCTATTTCATATGAAGGCACCCAC  
GAAATCAATGCACTCATCGTTGGNCGNCCATTCTGGGNCNTCTNTTCTTTTATATTAT

NACNCTTTTGAGGAGGATCTTCATGACTACTTCCACCACCCCAAACCATCGTTTCTTTTCG  
AAGACGCACCAACCCCTACCGGCCAGGACCTGGGCTTTTCGCAGTGGCGCACTGTCACCC  
AGGAGATGG

>RXN00819-downstream  
TGAACACCTTGGCGGACGCAACT

>RXN00832-upstream  
GAGATTGTGCTAGGTTCTGATGAGGCTTCGGGACGACCCGAAGAAATCTATGACAGCCTG  
GGAACGGCCCCAGAGTTCTTAAGAAAGTTTGACTAGAGAAC

>RXN00832  
ATGCCGTTTTCTTGGCTAAAACCAATTGATTATGCCCCGATCTTTGTGCGGCTGGGCATCG  
ATTTTTATCATCCCCCTCATCACACTGCCATCAATTATTGAGTTGGCGCTGATCGTGGCA  
GTCATCCTATTCTGCGCATTGGCGTGGTGAAGATGGCGGAGCGTTTGGCTCATATTTTG  
GGTGATCCTTTTGGATCGTTGATCCTTACCTTGTGATCGTGATCATTGAAGTGATTTTG  
ATCTGTGCGGTGATGCTGGGGCCTGCTGATTCAACCACTGCTGGTCGGGATTCCCGTGATG  
GCAGTGTCATGATCATCATGGGTTTGGTCGTGGGATTGTGCCCTACTCATTGGTGGTTTA  
AGGCATGGAAGCATGCCACACAATGGGGTGGGAACCTCCGACCTACTTGGTGCTGATCGCA  
ACTTTTCCGTAATCGCCTTGGCGTTCCAGCTTTCAGGGGAGAATACTCCACTGGGCAG  
GCACTTGTATTTCACACTGACAGCAGTGGTGTACGGGTCTTCCCTGTTTCGCCAAATG  
GGTGCCCCAAGCTGGTGAATTTCAAGAGGTCGAGGTGCGAGAAAAGGCAGACGACGCAGCA  
AAATGGGAGGTCCCATTTAGAGGCTTAATCTTGATTATCACTGTGCTCCCCATCGTGTTG  
CTGTCCCATGACATGGCCACGGTGATGGATGAAGTCTTGGCAAGCCTTGGTGACCCGTA  
GCAATGGCTGGATTAATTATTGCCACCATTGTCTTCTTGCCAGAGACCATCACCTCCTTG  
AAAGCTGCGTGGACAGGAGAGATTGAGCGAGTAAGCAACCTCGCGCATGGAGCCCAAGTA  
TCAACGGTGGGGCTGACAATCCCAGCTGTTCTAGTGATCGGCGTGATCACAGGTCAAGAT  
GTAGTTTGGGGGAGACCCGATCAACTTGTGCTGCTGGGAACCACCATTGCGGTGACA  
GCCATTGCGTTTAGCTCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTT  
TTCGGTGTACATGATGAGCATGTTTCGCC

>RXN00832-downstream  
TGATTTAGGTAGCCTGGTGGGAA

>RXN00842-upstream  
CCTTGTCGCGGAGGTAAGCGAGGGTATTTCTGGATGTGGAACAACGCGGATTATGGAAAA  
TCGTGACTTTCATAACGTTGAGCCTACTAAGGTTTGTTCC

>RXN00842  
ATGATTATTCAAATCCTAAGAGTGGCATTTGCCTTCGTCGGCATCATTGTTGGCGCCGGT  
TTCGCATCAGGGCAAGAGGTCATGCAATATTTGTGGCCTTCGGCATAGACGGAATTTGG  
GGAGTCATTGTTTCTGCAGTGATCATGTGCGTGATGGCGTTGATCATTTTGCAGCTCGGA  
AGCTATTTCAATGCAGGTGAACACGGTGAAGTGTTCCGCCGAGTAAGTCACCCCGTTTTTC  
TCCAAAATTTTGGACATCGGCGTTGTGGTGACGTTGTCTCCACCGTTTCGTGATGTTT  
GCAGGCGCGGATCAAATCTGAATCAGCAGTGGGGCTTCCGCTCTGGATCGGTTCTGTG  
ATCATGGTTCTTCTGGTGCTGGCTGCGGGCATGTTGGACGTGGATAAAGTAACCACAGTC  
ATTGGTGCAATTACTCCGTTTCATCATCATTTTCATCACTGCCGCCTCGATCTACACGCTG  
GTAGGTAATTTAGCTCAGTGGAGCAGCTTGATTCTGCTGCTTTAGAAGTCGGCACGACG  
TTGCCCTCACTGGGCTGTTGCAGCGGTGAACATATGTGGGATTCAACCTGATGGTTGCGGTG  
TCCATGGCTGTGGTCATTGGTGGATCAATGTTTAACCCGCGGGTCGCAGGTGCGGGCGGT  
TTGCTGGGCGGATTGATCCTGGGATTCTTGATCATCATCAGTGCGCTAACACTGTTTCGCC  
ACCGTGGAAGAAGTTGGCCAAGATGATATGCCATATGCTGACGATCATCAACAATTTGAAC  
CCGCTGGCTGGCCAAGTAATGGCAGTGGTTATCTACGGAATGATCTTCAACACGGCACTG  
GGTATGTTCTACGCATTGGGCCGTCGTCTCACTGCGAAAAACCCACAGCGATTCCGTCGG  
GTTTATGTGGTCACAGTGCTGATTGGTTTGTGTTGAGCTTTGTGGGATTCAAGAACTTG  
GTGGGCTATGTGTACCCAGTCTTGGGATACATTGGCCTGCTGCTGATTGCAGTGATGATG  
GTGGCGTGGGTGAGGGGACGCGTACGCATCTACAAGGAATCCGAACGCCGATGCGGATC  
GCAGACTTGTGAGATCGGCCATGACGGAGCGTTGAGTGGAGCAGAGCTGGCGGTGCTC  
AACCAGGAATCCAAGATTCAAACCTGGATGAGGAACAAATTAAAGCAGCGGTTAGGAAG

>RXN00842-downstream

TAGTTACTCTGCAGGGACGAGCT

>RXN00931-upstream

CCGTAACCTAATCGTTGAAACATCACCTTATTGCTGGGCTTTGCACGCTACTCTTTGTGA  
GTAACCTCACCGAAGTGCATAAATTAATTGGGAGTGATCA

>RXN00931

GTGAAAACATTGAAGATATTTTGACCTTGGGAAGAAATCGACCGCGATATTTACCGTGGT  
CCCGTTATCGAATCTTATTTAGCCAGGACTTTCCGGTGGCCAGGTGCGTGCCCAAGCTTTA  
GTAGCAGCAACGCATACTGTTGATAAAGCCTTTACTGTGCATTCTTTGCATGGCTACTTT  
ATAGCTCCTGGTGATCCAACAGCACCCGCAATTTATTTAGTGGATCGAGTTCGCGACGGA  
AAAAGCTACGTACCCCGCTCGGTGCGTGGCATCCAAGACGGCGAAGTAATCTTCAGCATG  
CAGGCCAGCTTTTCATCGTGGGGATGAAGGCATTGAGCACATGGACAAGATGCGTAAAGTT  
CCAGCTCCTGATGAGATCAAGGGAACAGTAGAACGTATGCCGATCTCAAGTAGGCGAGTG  
CTTGATGAATGGGCGGAATGGGATATCCGCGTTATTCCGCGAGGATCAATTAGAACTCAGC  
GATTTACCGCTACTGAGCAAGCTGTGTGGATTCCGGTGCACCGCTGATCTTCCGGATAAT  
CCCACCTTCCACCAGTGCTCACTGACTTATCTGTCCGATATGACTTTGCTGCATAGTGCC  
CTGGTGGCACACCCAGGTGAGAAAATGCAGATGGCCTCACTTGATCACGCTGTGTGGTTC  
CTGCGTCCCTTCCGCGTCGATGAATGGTTGCTTTATGATCAGCGCTCTCCATCGGCCTCA  
AGTGGGCGAGCCTTGACTCACGGGCGGCTTTTCAACCAGCAGGGAGATTTGGTTCGCTATT  
GTCAATCAAGAGGGAATGACCCGCACACTCCACGAGGGTGCGCAATCAATTCCGATGCGC  
AAAGAC

>RXN00931-downstream

TAAAATGCAGCGAAGTTGAAGAT

>RXN00934-upstream

CCAACCCCTGTGGTTTGGTGATTTGGATCCGGAGCGTCTCAAGCGCTCTAGGGAGCAGAC  
AAATGTTACAAACCGGTGGCATTACAGGAGGACAATTAG

>RXN00934

GTGCGAATTGGAATGGTCTGCCCGTACTCCTTCGATGAGCCGGGCGGTGTTCAAGCGCAT  
ATCCTTGACTTAGCGCGAACCTTCATTGCCCCAAGGCCATGAGGTTCAAGGTGCTTGGTCCG  
TGTAGTGCGGATACGCAGGTGCCCGATTTTCGTGGTGCGCGGTGGTGGCAGCATCCCGATT  
CCGTACAATGGCTCGGTTGCCCGCTTGAGCTTTGGGCGGAAAATGTTCAAGGCCGTGCGC  
ACGTTCCCTCCGCGAAGGCAACTTCGATGTGCTGCATATCCATGAACCGAATTCACCAAGT  
TTTTCCATGGCGGCGCTACGCTTTGCGGAAGGCCCCATCGTTGCTACTTACCACGCCTCC  
AGTAGCGGATCGAAGCTGCTCAAGGCTTTCTTACCAGTGCTTTGCGCCATGCTGGAGAAA  
GTGCGCGCAGGCATCGCCGTGTCTGAAATGGCTCGGCGCTGGCAGGTGGAGCAAGTCGGC  
GGCGATCCCGTGCTGATCCCCAACGGGGTAGAGACCTCCATGTTCAAAGCCGCGCGCCAA  
ATCGAACCGAATGATCCTGTAGAGATCGTCTTTTGGGTGCGCTCGATGAGTCCCGCAAA  
GGCCTCGACATCCTCCTGCGCGCTCTGACCAGGCTGGATCGCCCGTTTACCTGCACCGTC  
ATTGGCGGCGGCACCCCGCGAGAAGTCGCCGGCATCACTTTGTGGGCGCGCTCAGCGAT  
GAGGAAAAGGCAGCAATCTTAGGTGCGCGAGACATCTATGTCGCACCCAACACGGGCGGC  
GAAAGCTTCGGCATCGTGCTAGTTGAAGCGATGGCCGCGGGATGCGCTGTCTGTCGCCAGC  
GACCTAGAAGCGTTCTCCCTGGTCACCGATTCTGAAGCCGCACAGCCAGCGGGCGTGCTA  
TTTAAAACCGGCTCAGACGCGACCTAGCCAAAAAACTTCAAGCGCTTATCGACGACCCC  
TCCTCCCGTTCCACGCTTATCGCCGCGGGGCTAAAGCGCGCAAACGCCTACGACTGGTCG  
ACAGTATCCACCCAGGTGATGGCAGTCTATGAAACCATTGCGATCGACAAAGTGAGGCTT  
GGA

>RXN00934-downstream

TGACCCCTGTTTACCTCCTCATC

>RXN00960

ATGGCTCGGCATTGTTGCAGCAATCGCTACGCGTCCACCGTCTTCTCCGGTCTGATCGCC  
TACGGAGCATCCCAAGCGCTCTACCCATGGCTGCTGAAAGACCACCAAAGCGTCACCGAA  
ATCGACCTTGATGCAGGTGCCCTCCAGCCCTACTTCAACATCGAGATGCCACCACCATTT  
GAAGTGATGACCGCACTGCTGCTGGCATTCTGCCTCGGCCTGGGCATGGCTGTAATTAA  
TCAGACACCCTGTTCAAGGTAACCCGCGAAGTTCGAGCGCTAGTCATGAAGACCATCACC

GCCTTTGTCATCCCACTGCTGCCACTCTTCATCTTCGGCATCTTCCTCGGCATGGGCATG  
AACGGTGGCCTCCTGGAGATCATGTCCGCCTTTGGCAAGGTACTGATTCTCGCCGTCGTG  
GGAACCCCTGCTCTTCCCTAGCCATCCAGTTCATTATCGCTGGTGCAGTATCCAAGAAGAAC  
CCATGGAAACTGTTCAAAAACATGCTCCCTGCATACTTCACTGCACTGGGCATTCTCTCT  
TCAGCGGCAACCATCCCAGTGACCTACCAGCAGACCCTGAAAAACGATGTTGATGTCAAC  
GTCGCAGGCTTTGTTGTCCCACTGTGCGCCACCATCCACCTAGCTGGATCGATGATGAAG  
ATCGGCCTCTTCACCTTCGCTGTTGTCTTCATGTACGACATGGAAGTAGGCGTCGGCCTC  
TCCATCGGATTCTCTCATGCTGGGCATCACCATGATCGCCGCACCAGGCGTTCCCGGC  
GGAGCCATCATGGCAGCAACCGGCATGCTGGCCTCCATGCTCGGATTCAACACCGAACA  
GTCGCCCTCATGATCGCCGCTTACATCGCGATTGACTCCTTCGGCACCAGCAGCAACGTC  
ACCGGCGACGGCGCAATCGCAGTCATCGTGAACAAATTGCGCAAGGGCCAGCTGCACACC  
ACTTCCCGAGATGAAATCGAAGAAGACGACCGCGTTGCCCTTCGACATCACTCCATCGGAT  
GTGGAACATCACAAAG

>RXN00960-downstream  
TAGAAACCCGCATTTTCTGTAGT

>RXN00980-upstream  
AGAGAGAAAGGGAGAAATCATGAAAACGTGGAAGACCTGGGGGGTCGTGCGAGCTTCAGG  
CCTCTTGATTATTTTGTCTGGTTGAGTTCATCGAGCCCC

>RXN00980  
ATGCTGGCAGATGCATTCATGATCGCGGCTGCAATTGTTGCAGGTTGGCCGATCGCGCAG  
TCTGCATATCAAGCACTTCGCATTTCGAATGGTGTGCGATTGACTTACTGGTCGTTGTGGCT  
GCCGTTGGTGCCATGTTTCATCAACAACCTATTGGGAGTCTGCGGCGGTGACGTTCTCTTT  
GCCCTTGGCAAGGCACTGGAACGCGCGACAATGAACCGCACACGAAAAGCACTATCGGAT  
CTGGTGGATGCAGCTCCAGAACTGCAACAAGGCTCAACGCGGATGACTCAACAGAGGTA  
GTTGAGCTGTGGGAGCTTGAGCCCGGTGACATCGTCTTGGTACGCAATGGCGAACAATTT  
CCCGTGCATGGAACGCTGATTGCGGGTGTGCGGTGGAATTGATGAATCCAACATCACGGGT  
GAATCAATGCCGGCTGAAAAGGCTCAAGGCTCTGATGTGTATGCAGGAACCTGGCTGCGA  
TCTGGTGTTTTGTGAGAGTCGAGGCAACAGGAATTGGTTCAGACTCAACTTTGGCAAAAATC  
ATTACCGCGTTGAAGACGCCCAGGATGACAAAGCCCGCACACAAACATTCTTAGAGAAA  
TTCTCTAAGTGGTACACCCCGGGCGTCATGATCGCCGCGCGAGTGGTGGGACTTATCACC  
TGGGACGTAGAACTAGCACTGACGCTCTTAGTGATCGGCTGCCCGGCGCGTTGGTTATC  
TCCATCCCGGTGTCCATCGTCGAGGCATCGGCCGTGCTGCACGCGATGGCGTGCTGATC  
AAGGGTGGAGAAATACCTAGAAACCGCCCGCAAGTTCGACGTCGTTGTCTGAGACAAAAT  
GGAACGCTGACCACCGCCCGCCAGAACTCACAGACGTAGAAGTCATCGAGCCCGCCTAC  
AGCCAGGGCGAGGTGCTGGAGCTCGCCGCGCGCGCCGAGACGGCTTCAGAACATCCGCTT  
GCCGACGCCATCATCCGTGGTGCCAGGATCGGGGGCTGTCCACAACATTGGTGGAAGCA  
GCTGAAAACATCACCGGCCGAGGCATTATCGCAAATGTTGATGGACAGGCAGTTGCTGTT  
GGATCTGCTGAGTTACTTGATCATGAACCAGACTCGACCAGGATCCTGGAGCTAAATGCC  
GAAGGAAAAGACCGCGATGTTTGTGCGAGTGAACGGACACGCCATTGGAATCGTGGCCGTC  
GCCGACGCCGTTCTGTTAGATTCTGCCTCAGCAATCGAATCGCTGCATAAGGCGGGCATT  
CAAGTTGTATGGCGACTGGCGACGCTCACCGCGTTGCACAAAACGTGGCCTCCAAGCTG  
GGAGTGGATGAAGTCTACTCAGAGCTACTCCCTGAACAGAAATTAGAAGTGGTGCGTGAT  
CTGCAAGCTGCCGGCAAAACGGTCGCGATGGTGGGTGACGGAGTCAACGACACCCAGCA  
TTGGCAGCTGCTGATATCGGAGTAGCGATGGGCGTGGCAGGTTCCCCTGCAGCCATTGAA  
ACCGCTGATATCGCACTCATGGCGGATCGTCTCCACGGCTGGCACATGCAGTGACCTTG  
GCAAAACGCACCGTAAGAACCATGCGCATCAATATTCTGATTGCGTTGGCTACCGTGATG  
GTGTTACTAGCTGGCGTCCTATTTGGCGGAGTTACCATGTCGTTGGCATGCTCGTTTAC  
GAAGCAAGCGTGCTGCTTGTATCAGCATCGCCATGCTGTTGCTGCGTCCAACACTTAAA  
GAAGATGCTGCGCAAGCAAGTGATATTAAACGCTCGGAAATACAACAGATCGCA

>RXN00980-downstream  
TAACCAATGGCTGGGTACTGATG

>RXN01000-upstream  
CTTTCTATGCCTACGCGGATGTTTCCGTGATCATTCTGGAAATCCTCATCGTGGTGATTG  
TCATTGAAGTAATCTCCAACGCACTTCGAAAGAGGCTGGT

>RXN01000

ATGAGCACCTTAACCTCTCACCGCACAGTACCGGCCCCAGCTCTCCCCCGGCGCGCCCC  
AACAAACTGGCGCGCAATATCGTTGCAATTGTCGCTGCGCTGATTGTCCTTATAGCTACC  
GGCACGCTCAAGATCGAGTGGAATGAGCTTCCGCGAGATGCCCGCGCAGGTGTGGCATTAC  
TTAGAGCTGATGTTTAGCGATCCCGATTGGTCGAAGTTTGGCCGCGCCGTCCAGGAAATG  
TGGCGTTCCATCGCCATGGCGTGTTGGGTGCCATTTTATGCGTGGTGGTCTCTGTCCCT  
CTGGGAATGTTGGCTGCCCGCGGGGTGGGACCTTATTGGCTGCGTACCGTTTTACGGTTC  
GTGTTGCGCGGTGATTGTCGCTTCCCCGAAGTGGTTATCGCAATTATTTTGCTAACTGTC  
ACCGGCCCTAACTCCTTTTACTGGTGCGCTCGCATTTGGGTATCTCCGGTATTGGACAACAG  
GCAAAGTGGACCTATGAAGCCATTGAGTCCACTCCCACCGGCCCGTCAGAGGCAGTGCCT  
GCAGCGGGTGGAACCTACGCCGGAGGTCTGCGGTGGGCGTTGTGGCCACAGGTTCGCGCA  
TCCATTGCATCTTTTGCCCTGTACCGCTTTGAGATCAACATCCGTACCTCTGCGGTATTG  
GGCATCGTTGGTGAGGTGGTATCGGTAGTATGCTTGCCAAATTACACCAACTACAGGCAG  
TGGGACACCGTGGGCATGCTGCTCATCGTCGTGGTTGTCGCAACGATGATCGTCGATCTC  
ATCTCCGGCACCATCCGCCGCCGCATCATGAAGGGGGCTAGTGACCGTGTCTGTGGCACCA  
AGCAAC

>RXN01000-downstream  
TGACGCTCCACCAAGCATCCGCA

>RXN01002-upstream  
GACTGCTGATACCGCACAGGATGAAATCACTCGTTACGGCGAGATCCTGAAGAAGTTCTC  
CAACTAATTTCCCTGTTTCCAATACTCAAGGTGTGCGCAT

>RXN01002  
ATGAATTCTGATGCTTCGGCTACCACCAACTCCTGGGCTATCAACTTCGACCATGTGTGCG  
GTGACGTATCCCAATGGGACGAAAGCCCTCGATGATGTTTCCCTCACCATCAATCCCGGT  
GAGATGGTTGCCATCGTGGGTCTGTGAGGATCGGGTAAATCCACGCTGATTTCGCACGATC  
AACGGTCTTGTCCGCGCTACGGAAGGCACCGTGACGGTGGGGCCGCATCAGATCAACACC  
TTGAAGGGGAAAGCACTGCGTGATGCCCCGTGGGCAGATCGGCATGATTTTCCAGGGGTTT  
AACCTGTGCGAAGCAGCAGTGTGTTCCAGAATGTTTGGTGGGCCGCTTCGCGCACACA  
GCGTGGTGGCGTAACCTCCTCGGGTTTCCACGGAGCACGACAAGCAGATTGCTTTTCAC  
GCGTTGGAGTCCGTGGGCATTTTGCACAAAGTGTGGACCCGAGCTGGTGCTTTGTGCGGT  
GGACAGAAACAGCGCGTTGCTATTGCGCGCGCCTTATCGCAAGATCCGTCTGTATGCTG  
GCAGATGAGCCTGTGGCAAGCCTTGATCCGCCAACCAGCGCATTCGTGATGCGCGATCTA  
GAAAACATCAACAACGTGGAAGGCCTCACCGTGTGGTGAACCTTGCACTTGATTGATTG  
GCTCGTCAATACACCACAAGGCTTGTGGGTTTGCCTGCCCGCAAGCTGGTCTATGACGGT  
CCTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATCTATGGTCGCCCCATCCAGGT  
AAAGACCTGCTAGGTGATCGCGCA

>RXN01002-downstream  
TGACCACGCCTTCTTCTACACTT

>RXN01007-upstream  
TCTGAACCAATATACCGATCAGTCTAAAAGTGTGTTAAGTTCTGGAACATAAATTAGCTG  
ACACGTAAAGTAACCTAAAGATTCACTGGAGGTAAGCCTA

>RXN01007  
GTGTTTAAAAAGCACAGACACGGTCTCGGCTCCCCGAAACCAAACCACGCTCAATAACC  
CGCCGGTTTTTACCGCGGCGCGCGCTACGCTGGCAGGATTGGCAGTCTGTCCGGCTGC  
ACAGCACAAACCCTACAAGCAGAAGACAACACGCTCACTTACTTAGAGCCACAGTTCTTC  
CGCACCTGTACCCACCATCAGCGGGCTTTTACCCCAACGGCAGTGTGGTGAACAACATT  
GCAGACCGCTTGCTCTACCAGGATCCTGAAACCTTGGAACCTCAAGCCGTGGATCGCCACC  
GAACTCCCAGAAGTAAACGAAGACGCCACGGAATTTACCTTCAACATCCGCACCGATGTC  
ACCTACTCCGATGGCACCCCGCTGACGGCTGAAAACGTGGTGAAAACTTCGATCTCTAT  
GGCCTCGGCGATCAAGATCGACGCCTCACCATCTCTGAGCAGATCACCACCTACGACCAC  
GGCGAAGTAGTAGAGGACACCGTCCGATTCCACTTCTCTGAGCCTGCACCTGGTTTTT  
GCTCAGGCCACCGCTCCTTCAACGCTGGCCTTTATGCCGATTCCACCTTGGAGTTCCGC  
AATGAGGATTTGCGGCCAGGCAACGCCCCAAAACGTCATCGGCTCCGGTCTTTCTGTATC  
ACCGATGAAACCCTAGGCACCAACCTCACCTTGACTGCGCGTGAGGATTACGATTGGGCA  
CCACCATCACGCGAACATCAAGGTGCGCGCAAGCTTGACGCCGTCAATTATGTCCTCGCG  
GGTGAAGAATCCGTCCGCATCGGAGCCATCGTTGCTGGCCAAGGTGATATCGCCCGCCAG

ATCGAAGCGCCAGTGGAGGCACACCTGAAGGATGCAGGCATCCCGATCATCTCCGCAGCC  
ACCAACGGTGTGAACAACAGCTTCAACTTCCGCTTCAAAAACGAGCTGCTCTCAGACATC  
CGTGTTCGCCAAGCTCTGATCCACGCGATCGACCGCGAAAAGATCATGCGTGTGCTGTTT  
AGTGATTCTATCCGCTGGCAACTTCTGTGCTTGCAGAAAATGCACTGGGCTACAAAGAA  
CAAGTAGATGCCTATGTCTACGACCTAGACAAAGCAACAGCTCTGCTTGACGAAGCCGGC  
TGGACCCTTGATAGCGACGGCATGCGTCGCAAGGACGGTGAAGTTCTAGAGCTCACCTTC  
AACGAAGCCCTCCACAGCCTCGTTCACGCGAAGTTGTACCATGGTCCAAGAACAGCTC  
GGTGATCTGGGCATCAAGGTCAACCTCAACCCAGGTGACCAAGCAGCCAGGACGCTGAC  
TCCAAGGATCTCAACAAGATCCAGGTTCCGCCACACCATGGTGGGTGCGCGAGACTATGAC  
GTGCTGAAATCCCAGCTGTACTCCACCAACCGCAACGAGCTGTTGAACATGACCGTGGAA  
GGGAGAGACCGGATATTGGCGATCCTCATTGGAGGAACTCCTCATGGCTATTGCATCC  
AGCCCACGCGAAGAGGACCGTGCAGCAGCATCTGCCGAGCAGCAGGATTACATCACCGAG  
CAGGCATATGTTCTTCCACTGTTTGAAGAGCCAGTTGTCTACGGCGTGCAGCCTTACGTG  
AAGGGCTTTAGCCCCGAAGTGATCGGCCGCCCGAGCTTCTATGAGACCTACATTGACCAT  
TCCAGCGACCATTCAGTGAGGAGGAC

>RXN01007-downstream  
TAAATGACTACCTCGCAGATTCT

>RXN01090-upstream  
GCCGGTTTGGGCTGGTTGGAGCTCTAGATCGTAAGTGGTGTCTGACCCATGACGTACCAT  
TAACCACGAACGTTTTAAAGAAGCCACGAAGGAGCCTGAC

>RXN01090  
ATGGCGTTACCACTACCCAGCAAGAGCGCTCGAGCACTTGTACTGGGGCAAGCCAAGGC  
ATTGGCCTCGCCATCGCCAAAGATTGGCGCGGTATGGGCACAACCTCATTGTTGGTTGCT  
CGCCGCGAGGATGTCCTCAAAGAGATCGCCGAGATCTAGAGAAGAAGCACGGCGTGATC  
GTTGAGGTCCGCCCGGTGGATTTGAGTGATGAGCCAGCCCGCAAGGTGTTGATCGATGAG  
ATCAAGACAAGGGAAATCAACATCATCATTAAGTCTGCTGGCATCGCAAGCTTTGGGCCG  
TTCAAGGACCAGGATTGGTCTTATGAGACTGCCAGTTCTCACTTAATGCCACAGCCGTT  
TTTGAGCTACCCACGCGGTGTTGGGTGGCATGATTGACCGTGGCACGGGCGCTATTTGC  
AATGTGGGATCTGCGGCTGGCAATGTGCCAATCCCCAACACGCCACGTATGTGCTCACC  
AAGGTGGCGTGAACGCGTTACCCGAGGCAATGCATTATGAGCTGCGCGGAAGTGGTGTG  
GCGTGACTTTGCTGACCGCGGACCTGTCCGTGAGGCGGAGATCCCTGAGTCTGAGAAG  
TCGATCGTTGGACAAGGTTGTCCCTGATTTCTTGTGGACCACCTATGAGTCTGCTCCGCA  
GAGACCTTGCGTGCGCTGTCTAAGAATCAGCGTCGCGTTGTTCCAGGTCCGCTGTCCAAG  
GCCATGAATTTTGTGTCCTCTGTTGCTCCAACCGCTGTGCTCTCCCCTGTTATGGGCTGG  
GTTTATAAGAAGATGGGT

>RXN01090-downstream  
TAGTTTTTAAAAGTGTCTGAATC

>RXN01114-upstream  
TTCGGTGGAAGATATCCGCAAGCTGGTGCTGCCGAGCTTTTAGAAACGGCTCAAGCAAT  
TTCGACAGATCTCTTGCACTCTAAATTAAGGATCAAAA

>RXN01114  
ATGAACCCCTCAAGATATTGTCTATCTGTTCCCCATTGCGCACCCAGTTGGTGCTTACGGC  
GGATCCTTACCGGCGTCCCTGTTGAAGAATTGGCCACCACCGTGATCAACGCGATCGTT  
GAGGCAACCGGCATCACCGGCGACGATGTGGACGATCTGATCCTCGGCCAGGCATCCCC  
AACGGTGCGGCTCCAGCACTGGGCCGTGTTGTTGCTCTAGATTCCAAGCTTGGCCAAAAC  
GTTCCAGGCATGCAGCTTGATCGCCGCTGTGGTTCCGGCCTGCAGGCAATCGTCACCGCT  
GCTGCACACGTTGCATCCGGCGCTGCTGATCTGATCATCGCAGGTGGCGCAGAATCCATG  
AGCCGCGTTGAGTACACCGTGTCCGGCGATATCCGTTGGGGTGTCAAGGGCGGCGACATG  
CAGCTTCGTGACCGCCTTGAGAAGCACGCGAAACCGCTGGCGGACGCAACCACCCGATC  
CCTGGTGGCATGATCGAGACCGCTGAGAACCTGCGTCGCGAATACGGCATCTCCCGCGAG  
GAGCAGGACAAGATCTCCGCAGCGTCCAGCAGCGTTGGGGCAAGGCTGCTGATGCGGGG  
CTTTTCGACGACGAGATCGTGCCAGTCACCGTCCCTGCCAAGAAGCGCGCCAGGAGCCA  
ACCATCGTTTCTCGAGACGAGCATGGTTCGACCAGGAACAACCGTCGAAAAGCTTGCTGCT  
TTGCGCCCCATCATGGGCCGCCAGGATGCGGAAGCAACCGTCACCGCTGGCAACGCGTCC  
GGCCAAAATGATGGCGCTGCTGCCGTGATCGTGACCACTCGCGCCAAGGCCGAGGAGAAG



GGCCTGCGCCCAGTCATGCGTTTGGCTGGCTGGTCTGTGGCTGCTGTTCCCCCAGAGACC  
ATGGGTATTGGACCTGTTTCCTGCCACCAAGAAGGTCTGGATCGTTTGGGCCCTTACCCTG  
GAGGACATCGGCGGATCGAACTCAACGAAGCTTTCGCGAGCTCAGGCACTGTCTGTGCTG  
AAGGAATGGAACATTTCTTGGGAAGATGAGCGCGTCAACCCACTGGGTTCGGTATTTCC  
ATGGGACACCCAGTCGGTGCCACCGGTGCTCGCATGGCAGTAACCTTGGCTCACCGCATG  
CAGCGTGAAAACACTCAGTACGGAAGTGGCCACCATGTGCATCGGTGGCGGCCAGGGTCTT  
GCAGCTGTCTTTGAAAAGGAGAAC

>RXN01114-downstream  
TAAAAATGGCTATTTTGCACAGC

>RXN01139-upstream  
ACCACCGTGGCAGGCTTTTTTCAGTGGCAAGAAGATTAATTCTCCACCCCTTCATTTTCAA  
TAAGCTTTCAATAAGGGGAGAAGTGTGCTTAGCTGGGGTC

>RXN01139  
ATGGAAAGCCACGATCTTCAGCAGCGCAGTTATGCGCACAAATCCCGATGGCCACGACCAC  
AGCCATGACGGACTCGGACACTCACATGCTCCCAGCTCCCTCAAGGCTCTTTTTGCGGTC  
ATCATTTTACCTCGATCATCTTCTAGCGGAACATAATCGCCGGCCTTATTTCCGGATCT  
TTGGCACTGCTGGCTGACGCCATGCACATGCTGTCCGACTCCACTGGCTTGATCATTGCG  
GCTGTGCGCATGCTCATTGGCCGTCGGGCACGCACTTCTCGTGCGACCTACGGATACAAG  
CGTGCGGAAGTCTTGGCAGCGATGGTTAACGCCACCGTTGTTACAGCACTGTCTGTGTGG  
ATCGTCGTTGAGGCCATCATGCGTCTGGGCAAGGACCTGGAAATCCAGACCAACCTGATG  
CTCATCGTCGCGGTCAATTGGTTTTGTACCAACGGAATTTCCGCCCTGGTGTGATGCGC  
CACCAAGATGGCAATATCAATATGCGTGGAGCATTCCTTCACGTTCTCAGTGACATGCTG  
GGTTCGTTGCCGTCATTATTGCGGGCCTGGTGATTGCTACACGGGATGGATGCCGGCC  
GATACCATTGCTTCGATTGCGATTGCTGCGATTATTATTCCTCGCGCATTCAGCCTCCTG  
AAGGAAGCTCTCAATATCTTGTGGAGCGTGTTCCTACAGGTGCGGAGCCTGCAGAGGTC  
GACGCAGCCCTTCGTAAAGTCCCAGGTGTGAGCGATGTGCATGATCTTCACATTTGGAGC  
ATTGACGGCAAGGAAATCCTGGCCACGGTGCAATTGTTGGTGGTGGATTGCTCTACAAATCAG  
CTGCATAGTTGTGGCGTGTGGATCGGGCAGAAAGCGGAACATCCAAACTTGGGATCTTG  
CACTCAACAATTCAGCTGGAAAGCGCAGATCACAGTGATCATGAAAGTGTGTGC

>RXN01139-downstream  
TGATATAGAGTATGTCCCATGGG

>RXN01141-upstream  
AAAGAACACTCGGTATGGCACCTGATTTAAGGATGCTGCAATCGTGACACATATCCTCTT  
CGACAGCAGGCGTTTTCTGCAACTGGGCGCTTTTGGCTCC

>RXN01141  
TTGAGCACCGCATTGGCCGGAGCGGCCCCGCTACGTGACGTCGACAAGCAATAATGAACCT  
GCGGATAACACTCCCCTGACCATTGGCTACGTGCCTATTGCGGGCTCGGCGCCGATTGCT  
ATCGCAGATGCGCTAGGGCTGTTTAAGAAACACGGCGTGAATGTCACGTTGAAGAAGTAC  
TCAGGCTGGTCCGACCTGTGGACCGCTATGCAACAGAGCAGCTTGATGTTGCGCACATG  
CTGTCGCGCATGACTGTGGCGATTAAATGCTGGAGTGACCAACGCGTCGCGCCCGACGGAG  
CTGTCGTTTACCCAGAACACCAATGGGCAAGCAATTACCTTGGCGTCAAAGCACTATGGT  
TCCGTCAAATTCAGCGGCGGATCTTAAAGGCATGGTGCTGGGAATTCCTTTTGAATATTCA  
GTCCATGCGCTGCTCCTGCGCGATTATCTCGTCTCAAACGCAGTTGATCCCATCGCCGAT  
CTTGAGCTTCGCTGCTCCGACCTGCCGATATGGTCGCACAATTGACAGTTGAGGGCATC  
GATGGATTCAATTGGGCCCTGGGCGTTTAAATGAACGCGCCATCAGCAATGGCTCCGGCCGG  
ATTTGGCTGCTGACCAAACAACACTGTGGGACAAACATCCATGCTGCGCCGTGGCGATGGCC  
AAAGAGTGGAAAGCTGAACACCCACGGCGGCTCAGGGTGTGCTTAATGCGCTGGAGGAA  
GCCTCCGCAATTTTGAAGCAATCCGGCACAATTTGATTCTCGGCACGCACGCTGTGCGAG  
GAAAAATACCTCAACCAGCCTGCCACGTGCTGGATGGACCGTCG

>RXN01141-downstream  
TAATCATCGGCATCACCGGCTTA

>RXN01142-upstream  
ATCCCCATCCACCGGCACAGTCAGCGCAGGCAACGAAGAAATTAAAGGACCAGGACCTGA

CCGAGGCATGGTTTTTCCAAGACCACGCCCTCCTGCCCTGA

>RXN01142

TTGACCGCACGCGGCAACATCGACTTCGGGCTCCGCTCCGCGCGCCCCCTCCTTGAGCAAA  
ACCGAACGCGCCGACATCACCCGCACCCACCTCGAACAAGTAGGCCTCACCGACGCGGCC  
GAACGGCGCCCCGCCGCTCTCCGGCGGCATGCAACAGCGAGTCGGCATCGCACGCGCC  
TTCGCCATCGACCCACCAATCATGCTTCTCGACGAACCCCTCGGCGCCCTCGACGCCCTC  
ACCCGCCGCGAACTCCAGCTCCAATACTCAACATTTGGGAAGCCTCCCGCCGACCGTC  
GTCATGGTCACCCACGACGTCGACGAGGCCATCCTGCTCTCCGACCGAGTTCTCGTGATG  
TCCAAGAGCCCCGAAGCCACCATCATCACCGATATTCAGTGAATCTTCCCGCCCCAGA  
CACGAGCTGAGTGAAGACGCTTCTGTTGAAGCCGAGACCACAGCCCTGCGTAAGCGGATG  
CTGCATCTGCTGGAGCAC

>RXN01142-downstream

TAGTTTCTAACACGTCTTTTAA

>RXN01164-upstream

GCCGATCGTGATTGATGAAGACGAGATCCAAGCCTGGACTTCTGATCTCAAACCTGAAGA  
TTTACCAAAGGTAAAGATGAATCCGACGGTGAGAAATA

>RXN01164

GTGACACTGTTTGTTCGGCTCGCCCTTGCTGCTGTGGGCGGGCTTTTTGTCTTTGCTTCC  
AATGAACCGATCGGCTGGTTTGTTCGGGGAATTGTTGGCACTGCATTATTTTTTATCTCC  
CTTGCGCCGTGGGATCTGGGAGTTCCCCAAAAGCGGCGGAAGAAGAATGAGCCAGTCCCA  
TTTTTGCAACAGATGTCCACGGGCCCAACTGTTGTACAGGGCATGCTTTTAGGTTTTGTC  
CATGGCCTGGTGACATATTTGCAGCTGTTGCCGTGGATCGGTGAGTTTGTGGCTCACTG  
CCTTATGTCGCGTTGTGAGTTGTGAGGGCGCTTATTCATTGCTCTTGGTGCTTTCCGGC  
GTGCTCATTGCGCGTTGGAGGGACTGGAAGGTTCTCTGTTTCCGGCGATGTATGTGGCT  
GTGGAGTATCTAAGAAGCTCGTGGCCATTTGATGGATTTCGCGTGGGTTCGCCTGGCATGG  
GGTCAAATTAACGGTCCGTTGGCTAATCTCGCAGCGCTTGGTGGGGTAGCGTTTGTCACT  
TTTTCCACGGTGCTGGCTGCCGTGGGTGTGGCCATGGTGATTATTTCCAAGAAGCGACTG  
GCCGGCGCAATCATCACCGCGAGTGTGATTGCTATCGGCGCGGTGTCATCCCTGTACGTT  
GACCGCAATGGCACGAGCGATGAAAGCATCGAAGTAGCCGCAATTCAGGGCAATGTGCCT  
CGGATGGGATTGGACTTCAATGCACAGCGCCGCGCGGTGCTGGCGAATCACGCACGGGAA  
ACCCCTAAGCTGGATGAACAAGTGGATTTGGTGATCTGGCCGGAGAATTCCTCAGACGTC  
AACCCATTTTCCGATGCACAAGCAAGAGCCATTATCGATGGAGCAGTGGAACATGTTTCA  
GCACCTATTTTGGTGGGCACGATCACCGTCGATGAGGTTGGTCCACGCAACACCATGCAG  
GTATTTGATCCTGTTGAAGGTGCCGCGGAGTACCACAATAAGAAGTTCTTGACCGCGTTT  
GGTGAATACATGCCGTTTTCGCGAATTCCTGAGAATTTCTCGCCCTACGTTGATTCCGCT  
GGAACTTCCAGCCCGGTGATGGCACCGCGCTAGTGGAGATGAATGCTGCGAATTTAGGC  
CGCGCTGTGACAGTGGGCGTGATGACGTGTTACGAGGTCATCTTCGACCGTGCTGGCCGC  
GACGCCATCGCCAATGGGGCTGAATTTTGACCACGCCCACCAACAACGCCACCTTCGGA  
TTCACGGACATGACGTATCAGCAATTAGCAATGAGCAGGATGCGTGCCATCGAATTTGAT  
AGGGCGGTGGTTGTTGCAGCTACATCGGGTGTTCGGCTATCGTCAACCCTGATGGAAGC  
ATTTCCCAAAACACCCGAATTTTGGAGCCGCCACCTTGACGGAATCCATTCCACTCAAG  
GACACTGTCACCATCGCAGCGCGGGTGGTTTCTATGTTGAATTACTGTTGGTTATCATT  
GGTGTATTAGCTGGACTATTCGCCATTGCAATGAATAGCCGTTCAAAGTCTGCGAAAGGT  
TCCGCTCGGCCCGCAAGTTCCGGTTAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAAT  
CGTCGAAAAGTAAAA

>RXN01164-downstream

TAAAAACGTCCCGAAGGGACGAG

>RXN01168-upstream

CCGCACAAGTTCGGGTAAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAATCGTCGAAAAG  
TAAAATAAAAACGTCCCGAAGGGACGAGGAGGACAACACC

>RXN01168

ATGAGCAGTGAGGCAGTAGATGCTACGACGCTGGTGATTATTTCCAACGTACAACGAGCTG  
GAAAACCTTCCACTCATCGTGATCGCGTGCGCACCGCAACCCCTGACGTTACGTACTC  
ATCGTGGACGACAACAGCCAGACGGCACCGGCGAGCGCGCAGACAAGCTTGCTGCTGAC

GACGACCACATTTTTGTCTCCACCGCGAAGGCAAAGGCGGCCTGTGCGCAGAGTACATG  
GCTGGCTTCCAGTGGGGCCTGGAGCGCGACTACCAGGTCTGTGCGAAATGGACGCCGAC  
GGCTCCACGCACCAGAACAGCTGCACCTGCTGCTCGCTGAGATCACCAATGGCGCTGAC  
CTGGTCATCGGCTCGCGCTACGTGCCAGGCGGCCGCTAGTCAACTGGCCCAAGAACCCT  
TGGCTCTTGTCCAAGGGCGGCAACGTCTACATCAGCGTCGCGCTCGGCGCCGGCTTGACC  
GATATGACCGCAGGGTACCGCGCTTTTCGACGTGAAGTGCTAGAAGCACTGCCGCTTGAT  
GAGCTCTCCAACGCTGGGTACATTTTCCAAGTTGAGATTGCCCTACCGTGCAGTTGAAGCC  
GGATTGATGTTTCGTGAAGTTCCCATCACTTTCACCGAGCGTGAGATCGGCGAATCCAAG  
CTGGACGGCAGCTTTGTCAAGGATTCCCTGCTCGAGGTAACCAAGTGGGGCCTCAAGCAC  
CGCGGTGGCCAGGCCAAGGAACTGTCCAAGGAAATGGTCGCGCTGCTGAACTATGAGTGG  
AAGCACTTCAAAAAGCGCAACACCTGGCTC

>RXN01168-downstream  
TAAACTGCTTGCCGGTTAGTGAA

>RXN01191-upstream  
CGCTGCTTTACGCAACTGAAACCGCACCGGATCAAGTTATTTGGGGTTGTTCTTTGTGG  
CGTGTGGTGGCGCTCGCGGGGTTGGTAGGGCCCTGGGCG

>RXN01191  
GTGGGTGGACTCGTCGATAAGCTCCTTGCAACCCCGAGCATGCGCGACGTTGTAGTGTTT  
GCGCTGCTTATCGTGGCTGGCGGCGTTGTTTCGAGCCTGGGCACGTGGTGGGGCAGCGCG  
CTGATGGCGCGCGCTTGGAGCCGGCGATCGCGGGGCTGCGCGAGGATGTGTTGCGCGCG  
GCGGTGAGTTTGGATGCGAACACGATTGAAACGGCGGGGCGCGGCGACGTGATTTGCGGT  
ATCGCGGATGATTCGCGGGAGGTGTCCACTGCGGCGAGCACCGTGGTGCCGCTGATGGTG  
CAGGCGGGCTTTACCGTGGTGATTTCCGCGTTTGGCATGGCGGCGGTTGATTGGCGCCTC  
GGCCTTGTCGGTTTGGTTCGCGATCCCGCTGTATTGGACCACGTTGCGCGTCTATTTACCC  
CGCTCAGTCCGCTTTATACGCGTGAGCGCGAGGCCTTTGGGGTGCGCACGCAGCGGCTT  
GTGGCGCAGTCGAAGGCGCGGAAACCTTGCGCGCTTTCCGCGCAGAAGATACAGAATTA  
AAGCGTATCGACGCAGCCTCCGGCGAAGCCCGCGACATTTCCATTTCTGTTTTTCAGGTTT  
CTCACATGGGCATTTTCCCGCAACAACCGCGCGGAATGCATCACCTCGTGCTCATCTTG  
GGCACC GGCTTTTACCTGGTCAACATCGATCTGGTCACCGTCGGCGCAGTCTCAACCGCC  
GCACTGATCTTCCACCGACTCTTCGGTCCAATCGGCACGCTCGTGGGCATGTTCTCCGAC  
ATCCAATCCGCCAGCGCATCGCTGATCCGCATGGTGGGCGTTATTAACGCGGCATCGAAC  
CAGGTCAGCGGCACCTCGCCGGCGTCTGCCAGCACCGCTTTAACGCTTTTCGACGTCTCC  
CACCCTATCACACTGCACCGCTCATCAAGAATGCATCCGTGCAGCTGGAACCGGGGAA  
CACATCGCCATTGTGGGTGCGACCGGCGCTGGTAAAAGCACGCTCGCCCTCATTGCGGCA  
GGCCTGCTCAGCCCAACTTCCGGGCGAGGTGGCTCTCGGCGGATCGAGTTTTTCTAACGTC  
GAACCGGAAGCATTGCGCCAGAAGATCGCGATGGTCAGCCAAGAAATCCACTGCTTCCGA  
GGATCTGTTTTAGATAATCTTCGTATCGCACGCCCCGAAGCCACCGATGCGGACATCCAC  
GCCGTTCTCGCCGATATTGGTGATTCTTGGTGGAGCGCTTACCAGCAAGGCATAGACACC  
ATCGTGGGTGATGGCGCTTTCCGTTTAACTCTGTGGAAAACAGATCATGGCGCTTGCT  
CGCGTACATTTGGCCGACCTAGCAATCGTCATCCTTGATGAAGCAACGGCTGAATCAGGC  
TCTGATCATGAAAACAGCTTGAAGATGCAGCCCTTAAAGTCACTGAAAACAGATCAGCC  
ATCATCGTGGCTCACCGCTCAACCAAGCGAAAACCGCCGATCGCATCATCGTCATGGAC  
TCCGGAGAAATCATAGAATCTGGAACCCATGAAGAGCTTCGAGCGATCGGCGGCCGATAT  
GAACAACGTGGACTGCGTGGTCTGCGCGC

>RXN01191-downstream  
TAATTAGCCACCCAAGACCACGC

>RXN01212-upstream  
TTTAGAAGCCACATGACATATGTCATGAAAATTATGTGCAAAGTGCAGTAATACTCCTGA  
CATATGGCTCTACCAGCGCCAATGCGAAGTAGGAAGAATT

>RXN01212  
ATGCCTATGACAACGACACCAGCAATCGACGTAACAGACCTCGTGAGAACCTACGGCGAC  
TACACCGCAGTCAAGGGCCTGAATTTCATGTACAGCGCGGTGAAGTATTTGGTCTGCTC  
GGCACCACGGGGCCGGCAAAACCTCCACCTTGAAGTCATCGAAGGACTTTCCGCACCC  
AGCTCCGGCACCGTGCGCATCTCCGGGCTTGACCCCGTTGCCGACCGCGCGATCCTGCGC

CCCGAGCTCGGCATCATGCTGCAATCAGGCGGCCTGCCATCACAGCTCACCGTCGCCGAA  
 ACCATGGACATGTGGCACGGCACCTGCACGTATCCGCGCGCCATTAAAGATGTGCTTGCC  
 GACGTCGACCTCCTACACCGCGAAAACGTCAAGGTCGGCGCGCTTCCGGAGGCGAACA  
 CGACGCCTTGATTTGGCCTGCGCACTGCTTGGCGACCCCTCAATTTTGTTCCTCGACGAA  
 CCCACCACCGGCCTCGACCCAGAATCTAGGCGCCACACCTGGCAACTCCTGCTGGACCTG  
 AAACAGCGCGGCGTCACCATGATGCTGACCACCCACTACCTGGAGGAAGCCGAATTCCTC  
 TGCGACCGGATTGCCATCATGAACGCCGGTGAGATCGCAGTGGAAGGCACCTTGATGAA  
 CTGGTGGCCCGGAGAAGTCGATCATCAGTTTCGTGCTGCGTGGCGGGCAGGTGGAGTTG  
 CCGGTCTTGAGTGGGGCTGAAATCATCCGCGACAACAACCACGTCCGCATCGCCACCACC  
 ACCCTGCAGCAGCACACCTTAGAAATACTTACCTGGGCTGCAGAGACCGGGATCGCGCTG  
 GAAGGCTTCGCTGCAAACCCGCCACCTTGAATCCGTATTTCATGGACATCGCCTCACTC  
 GAGAACACCTCGCTGCAAACCGCC

>RXN01212-downstream  
 TAGAATCTTTAAGGAGACCACAA

>RXN01285  
 CTCAACGTCACCATCCCCGACAACACCTTCACCGCCATCATCGGCCCCAACGGCTGCGGC  
 AAATCCACCCTGCTCCGCGGTTTCTCCCGCGTGCTCAATCCGCAGCACGGCAAAGTGCTT  
 CTCGACGGTCGGCAACTCGATTTCATTCAAGCCTAAAGAGATCGCCCCGAGAACTAGGCCTG  
 CTGCCACAGACCTCCATCGCCCCAGAAGGCATCCGGGTTTACGATCTCATCGCGCGCGGG  
 CGCGTCCCCTACCAAAGCCTCATACAACAATGGCGCACCTCCGACGAAGACGCCGTGCGG  
 CAAGCGCTCGCCTCCACGAATCTCACCGAACCTGCGAGCTCGCCTCGTCGATGAACTCTCC  
 GGTGGCCAGCGCCAACGAGTGTGGGTGGCCATGTTGCTCGCCCAGCAAACACCGATCATG  
 CTTCTCGACGAGCCCACCACCTTCCTCGACATCGCCACCAATACGAACTCTTGGAATTG  
 CTGCGCGCATTCAACGAGGCCGGGAAAACCTGTGGTCACTGTGCTTCACGATCTCAACCAA  
 GCCGCCCGCTACGCCGACCACCTCATCGTGATGAAAGATGGGCACGTACATGCCACGGGC  
 ACACCGGAGGAAGTCTTAAGTCCCGAGATGGTTCAAGGAGTTTTTGGCCTGCCCTGCATC  
 ATCTCCCCAGACCCCGTCACAGGAACCCCCACCGTCGTTCCCCTCAGTCGGTCTCGCGCA  
 GGAGCT

>RXN01285-downstream  
 TAAGTAGCTACCCCTCCAACGGA

>RXN01298-upstream  
 CTTAAACGTCACCTTATTTATGCATTATGTTGGTTTTAGACTCGAACAATTCAATTAGAA  
 AACACTAATCGGACATTTAGGTACATAACATTTCCGCTC

>RXN01298  
 GTGTCCACATTAATTTCTGAACCCGAGGTGGATAAGCTACGTAAACGTGCCAAGAGATCA  
 AGGCGGACAGAATGGTGGCTTGCCGCCGCACTTCTTGCCCCAACTTGCTTCTCTTGCC  
 ATCTTTACGTATCGGCCACTGTTAGATAACTTCCGGTTGTCCTTTTTCAACTGGAACATT  
 TCCTCGCCACATCAACCTTCATTGGGTGTTGATAACTACGTTGAGTTCTTCACTCGTAGT  
 GACACTCTCCAAGTTGTTTTAAACACCGTCATCTTCACGGCATGTGCTGTGATCGGATCG  
 ATGGTGCTCGGTTTGCTCCTGGCCATGTTGTTGGATCAGAAGCTTTTCGGCCGTAACCTT  
 GTGCGTTCCATGGTGTGTTGCCCCGTTTGTTGATTTCGGGTGCTGCCATTGGTGTGTTTC  
 CAGTTCGTTTTTGACCCTAATTTTGTTGTTGTTTCAGGACTTGCTGGGACGCATCGGCGTT  
 GATTGCCACAGTTCTACCAAAAACCTAACTGGGCATTGTTTCATGGTGACGTTCACTTTC  
 GTGTGGAAGAACTTGGGCTACTCCTTTGTTATCTACCTGGCTGCATTGCAGGGGCTAAAC  
 AAGGATTTGTCTGAGGCCGACCGGTGGATGGCGCGAGCGGTGGACACGTTTTTGGAAG  
 GTTACTCTTCCGCAGCTTCGCCCCAACACGTTCTTCCTTTCTATTACTGTCACGCTGAAC  
 TCGGTTACAGGTCTTCGACATCATTCACACCATGACTCGTGGTGGCCCCCTTGGGTAACGGT  
 ACGACCACCTTGGTTTACCAGGTGTACACCGAGACTTTCACCAACTATCGCGCGGGATAT  
 GGTGCAACAATCGCAACGATTTTGTTCCGTGTTGCTGCTGATTATCACTGTTATCCAGGTT  
 CGATACATGGATAAGGAGAACAAGCAGAAA

>RXN01298-downstream  
 TGATCTCGACTGATAGAAACGTT

>RXN01338

AAAACCTTATACCCCAAATCCCTGGATGTTATTCATCCGCTCATTGATGGCATCATCACT  
 GTCGCAGCCCTTGTGGCATCGCAATACATCTCATTATGCTGGCTCTAGATCTAGAT  
 GGCCTTGCTAAAAACTGGCCTTAATAGCCATCGTTATCGTAGGTGGCATTCCGTTGATG  
 TGGGATGTGCTGAAATCAGCCATTAAACTCGCGGTGGCGCGGATACTTTAGCAGCAGTC  
 TCCATCATTACTTCTGTGTTGTTAGGGGAGTGGTTGGTTGCCGCGATCATCGTGCTCATG  
 CTCTCTGGTGGTGAAGCGCTAGAAGAGGCGAGCATCACGGCGAGCCAGTGGCACCTTGGAC  
 GCACTTGCCCGGCGCGCACCAAGTACAGCTCACCGCCTGTTGGGTGCAACCATTCTTGAT  
 GGAACCGAAGAGATCGCCGTGGAAGAGATCACGGTTGGTGATTTAGTGGCGGTGCTCCCG  
 CATGAACTTTGTCCCGTGGATGGTGAAATCGTGGCAGGCCACGGCACCATGGATGAGTCT  
 TATCTCACGGGTGAGCCCTATGTGGTGAGTAAATCTAAAGGTTGCAAGCAATGTCGGGT  
 GCAGTCAATGGTGATACTCCGCTGACGATTGTTGCCACAAAGCTTGCCCATGATTCCAGA  
 TACGCCCCAAATTGTTGGTGTACTCCATGAAGCAGAAAAACAACCGCCCAGAAATGCGCAGG  
 ATGGCTGACCGTCTTGGCGCGTGGTATACGGTGATTGCACTGCCCTCGGTGGTCTTGGC  
 TGGATTGTCTCCGGCGACCCAGTGAGGTTCTTGGCTGTTGTCGTTGTCGCCACCCCATGT  
 CCATTGCTCATTGCGAGTGCCAGTGCGGATCATCGGTGCGATTCTCTTGCGGCTCGTCGG  
 GGCATCATCGTGAAGAACCCTGGAATGCTGGAACACGCTTCAGGAGTAAAGACAGTGATG  
 TTCGATAAGACTGGAACGCTCACCTATGGCAGGCCAGTGATTACTGATATCCACACTGCT  
 CCCGGAGTTGAGGAAGATACAGTCTTAGCTTTGGCTGCTTCAGTAGAGCGCTACTCCAGA  
 CACCCGTTGGCTGACGCGATTCTGTGAGGGCGCAAAAGCCAGGGAACCTCATCTGCCTGAT  
 GTAGTGAAGTATCGGAACGTCCAGGACAGGGACTAACCGGCACGGTGGGCGAGCACCTG  
 GTTCGAATAACCAATAGGCGCAGCACACTAGAAATTGATCCAGACAGCAAGAACTACATT  
 CCGGTGACAAGTTCCGGCATGGAATCTGTGGTGCTTGTGATGATAAATATGCAGCACTC  
 ATTCGCTCCCGGATGAACCTCGTGATCTGCCAGTGAGTTTCATCGCGCACTTGCCCAAG  
 AAGCACAAAGTGGACAAGCTCATGATTATCTCTGGTGATCGCGCATCTGAGGTTCTGTTAC  
 CTTGCGGACAAGGTTGGCATTGATGAGGTACACGCAGAGGCCTCACCGGAAGACAAGCTG  
 AACATTGTTAATCGGCATAATGAGCACGGCGCCACCATGTTCTTAGGTGATGGAATCAAC  
 GATGCGCCAGCCATGGCCGTTGCCACCGTTGGTGTCGCGATGGGAGCAGACTCCGATGTC  
 ACGTCCGAAGCAGCAGATGCTGTGATTTTGGATTCTTCCCTGGAACGTCTCGACGATCTG  
 CTCCACATCAGTGACGGATGCGTCGAATAGCGTTGCAATCTGCGGGCGGTGGCATGGCG  
 TTGAGTGTCATAGGAATGATCCTCGCGGTATTGGATTCTTGACGCCACTGATGGGTGCG  
 ATCTTCCAAGAGGTCATTGACGTGCTGGCTATCCTCAATTCCGCTCGGGTTCGCACTGCCA  
 CGCGGAGCGATTAGTGATTTTGATACGCAAGAAAAAGTTTCT

>RXN01338-downstream  
 TAGCAGGGTAACCTAAATGTCTG

>RXN01382-upstream  
 AAAGGATGTACCTCATGAGCACACGATTACTCGCCGCAATTTCTCTCCGAGCAACCGGAA  
 TCCTCGGTGTGCGAGCTGGCATCGGCGCAACACTTGCTGC

>RXN01382  
 ATGTGCACCAACAACACCGGCACCAGCGGATCCACCTCCACCGCAGCTGGCACCGGAACT  
 GCAAATGAAGAAGGCACCATCACCGCAGCCATCTCTACGAACTGGGAACCAACGGCTAC  
 GACCCAATGACCACACCTCGGCTCTCACTGTGGCAGCCAACCTGGCACACCCTTGAAGGC  
 CTCACCGAAATCGACCCAGCCACCGGCGAGGTCTACGCAGCACTCGCCAGCGCACTGCCT  
 TCAGCCGATGCGACCTCCCTAGACATCAAGCTTCGCGACGGCGCCACCTTCCACAACGGC  
 GACGCAGTCACCGCAGACGACGTAGTCTTCTCTTTTGGAGCGAGTCTCGATCCAGCCAAC  
 AACTCCCTTTACGCATCCTTCATCCCATTCATCAAGTCAGTCACCAAGAAGGATGACACC  
 ACCGTCACCATCGACCTCGACTACGCAACCGGCATCATCAGCGAACGCCTCGCAGTAGTA  
 AAGATCGTGCCAAAGTCCGTGCTGGAAGCAGACGCATCCGGATTGACGCCAACCCAATC  
 GGCTCCGGGCCATACAAGATGACCGACAACGGTGATCCAAGGTGGTCAAGTTGAGCGC  
 AACGACGACTACAACGGCCACGCCCAGCACGTGCCGCCAAGATGGAATGGCAGATCATC  
 CCCGACGCTCCACCCGACCACTCCCTTCAGTCCGGCAGCACCATGGCCATCGACTCC  
 GTTCCATACCTGTGATCCACAGCTTGAAGCCACCAGCACCGTAGAATCCGTCCAAGGA  
 TTCGGCTCCTGTTGCGCATGTTCACTGCTCCGAAGGCAACCCCTTCAACGACGTCCGC  
 AACCGCCAGGCATTCTCTACGCACTGGACATGGACAAGATCGTTAAGACCGGCATGTCC  
 GACCAGGCAACCCAGCCACCTCCTTCGTGCAGAAGGAACACCCCAACTACAACCAGGCA  
 TCCACGGTCTACTCCCTCGACGCCGACAAAGCCAAGGCGCTGTTGCTGAAACCGGCCTT  
 ACCAGCCTCAACCTCCTGTGCACCGACACGACTGGGTCAAGAACTGCACCCCACTGATC  
 CAGGAATCCCTC

>RXN01411-upstream  
CTTATCGACGTCCCCATCCCCCTCGCCAATGCTTCGGCGAGGGGTTCTATTTATTGTGTG  
TGCTAGCCTTTTCGCAATCGTTCAGCCCGCCCCGACGTCA

>RXN01411  
ATGTTGGGAGTGGGCTGGCGCATTCCATTCTGATGGCCGTGCCACTAGGGCTTATCGGC  
TGGTGGATCCGCACCGGTGCCAGGAAATGTACGCCCCGCATCCGAACGCCCGAAGCT  
CCTATTAAGCAGGCATTGCGTACTGAGTGAAGATGATGTTGCGGGTAGGTGGCTTTATC  
TCTTGACCCGGTCTGAGCTTCTACATTTTACCACGTACATGACCACTTTCCTGCGCAGC  
ACCGTCGGACTGGAGGGCACGTTAGTGCTGGCTGGAAACATCATCGCTCTCAGCATGGCA  
GCAATTGTGGCCCCATTTGTTGGCCGCGCAATTGATAAATTCGCCCGCCGAACATCATG  
GCTTTCGCTACCTTAAGCACAGTAATTATGGCGATCCCGGCCCTACATCATTGCAGGTCAA  
GGTACTTTGACTGCTTCTTTGATTGCGCAGGTAATGCTTGGAATCGGCGCGGTTACCGCT  
AAGTGGCTTACCTCAGTAATGATGGCCGAGGCTTCCAGAGGTACCCGCGGTAATCC  
GCCGGCATTACCTACAACGTCACTTACGCAATCTTCGGCGGCTCGGCTCCATTTATCTCC  
ACCGCATTGGTCTCCTGGACCGGCAGCCCGCTGGCCCCCTGCGGTATACATGATCATCATT  
GCGCTCTTCGCCTTACCGCGTCCCGCTTCATTCTGAAACCTCCCCAGTTTTTGTCAAC  
GCAACCCCGGCCATTAAAGCACCAAGGTGCTGGTCAACCCGGGT

>RXN01411-downstream  
TAAACCACGCTTTTCGACGAAAA

>RXN01421-upstream  
TTGATGCACGTGCAGAAATCGTCGGCGGTCCGTGGCACCCTCTGTTAAGGGAGACTCGG  
TTACTGCAGGGATCCTGCGAGATCGAGTAAACGCCTAAAG

>RXN01421  
ATGACGTCGAAAAGCATTAGCGGCAAGCGCCCGAATCTGCCGTGCGTCACTGGAGCGCGG  
TGGCTCGCGGCGCTCGCTGTTTATTTTTCATGCGTTGGTGTTTTGTGCGGTGATCCG  
TTCCAGCAGTCGGAACGTTTGGCACAATCCATAAATTTGTCCCATGCAGCTGGGTTC  
GCTGGTGTAACTTCTTCTTTATCTTGTCCGGATTTTGTATCTATTGGTCAAATAGCCAG  
CTCAAGGGCATGAAGAATGTGCTGTATTACTGCAAGCGCCGCATCACCAGATTTATCCC  
ATGCACTTGATTGCGTTGCCGATGTTTATTGAGGCGTCGGCGAAGTTCACGACTACAGGC  
ATTACCTGGGTGCTGATTTTGCAGGAG

>RXN01421-downstream  
TAAAGCTGTGGCTGCGGAATGCG

>RXN01602-upstream  
TGCAGGCCACATGCCTCCCAGTGCCGTCTCTGCACGTTGATTTTCCCCTGCCACGACTGG  
TCGAGGGCGACTTTCTAGCACTTTTAAAGGAATTTTTTA

>RXN01602  
ATGGCTAAAACCCATATTTCGGTTACAGGACCTTTCCCTGTCATACACCTCAACCCCGTTA  
ATTACGAAGCTCAATATCACTGTTTCTTCTGGACAGTGCGCAGTGATTGTTGGTGAGAAT  
GGTCGAGGTAAAACCACACTTCTGCGAGCACTGGCTCGAGAATTCCCGCCATCTGCAGGT  
GAGATTCTCACTCATGGCACGGTAGCAATTGCTCATCAACACATGCCTGCAGGTGATCTG  
TCCGTGCGAGAGATCTGTGATGAGGCAATTCGTGATTCAAAGAATGCTCTCGAAGAGCTT  
GAGAGAGCTGGAGCTCTACTTGAGACAAACACTGCGCACGCACTTGATGGATATCAACAA  
GCCCTTGATGCCGCTGAAGTGCTTGACGCATGGAACGCTGAACATCGATTAGAAAAAGCT  
CTGCGCAGCTTTGGCGCGATCACCGATAGATCCCGTGCACTCAGTGAGCTATCGATCGGG  
CAAAGGTATCGGGTACGGCTGGCCTGCCTCATCGGTGGCGATGCTGATATTTGCTTCTC  
GATGACAAACCAATCATCTTGACCGGGGCGCGCTTAAGTATCTCACCAGGACCAATACC  
TCCCAAAAGGTGTGGTACTTGTGTTTCTCATGATCAAGCACTGATCAAAAGATGTCGCG  
GATTTTCATCATCGATATTGATTCAACCCAGACGGCCTACCACGGATCTATCATGAGGGT  
TTTGATTCTTATCGACGCCAAAGGAGTGCGCTTCTTGAAACTTGAGGCGAGGATTATGCC  
GCTGCACAAACTGTGCAACAGCAATTGCAGGAGGATCTAGAGCACGCACGCCAGCGGGTG  
AATTCTTCGTGGAAACCTCCAAAAGGAACGGGAAAACACACTCGCGCATCTCGGGCTCCC  
GGAGTGGTGCAGGCCCTTAAAGCGAGCACAGGATGCGTTGGATAGCAAAGCGTTGGACGTT  
CCCCGGGCTCCGGCCCCATTGCTTCTGCCTACCTTGAAAGTGCGACCAGATAAACCCATG

GTGGACTTTTCGGACCTTTTTGTACCCACCGCTTGCGTCTGCCAGGCTCACATTACAGTG  
GTATCAGGTGACAAAATAGTGATCACTGGTGACAACGGCGCTGGCAAATCAACGCTCATC  
GAAGTCTTGTCTGGGGTTTTGACTCCGGCAAGTGGTTCGGTTGCAAACCATGCCCCAAT  
GGGGTTCTCGGCCAAGAATCACTTGTGGCGAGGTGCCATCAATAGCACGAGATCACGCA  
GTTAAGTGGGGACTTTTAAAGTGTGAGGAGAGCCGATTGCCCCACAGGAATTCTCAATT  
GGTCAACGCAGAAGACTAGATTGCGCATGTCTAGCTGGCAATCCTGAACGTGTGCTT  
CTCGATGAACCTTCGAACCATCTGTCTATGCACTTGGTTTCCGCACTTACAGAGTGGCTG  
GACACGACCGCGGCTGCAGTGATCATGGTAACGCATGATCGACAGCTACTCCGCGATACG  
GCTCATTGGAGGCACATCGAGTTGAAATCT

>RXN01602-downstream  
TAAGAATTCGCAAGGGCTTTCAC

>RXN01604-upstream  
CTCTCATGTTGTTGTCCTTAGTTGACAGCGGGGTGGTGGTGGTCTAAAATAGCCTAC  
GATAACTGATAGTGTTCCTCCACTTACGGAAGAAGATAC

>RXN01604  
ATGAATACCCCTCTTTTGAGAAGCTCTGGGCTCTCCATCCGCGACACACCCTTCGCCGAT  
GTTGAGATAGCTCCAGACAGCGGACTCACTTTGCTGAGCACCGGGCGCGAATCCCAATCC  
AGTTCCTTTTCTTTGGTACTTTCCGGCCGATGCGCGCTCCACCGGAACCATCGAATTA  
AACGGCGAACCCATCAAGGCAACCAAGCTGGCCAAGCATGTGGCTTTGGCGGGCATCCCT  
GAAATCGATCTACTCGAGCGACTTGTCACTGTGCGCACCGTTGTCCGTGAACAACCTCGCC  
TGGTCAAGCCCTTGGTACCTGATGGTGCCAGGGATATTAGTGATTCCGGACGGTGGGT  
GACGTCGAAAAGCATCTTGGCCTGAACCTGAACCTAAAACCTTAATCGGCGACCTCAGC  
GTGCTCGAGCGTTTTTAAGCTGCGCATCGCGCTGGCGCTGCTGGCGCGGCCAGAGGCGCAA  
CTGTTGGTCTGGATGATCCCGATCAAGTGCGCAGCATGGAATTGCGTGCGGAGGTGTTG  
CACGCATTGAAAGGCGTTGCAGAGGATCTCCCTGTGGTCTGGTATCCACCAACCCAGAT  
TTTGATTCCCTTGGCCGATACCGCTTTGACCATTACGGGGGGCTGGAAAC

>RXN01604-downstream  
TAATGGCATTTTTTACACTTTGGC

>RXN01722-upstream  
CTCATTCCTCGCTAAAAGCTGCATAAAGTTTCGACGTTTTCAAAGTTGATTGCTTGCA  
CTGTCGTTGCGTGTGCGATGCCCCGGCTATTGTTGATTGC

>RXN01722  
ATGCTCAGCAGCATGCAGGACGTCCCACTGTCAATTAACCAGAATCCTCGAGTACGGGTCC  
ACTGTTACGGTGATACTTTGATCAACACGTGGGGCGGTGCCGATGGCATTGAACAAGCA  
CAGCAAACCTTTTAGTGCTGTGGGGGCTAGAGCTGCGGCTTTGGCTCATGCGCTGCATGAT  
TCTTTAGGTATTACTGGGGATCAGCGAGTGGCGTCGATGCTCTATAACTGCGCGGAACAC  
ATGGAAACTATGTTTGCAGTCGCATGCATGGGTGCCGTGTTTAATCCGCTGAACAAGCAG  
TTGATGAATGATCAGATTGTGTTCAATCTCAATCACTCTGAAGCTGAAGTGGTTATCGCT  
GATCCGCGCATGGCTGAACAATTGGGTGAGATCTTAAAAGAAACACCAAAGTTCGTGCC  
GTGGTGTTTATTGGACCGAATGATTTCTCTAGCGCGGCGGCCACATGCCGGAGGGAATG  
AAGCTGTATTTCCTATGAAGCGCTCCTTGACGGCCGTTCCACTGTTTACAACCTGGCCCGAG  
CAGGATGAACGCACTGCTGCTGCAATTTGCTATTCCACCGGTACATCGGGACCGCGAAG  
GGTGTGGTGTATTCCACCGCTCGCTTTATTTACAGTCGTTGAGCTTGCGCACCAACGGAT  
TCCCTCGCAGTGGAACACGGCGAAACGTTCCCTGTGCTGTGTGCCGATTTACCACGTCTC  
AGCTGGGGCGTGCCGATCGCAGCGTTTATGTCCGGCACTCCCTGGTGCTTCTGGACCG  
GATCTTTCTGCGCCGACATTGGCAAAGATCATTTCCACACGCTGCCTCGCGTGGCGCAT  
GGCGTGCCCTACTCTCTGGATTGAGCTGATGGTTCACTACCTGAAAAATCCCCAGAGCGT  
ATGTCTCTGCGTGAGCTATACGTGGGCGGTTCTGCGGTGCCTCCAATCGTGATCACCATG  
TGGGAGCAGCGCTATGGCGTGATGTTGTCCACGTGTGGGGTATGACGGAAACCTCCACC  
GTGGGTACTGTGTCTCGCCACCATCAGGTGTTTCTGGTGAAAGCCGGTGGAATTATCGA  
GTCTCCAGGGCCGATTCCCCGCTCCCTGCAGTACCGCATTTGTCAACGACGGCCAGGTC  
ATGGCGTCCACCGACCGCAACGAGGGCGAGATTCAGGTCCGCGGTCCGTGGGTGACTGCA  
AGTTACTTCCACCCCGATGTGGAAAAAGAAGGTGGCACCGCCTCAACATTCCGCGACCAT  
GACGTTGAAGAGGAAAACGATGAGCTCTTACCAGCGACGGCTGGCTGCGCACCGGGGAC  
GTTGGATCTGTACCAGCGATGGATTCTCACCATCCAAGACCGCGCCCGCATGTCATC

CGTTCTGGCGGCGAGTGGATTTACTCCGCTCAGCTGGAAAACCTCATCGTGGCTACGGAA  
GAGGTTGTGCAATGCGCCGTCATTGGCTTCCCCGATGACAAGTGGGTGGAACGTCCCCTC  
GCAGTCACCATGCTCTACCCCGGCATTGAACGCACCCGGGAAACCGCCGAGCGCCTCCGC  
GATCAACTTCGCGACCGCCTACCCAAGTGGATGCTGCCAGAATATTGGACATTTGTTGAT  
GAGGTGGATAAAACCTCCGTCGGTAAATATGACAAGAAGGACCTCCGCAACCACCTGCGC  
AACGGCGATTTGCAAGTAATTAAGCTTAAAGGGCCAGGTGAAAAA

>RXN01722-downstream  
TAACTTCCCTATTTATTCCGGCT

>RXN01732-upstream  
GATTCTATCGCTGATCTCCCTCTCCTTGCCCTGGGTTTGTTCCTCCGGGTCTCCTCTTCTTAA  
CTTTCTTGCTCATGTGCTGAAAGGTTTTTAAAGATCTC

>RXN01732  
ATGTTCAAGCTCTCTAAGCCATCCAAGTCCATGCGTGTTGCTGTTTCTACGCTTGCGATC  
TCTACCCTTGCTCTAGTTGGTTGTTCTCTTCCGATGAGTCTTCTTCTCATCATCTGCG  
TCTTCTTCTTCGGATGCTGCAAGCCAGTGGCCTGAGTCCATTACTTTGTCTCTTGTTCCT  
TCTACTGAGGGTGAGGATTTGGCTGAAGCGTTGGCTCCTTTGACTGATTACCTGTCTGAG  
AACCTTGGTATTGAGGTCAATGGTGTGGTGGCGTCTGATTACGCTGCAACCGTTGAGGCT  
TTGGGTGCTGATCAGGCTCAGGTGATCATCACTGATGCGGGTCCCTGTATAACGCGATT  
GAGCAGTACGATGCGCAGCTGATTCTGCGTGATGTGCGTTTCGGTGCCACCTCGTACTCT  
GCTGTGGCGTACACCAACAATCCTGATAAGTACTGCGACGATGCCCCAGTGGCTGCGTCT  
TATGCTGCGTCCGATGTAGACATGCTTTACTGCAACGGTATTGAAACTGAGGGCCAGGCT  
GCTACCGGTGAGGGCCCAGCAGCTCTTGATGCGCTGGAAAAGATCGAGTCCGGTGACAAG  
GTAGCGCTGCAGGCTGCAACCTCTCCTGCGGGTTACCAGTACCCTATCGTCGCTATGCAG  
GATCTGGGCATGGATACCGATTCCGCTTTTGTTCAGGTTCCAGTAGAGGGCAACAACAAC  
GCTGTGCTGTCTGTCTGAACGGTGACGCGGAAGTGTCCTTCGGTTTCTGGGATGCGCGT  
TCCACCGTGCTGTCTGAGGCTCCTAACGCAGCTGAGGATGTCGTAGCGTTTGCCTACACC  
GAGATGATCCCTAACGGTGGCGTCCGAGCGTCCAAGTCCCTTCCATCCGACCTGGTGGA  
AAGCTCACCGAGTTGATGGATGATTACGCAGATTCTCCGAGGAAGCCAAGGATGTCATG  
TTCGACATGGTTGGTCTATCTGACTGGACTGCTGATACCGCACAGGATGAAATCACTCGT  
TACGGCGAGATCCTGAAGAAGTTCTCCAAC

>RXN01732-downstream  
TAATTTCCCTGTTTCCAATACTC

>RXN01762-upstream  
TGGAGTGATGAATTTTCCTATAGAACGTTTTTTTAAACGATTGACTTTTTTAAACGTTTACG  
CTTTTAATGACTTCAAACGTGATCTAAAGCACAAAGGAGA

>RXN01762  
ATGAAAGTGAACCTCGGAATAGGAAGCTACCCACGACGCAGGGCAACTGTTTCGACCAGAG  
TCCACTGCAATCGAATTCGAAGGCACCAGCATCACCTACGGAGAATTCAGCAAACGAGTC  
AATCGGCTTGGACATGCTCTTCTAGACCTCGGCGTTGCGCACCAGATCGAGTAGCTTAT  
GTCGGATTCAACCACCTGCCCTGCTAGAAGTGTCTTTTCAACGAACCTCATTGGGGCA  
ACACCCGTGCTTGTAAACCCTCGCCTATCGGCAAACGAAATCGATTACATCAACAGAC  
AGCGGTGCGAGCATCGTGTTTTACGGAATCGACCTCATCGAGCACGCCACTTACCTCCAA  
GAACTCCATCCAGAGATCATCATGGTGGCCGTTGAAGGCGATGAGGGTCCAGGTTTGCCT  
CGAAAAGCGCTTATTGAAGCGGCGAGCGACGCCGACATCGACCTAGAAGTCAGCGATGAT  
GACCTGGTGCTGCTCATGTACACCTCCGGAACCACTGGCCGCCCAAAGGGCGCCATGTTA  
TCCCACCGAAACCTCTTCTTTAACTACTTCAATGCCCTGCTCAGCCAGGAAATTGAACAA  
GGCGCGGTACTTTTATCCACTGCGCCGTTATTCCACATCGCGGGCCTCAACATGACCACC  
ATCCCGGTGATGATGAAGGGCGGAAAGGTGATCATCCACCGCAATTCCGGGCAGAGCAC  
GTCTCGACGAAATCGAACGCTCCAAGGTATCCGAATCCTTCATGGTGCCAGCGATGATC  
GACATGTTGTCCAACCAACCATCATTTTGCCGAACGCGACCTTTCTTCCCTTCGCGCCATC  
ATGGTGGGCGGCTCTCCCTTAGCGAACGTGCGCTGCGAATCTGGCAAGGACGCGACGTA  
AAAATTGTCCAAGGCTTCGGCATGACAGAAACCGCACCGGGCGCCTGTATCTCGAGGCA  
ACAGACACAAGCACACCTTGAACCGCAGGTGAGCCCACTTCTTACCGACATCAAA  
CTAGTGGACCCGAAACCGGCGAAGAAGTCCCCACCGGAGAGGCCGCGAAGTTCTCATC  
CGCGGACCACATGTGATGACCGGATACTGGAACCGACCAGAAGACACCGCCAGCGCACTA



CAAAATGGCTGGTACCACTCCGGAGATATCGCCATCAAAGATGAAGACGGCTACTACACC  
ATCAAAGACCGCATCAAAGACATGTACATCTCCGGCGGCGAAAACATTTACCCCGCAGAA  
GTCGAACAAGCACTCCAGGAAGTGAAGCAGTCCTTGATGCCGAGTCATCGGAGTCCCC  
GATGAACGATGGGGCGAAACTGGCATCGCCTTTGTCTCCATCCGAGAAAGCTACCTGACC  
AACCACCAACCGGACCGGAAGTACGAGAACTACTAGGCAGTGTCTAGCCAGATACAAA  
CTTCCACGAGAAATCCACATCATCGAAGAACTCCCCCGCAACGCCACAGGCAAAATCCAA  
AAGAACATCTGCGAGACTTCACCATCCCCGTTTCA

>RXN01762-downstream  
TAAACCCCCAACGTCACCTTGA

>RXN01881-upstream  
ACCGGCCCTGCGGCCCTCAACCGCCGACCAGCGCGGCGCACACATTTTGAAGTGTTCATAA  
TAAAGACAAACTTAAGTATCGGAGTCGAAGAAAAACCACA

>RXN01881  
ATGGCCAATCTGATTAATCTCGAGAACGTCTCCAAAACCTGGGGATTAAAAACGCTTCTC  
GACGGTGTCTCCTTAGGTGTTCAAACCGGCGACCGCATTTGGCGTCGTCGGCCCTCAATGGT  
GGCGGAAAAACCACCCTGCTGGAAGTACTTACTGGCATCGAAAAGCCGGATCAGGGCCGT  
GTGTCTCACAACCTCTGACCTGCGCATGGCTGTGGTGACGCAGCGTGTGAAGTCAATGAT  
GACGACACCGTCTGCTGACGTGGTGTGGACCTTTGGGTTTGGAAAGTTTTCGAATGGGCA  
TCAAACGCCACGGTGCAGCAGCTCCTCGGTGGCTTGGGCATTGTTCGATCTTGGCCTTGAC  
ACCAAGGTGGGCAACCTTTTCCGGTGGGCGAAGCGCCGACGCACCAACCTGGCCGCGCG  
GCTGGTTCGCGACCT

>RXN01881-downstream  
TGACCTGATCGTGCTCGACGAGC

>RXN01936-upstream  
GCGCGGTGACACCACAGCCGTTGTGACGCGCGCTTGGTCTGTGGAGGATCGCCGAGGTTA  
CTAACAAATAGGCCCAACAAAGAGGTCTAAGCTCTACCTG

>RXN01936  
GTGAGTTTCCGAGATATTTTCGCTGACACCAGACCGCTGAAAGAACCGGCCTTCAAACGC  
CTCTGGCTTGGCAATGTTGCCACCGTCATTGGTGCCCAATTAAGTGTGTTGCCGTTCCG  
GTGACAGATTTACCAAATGACTGGGTCTCCGGCTATGTGGGCTTGACCGGGCTTTTTGGC  
CTTATTCCTTTGGTTATTTTTGGCCTTTATGGTGGATCCATTGCGGATGCTTTTGATAAA  
CGCATCGTGCTGATCTGCACCACGATCGGCATGTGTGTCACCACTGCCGGTTTTTGGGTG  
CTGACCATTTTAGGCAATGAGAATATTTGGCTCCTGTTAATAAACTTTTCTTTACAGCAG  
GCATTTTTCGCGGTGAATCAACCCACCGAACGCGCATCCTTCGAAGTATTTTGCCGATT  
GATCAATTAGCGTCGGCAACATCACTGAATATGCTGCTCATGCAGACCGGCGCAATCGTT  
GGCCCGCTGATCGCAGGTGCGTTGATTCCGCTGATCGGTTTCGGGTGGCTGTATTTCTT  
GATGTTGTCTCCATCATCCCCACACTGTGGGCTGTATGGTCACTGCCTTCGATCAAGCCA  
TCCGGCAAGGTGATGAAGGCTGGTTTCGCCAGTGTGGTGGATGGCCTGAAGTATTTGGCT  
GGCCAACCCGTGTTGTTGATGGTGTGCTGGATCTTATCGCCATGATTTTCGGCATG  
CCACGTGCGCTTTACCCCGAGATCGCAGAAGTGAAGTTCGGTGGGGGTGACGCCGGTGCA  
ACGATGCTGGCGTTCATGTACTCATCCATGGCTGTTGGCGCAGTTCTTGGCGGCGTGCTG  
TCTGGTTGGGTGGCCCGGATTAGCCGCCAGGGTGTGCAAGTTTATGGTGCATCATCGCC  
TGGGGCGCAGCCGTTGCTTTGGGTGGTGTGGCAATTGTTGTGACCCCGGCGCGGTGACT  
GCGTGGGCGTGGATGTTTCATCATCATGATGGTCATTGGTGGCATGGCTGACATGTTTACG  
TCGGCAGTTCGAAACGCTATTTTGCAGCAGTCTGCTGCGGAACATGTGCAGGGCCGAATC  
CAAGGTGTGTGGATCATCGTGGTGGGTGGACCTCGTTTAGCTGACGTCCTTACCGGT  
TGGGCCGCTGAGCCCCTCGGCGCAGGTGGACGGTATTATGGGGCGGAGTAGCGGTGGTT  
GTACTCACTGCAATTTGTATGGTGGCGGTGCCATAATTCTGGAATACGAGAAACCAAAA  
ATTACCGGCATC

>RXN01936-downstream  
TAAATACTTATCCATGCCCATTT

>RXN01946  
ATCCGCAAGTACTCCAGGCTCGAGGAACAATTCCAGTCGCTCGGCGGCTACGAAGCTGAC

GCGGAAGCAGCCAGATCTGCGACAACCTCGGCCTCGAGGCACGCATCCTCGACCAGCAG  
 CTTAAAACCTGTCCGGCGGCCAGCGCCGCGCGTTCGAGTTGGCGCAGATCCTCTTCGCC  
 GCCACCAACGGCTCCGGCAAATCAAAAACCACATTGCTTCTCGACGAGCCACCAACCAC  
 TTGGACGCAGACTCGATCACCTGGCTCCGTGACTTCCTGGCGAAGCACGAAGGTGGACTG  
 ATCATGATTTTCGCACGACGTGCAACTGCTTGGCGCCGTATGTAACAAGATTTGGTACCTC  
 GACGCAGTACGCAGCGAAGCCGATGTCTACAACATGGGCTTTAGCAAATACGTGCATGCA  
 CGTGCACTCGATGAAGCACGCCGACGCCGTGAGCGCGCAAACGCCGAAAAGAAGGCCGGA  
 GCCCTCAAGGACCAGGCTGCACGCCTCGGCGCGAAAGCAACCAAGGCTGCCGCAGCTAAG  
 CAGATGATCGCCGTGCGGAACGAATGATCGACAACCTCGACGAAATCCGCGTAGCTGAC  
 CGCGCCGCCAACATCGTTTTCCAGAACACGCCCTGTGGAAAAACCCCACTCAACGCC  
 AAGGGCCTGACCAAGATGTACGGCTCCCTCGAAGTCTTCGCCGGCGTCGACCTAGCCATC  
 GACAAAGGCTCCCGCGTAGTCTCTCGGATTCAACGGTGCAGGTAAAACCACCCTGCTC  
 AAACCTCCTCGCCGGTGTGGAACGCACCGACGGCGAAGGCCGCATCGTCACCGGATACGGC  
 CTCAAAATCGGCTACTTCGCCCAGGAACACGACACCATCGACCCCGACAAATCCGTCTGG  
 CAAAACACCATCGAAGCCTGCGCCGACGCCGACCAACAAAGCCTCCGCAGCCTCCTCGGA  
 TCCTTCATGTTCTCCGGCGAACAACCTCGACCAACCAGCAGGAACACTCTCCGGCGGTGAA  
 AAAACCCGCTCGCACTGGCCACCCTCGTGTCTCCCGCGCAAACGTCTGCTTCTCGAC  
 GAGCCCAACCAACCTTGACCCGATCTCCCGCGAACAGGTCTCGACGCACTGCGCACCC  
 TACACCGCGCAGTCTGCTGTTACCCACGACCCGGGTGCAGTCAAGGCCCTTGAGCCA  
 GAACGCGTCATCGTGTCTCCTGATGGCACCGAGGATCTTTGGAATGATCAGTACATGGAA  
 ATCGTGGAATTGGCG

>RXN01946-downstream  
 TAGGTTCTAAGGCTGTTTATGCT

>RXN01995-upstream  
 CCGACGCAAAGGCATGCGCCTGCGTGTCTCGAGTAGTCTCCTCCCTTCCTCGTCCCCAA  
 CCTCGACCATTACGGTCGCCCTCTCCTAAAGGAGCCTGGC

>RXN01995  
 ATGGATATCCGCCAAACAATTAACGACACAGCAATGTTCGAGATATCAGTGGTTCATTGTA  
 TTTATCGCAGTGTGCTCAACGCACTGGACGGCTTTGATGTCTTCGCCATGTCTTTTACT  
 GCGAATGCACTGACCGAAGAATTTGGACTGAGTGGCAGCCAGCTTGGTGTGCTGCTGAGT  
 TCCGCGCTGTTCCGGCATGACCGCTGGATCTTTGCTGTTCCGGTCCGATCGGTGACCGTTTC  
 GGCCGTAAGAATGCCCTGATGATCGCGCTGCTGTTCAACGTGGTGGGATTGGTATTGTCC  
 GCCACCGCGCAGTCCGCAGGCCAGTTGGGCGTGTGGCGTTTGATCACTGGTATCGGCATC  
 GGCGGAATCCTCGCCTGCATCACAGTGGTGTGATCAGTGAGTTCTCCAACAACAAAACCGC  
 GGCATGGCCATGTCCATCTACGCTGCTGGTTACGGCATCGGCGCGTCTTTGGGCGGTTTC  
 GGCGCAGCGCAGCTCATCCCAACATTTGGATGGCGCTCCGTGTTTCGACGCCGGTGCGATC  
 GCAACTGGTATCGCCACCATCGCTACTTTCTTCTCTCCAGCAATCCGTTGATTTGGCTG  
 AGCACTCGCCGCCCTGCGGGCGCTCGCGACAAGATCAATTACATTGCGCGCCGCTGGGC  
 AAAGTCGTTACCTTTGAGCTTCCAGGCGAACAAGCTTGTTCGACGAAAAAAGCCGGTCTC  
 CAATCGTATGCAGTGTCTGTTAACAAGAGAACCCTGGAACCAGCATCAAGCTGTGGGTT  
 GCGTTCCGGCATCGTGTGTTCCGGCTTCTACTTCGCCAACACTTGGACCCCGAAGCTGCTC  
 GTGGAAACCGGAATGTCAGAACAGCAGGGCATCATCGGTGGTTTGATGTTGTCCATGGGT  
 GGAGCATTCGGCTCCCTGCTCTACGGTTTCTCACCACCAAGTTCAGCTCCCGAAACACA  
 CTGATGACCTTCATGGTGTGTCCGGCCTGACGCTGATCCTGTTCAATTTCTCCACCTCT  
 GTTCCATCCATCGCGTTTGCCAGCGGCGTGTGCGTGGGCATGCTGATCAATGGTTGTGTG  
 GCTGGTCTGTACACCCTGTCCCCACAGCTGTACTCCGCTGAAGTACGCACCACTGGTGTG  
 GGCGCTGCGATTGGTATGGGTGCTGTGCGGTGCGATTTCCGCGCCACTGCTGGTGGGTGGC  
 CTGCTGGATTCTGGCTGGTCCCCAACGCAGCTGTATGTTGGTGTGGCAGTGATTGTTATT  
 GCCGGTGCAACCGCATTGATTGGGATGCGCACTCAGGCGGTAGCCGTGAAAAGCAGCCT  
 GAAGCCCTAGCGACCAAA

>RXN01995-downstream  
 TAGGGCCGCGATTCTTAGCATGC

>RXN02062-upstream  
 TTGTCTAAACATCGTTTTGGGGTCCGAATGATAGCCCTTTTAATGCCCCCATTTCCGGTA  
 TCGCTGCGCAACTGTTTTTAGATGGCTAATCTTTGAAATT

>RXN02062

ATGAGAGTCGGAATGATGACAAGAGAGTATCCACCAGAGGTTTACGGCGGCGCTGGCGTG  
CACGTCACCGAATTGACCCGATTCATGCGTGAGATCGCTGAAGTTGATGTTCACTGCATG  
GGTGACCTCGCGATATGGAGGGAGTTTTTCGTCCACGGCGTCGATCCTGCCTTGGAAAGC  
GCGAACCCTGCGATTAAGACACTGTCCACCGGTTTACGCATGGCAGAAGCTGCAAACAAC  
GTGGATGTCTGTCACACTCACACACTTGGTATGCAGGTCTTGGCGGCCACCTTGACGCTCGT  
CTCCACGGCATTCTCACGTGGCTACCGCGCACTCTTTGGAGCCAGATCGCCCATGGAAG  
CGTGAGCAGCTTGGCGGTGGATACGACGTGTCTCCTCGGTCTGAAAAAATGCCATGGAA  
TACGCTGACGCGGTTCATCGCTGTGTGCGCTCGCATGAAAGATTCCATCCTCGCTGCGTAC  
CCTCGCATCGAGCCGGACAACGTGCGTGTTGTCTCAACGGCATCGACACTGAGTTGTGG  
CAGCCTCGCCGACTTTCGATGACGCGGAAGATTCCGTAATCCGCTCCCTAGGCGTTGAC  
CCACAGCGGCCCATCGTCGCATTTGTGCGCCGCATCACCCGCCAAAAGGCGTCGAGCAC  
CTCATCAAGGCAGCAGCGCTTTTCGACGAGTCCGTGCAGCTTGTGCTCTGTGCCGGCGCG  
CCAGACACCCCCGAAATCGCAGCTCGCACCACCGCCCTGGTGGAAGAACTCCAGGCAAAAG  
CGCGAAGGCATTTTCTGGGTTTCAGGACATGCTGGGCAAGGACAAAATCCAAGAGATTCTC  
ACCGCTGTGACACCTTCGTGTGCCCATCCATTTACGAGCCACTGGGCATCGTGAACCTG  
GAAGCAATGGCCTGCAACACCGCAGTTGTGCGCATCCGACGTTGGAGGCATCCCTGAGGTT  
GTTGTGACGGCACCACCGGCGCCCTCGTTCACTACGACGAAAATGATGTGAAAACCTTC  
GAGCGCGATATCGCCGAAGCGGTGAATAAAATGGTCGCTGATCGAGAGACCGCAGCCAAA  
TTTGGTCTCGCAGGGCGCGAACGTGCTATCAATGATTTCTCCTGGGCAACGATTGCTCAG  
CAGACCATTGATGTGTACAAATCCTTGATG

>RXN02062-downstream

TAAAACCGAAAGCCGGGGAACCT

>RXN02074-upstream

CGGGGGAAGGCGGTGTGCGATGCTCGGGCTAGCCTTGGATCTCAAGAAGAATTGACTGG  
TTTAAAGTCTGGGCTTTAAGTGCAGAAAGGTTGTGGATTG

>RXN02074

ATGCGCTCCCTGCTTCGTGATATCCCTGCGGTGGGTTGGCTAATCACCGCGACGATTGTT  
GTGCGCACGCTCGTTGTTGCGCTGGTCATCGTTGGGATCGGCTTGCTTATCGACGTCCCC  
TCGCCCCTCATTCAGCCATGTTGTGGTGGGTTCTGCGAGGTGCCACGGCAGCAGCTGCG  
CTGCTGTGCGCGGAAGCGGTGCTCCCCAACGTATTCGTGCACGAGTTGAACGATCCTGG  
CGGCGGCAGTTGGCTGCTAAAAATCTGGAGCTGAATTCCAGTTCGTGATGATGCCCAG  
TTGATCACACTGGCAACTGAAGCCACCTCAAAAGCATCCACTTACACAGTGATGTTTCTG  
GGGCTTACTTTGAGTATTTTGGCCCCACTGACAGTTATTGCGGTTGTGCGCGCGGCT  
ATTTCTGGCCGATTGCGGGGATACTGTGCTCGGTTGTGCGTGATACCTTTCGTTATT  
TCTTGGGCACAGCGCATGTTGAAAGGCGCTGGCGCGGGATACGGGCGAGCATCTGGGCAG  
TTGGCAGGCGTGTTTTGAATCGGTGCGCACACTAGGCACCACGATGATGCTGAATGCC  
GCTGGGCAGCGCAGGCAGATCATCACACAGCGCGCAGAGAATATGCGCTCCCAAGTGATG  
TCATTGCTGTACCGAAATCAGTTGATGATTCTGGTGACCGACGGCGTGTGAGATTGCC  
ACCACAATGGTTGCTGCGGTGTTGCCATTGGAGGATTCTTTTCAGGCTCTCTTACTCTC  
GGCCAAGCTGTAGCACTCGTATTGCTGGCCAGGCTGCTTATTGATCCCATCAACCGCATG  
GGTCGCACGTTTTACACCGGCATGGCAGGCAAAACCTCGCTGATCGCCATTGAAAAAGCC  
CTCGCGACAACCTTTACTGATCAGCCAACCAACAGGGACAGCGCCACGATGGGGATCTG  
GTGGTCAACAACCTGAAGATCGCCCGCATCACAGGGACATTGTGCACGGTATCTCTTTC  
AGCATTTCCCGCGGTTCCACATCGCGGTGGTAGGTCCAGTGGCGCTGGTAAATCCTCT  
GTGGCTCTAGCGTTGTCCGGACTTTTAGAGTTTGATGGTGCGATTTCCCTCGGCGGCCAC  
AACTGTGAGATGTTAGATCTTCGCGCCTCAGTCAGTTTCGTGCCCCAATCCCCACGCTG  
TTTAGCGGAAGCATCAAAAGCAATATCGATCTGGCGCGACGGGTGTTGATTCTGATCAC  
ATCCACGCAGCACTTTTAGGCGAAGAACTCCCGCGGACCTCAAAGTCGGTGAAACCGGC  
AAAGGTGTCTCCGGCGGCCAAGCAGCACGCATTTCCATTGCCCGAGGTTTAGTAAAGAAT  
GCTGCCGTGATTGTTCTCGACGAGGCGACCGCACAACTCGACTACACCAACGCCCCGCGAG  
GTTTCGACATCTTGCCAAATCCCTTGAGTGCACGTTGGTTGAGATCACCCACCGCCCATCA  
GAAGCCCTCGATGCAGACTTCATCATTGTTTTAGAGGATGGCCAATTGACCATGATGGAT  
ACACCCAGCAACGTTTCCAGCACAAATGCGTTTTTCCGCACCGCTGTGATGGAGGAAGAA  
CAA

>RXN02074-downstream

TGATTTCCCGACTTCTCCAATTG

>RXN02096-upstream

CGCTTCGACGACCTACCCACAGCGATATCCGCAGGAATCTCATCGCGGTTTTTGTAGAG  
CCGTTCTTGTACTCCTCCTCCATACCGCGAGAACATCTCG

>RXN02096

ATGGGTTTTGGATGTCAGTGATGAGCAGATCGAACACGCAGCCAGGCTTGCCCAGGCTCAT  
GATTTTATCGATCGCCTTCCAAACAAATACGAGGAAGTCATTGGCGAACGCGGCCTGACG  
CTTTCTGGTGGTCAACGCCAACGCATCGCCCTCGCACGGGCTTTCCTGGCGCATCCCAAA  
GTGTTGGTGCTTGATGATGCCACCTCTGCCATTGATGCCTCCACTGAGGACCGCATTTTC  
CAGGCCCTTGCGCGAAGAACTGCACGATGTACCATTTTGATCATCGCGCACCGCCACTCC  
ACTTTGGAGCTCGGCGATCGGGTTGGTCTGGTCTGAAGATGGACGGGTAACAGCACTGGGA  
CCGTTGAGTGAGATGCGTGATCACGCTCGTTTCTCGCATCTGATGGCTCTTGATTTCCAG  
GATTCTCACGATCCGGAATTCACCCTCGACAACGGTTCCTACCCAGCCAAGAGCAATTG  
TGGCCGGAGGTTCTCCACAGAAAAGCAGTACAAGATTCTTGCGCCTGCCCTGGTTCGAGGC  
CGTGGCATGTCCATGCCAGCAACCCCTGAGCTGCTCGCCAGATTGAGGCGCTGCCAGCA  
GCAACGGAAGAAACACGAGTTGATGCCGGGAGGCTACGCACCAGTACCTCCGGTTTCAAA  
TTGCTCAGTTTATTCAAGCAGGTCCGTTGGCTCGTCGTCGCGGTCATCGCGTTGTTGCTG  
GTGGGCGTAGCCGCCGATCTAGCATTTTCCAACACTGATGCGCGCAGCCATCGACAACGGT  
GTGCAAGCACAAAGCACCTCCACGTTGTGGTGGATCGCCATCGCAGGCAGCGTAGTAGTC  
CTTCTGTCTTGGGCCGCCGCCGCGATCAACACGATTATCACGGCACGCACCGGTGAACGG  
CTGCTTTACGGCTTGCGTCTGCGCTCATTGTGTCATCTATTGCGCCTGTCCATGAGCTAT  
TTCGAACGCACCATGTCCGGCCGCATCATGACGCGCATGACCACCGACATCGACAACCTC  
TCGTCTTCTCCAATCAGGTCTGGCGCAAACAGTTGTCTCTGTGGGCACGCTCATCGGT  
GTGGTCACCATGCTCGCCATCACCGACGCACAAGTAGCACTCGTTGCGCTGTCCGTGGTG  
CCGATCATCATCGTGTCTACTCTCATTTTCCGACGCATCAGCTCCAGGCTGTACACCGCT  
TCACGCGAGCAAGCCAGCCAGGTCAACGCGGTATTCCACGAGTCCATCGCCGGTTTACGC  
ACCGCGCAGATGCACCGCATGGAAGACCAAGTCTTTGACAATTATGCGGGCGAAGCAGAG  
GAATTCGACGCTGCGTGTGAAATCCAGACGGCCATCGCCATCTACTTCCCCGGCCTT  
GGCGCGCTCTCTGAAATCGCCAGGCACTCGTCTCGGTTTCGGCGCACTGCAAGTAACG  
CGCGGCGACATCTCCACCGGCGTACTCGTGGCATTCTGTGCTGTACATGGGCCTGATGTTT  
GGCCCCATCCAACAATAAGCCAAATCTTCGACTCCTACCAACAAGCCGCGCTCGGCTTC  
CGTCGCATCACCGAAGTGTCTGCAACGCAGCCAGCGTCCAGATCTGGGCACCAACAGGC  
ACGCTAGGCAGGCTGCCACGCAGCCTTTATTGCTTGACGACGTCACCTTCGGCTATTAG  
ACGATCCGATCC

>RXN02096-downstream

TAGACAACGTCACCGTCCAGATC

>RXN02148-upstream

GCCTCAGACTACGGAATCCCTGTGCAGGTGGTATCTGTTGATTTCAGCACCGTTTTATGGT  
GCGCGTCGCTACTAAGAAATAGTTTCGTGAGGAGAATCTTT

>RXN02148

GTGTCTGCATCCCGAAAACTCTCGTTGTGACCAATGATTTTCTCCACGGATCGGCGGA  
ATCCAAAGCTATTTGAGGGATTTTCATCGCTACTCAAGATCCTGAGTCGATCGTGGTGTTC  
GCGTCGACTCAAAACGCTGAGGAAGCGCATGCCCTACGACAAGACTTTGGACTATGAGGTC  
ATTAGGTGGCCTCGTTTCGGTGATGCTGCCACCCCAACAACGGCACACGCTATGGCGGAG  
ATCATTCGTGAGCGAGAGATCGATAATGTGTGGTTCGGTGCTGCGGCTCCGTTGGCGTTG  
ATGGCAGGCACAGCGAAGCAGGCAGGTGCGAGCAAGGTTATTGCCTCCACTCATGGGCAT  
GAGGTGGGGTGGTCAATGCTTCTTGATCGAGACAATCGTTGCGCAAAATCGGCACTGAG  
GTGGACGTGCTGACTTATATCTCGCAGTACACGCTGCGCAGATTCAAAAGTGCTTTTGA  
TCGCACCCGACTTTTGAACATTTGCCTTCCGGCGTGGACGTTAAGAGATTCACTCCGGCC  
ACGCCAGAGGACAAAAGCGCAACAAGGAAAAAGCTAGGATTACGGACACCACCCCGGTT  
ATTGCCTGTAAGTTCGCTTTAGTGCCGAGGAAAGGCCAGGACTCGCTGATCAAGGCGATG  
CCACAGGTGATTGCGGCGCGCCAGATGCGCAGTTGCTCATTGTGGGCAGTGGGCGATAC  
GAGTCGACTTTGCGGCGCCTTGCCACTGACGTGAGCCAGAACGTGAAATTCCTTGGGCGC  
CTTGAATATCAAGATATGATCAACACGCTTGCCGCGCAGATATTTTCGCGATGCCAGCG  
CGCACCCGCGGTGGCGGACTTGATGTTGAAGGCTTGGGCATTGTCTATCTCGAGGCACAA  
GCCTGCGGAGTGCCGGTGATAGCCGGCACCTCTGGCGGCGCGCCAGAGACGGTGACTCCG  
GCAACTGGCCTGGTTGTGGAGGGTTCGGACGTCGATAAGCTGTCTGAGCTTTTAATTGAG

CTTCTCGACGATCCGATCCGCCGCGCCGCGATGGGCGCTGCAGGTAGGGCGCATGTGGAG  
GCCGAATGGTCTGGGAAATCATGGGGGAGCGGTTGACCAATATTTTGCAGAGTGAACCA  
CGA

>RXN02148-downstream  
TGATGGTTGGACAGCTGTTGATA

>RXN02168-upstream  
AGGGTTTAGTCATCTATTTTCGGCTACGCTCACGTAACCTACGCATTCTGTAAGTGGTCATG  
GGTCCAAGAAGCCCATTTCCAAGACTTAGGAGCTTTATTTTC

>RXN02168  
GTGAGTATTTCTTCACTGACACCGCTGCACTCTTTCAAAGAGCCAGCAATTCTGTACGCC  
GGTCAGGCTTCTGCCTGGCAGCAGGTGATCGCTGATTCCAGCGAAGACCACATCACCGCA  
ACGCACCTGCGCGAGCTCCTGTCTCGCTCCCGTGCAAAGACTGCACCTTTCGCTCGCCAA  
ATCACCGCCATCGTGCCTGGCTCACTTGCTCGTCTTGAGGAAGTACCCGCGAAGACGCA  
CAAATCGGTGCAGACATCGACGCACAGCCTGCCGTTTCCATTCCAGGCATTCTGCTGGGA  
CAGATCGCTGCAACCCGTCAGCTGCGTGACCTCGGACTCGATGTCGCAGCAGCTTCCCGC  
CTTGGACACTCCCAGGGCATTTTGGGCGTTGAAGCAGTAGACAATGAAGAAGACGTTTTTA  
GCTTTCGCCATCCTGCTGGGCGCAGCAGCTTCCAGTTTCGCTGGCAAGGGCGCACATATG  
CTCTCTGTTTCGCGGCCTGTCCCGTGAGATCATCCAGGACACCATCGCTGGTGTGATGGG  
GTAGAGGTCTCCCTGCGCAACGCTCGTGACACTTTGTTGTCTCTGGTAAGCCAGAGGCA  
CTGAAGAAGGCTGCTGCTGCTCTACAGCGCGCAGCTGATGTTTACAACGAAGACATCAAC  
GAAAAGCGCAAGGGTGGATCCCTGGCAGAGCCTAAGTTTGACTACTTGGATGTGGCCATT  
CCTTTCCACCACTCCTCCATGCAGGACGCGAGCCGACTTGGCTGTGAGTGGGCAACC  
TGTGGCCTAAACGTCAACGCGCGCGCTTGGCAGAAGCAATTCTAGTTAACCAGCTGAC  
TGGGTTGAGCAGATCGCAAACCTCAAGGCTGATTACGTTCTTTCCCTCGATGCAGGCGTC  
AGCCGTTTACCAGCTCCATTGCTAGACGGTCGCGGAATCTCTTTGGTTCTGCGTTCTCC  
GCTGCAGAGCGCGACAACCTTGGCTCGCCCTGGCTTCCACGTTCCCTACCAGCTGAGGATTGG  
TCCGAGTTTCGCTCCAAAGCTGGTTAAGCTTCCAAACGGTGAGCACAAGGTTCTCACCGGG  
TTCTCCCGCCTGACTGGTTATTTCCCAATCGTCTGGCTGGCATGACCCCAACCACCGTT  
GATCCTGAGATCGTTGCAGCTGCAGCGAACGCTGGACACTGGGCGCAAATGGCCGGTGGC  
GGACAGTACTCTGAAGAAGTCTTCAACAAGAAAGGAAAGCTCGTTTCCCTGCTCAAG  
GTTGGACGCTCCGCACAGTTCAACTCCATGTTCTTCGACCGCTACATGTGGAACCTGCAG  
TTCGGTGCACAGCGCATCGTTTCCAAGGCACGTGCAACCGGTACCTCCATCAACGGTGTT  
GTTGTCTCCGCTGGTATCCCAGAGGTTGAGGAAGCAACTGAGCTGATCAACGATCTGAAC  
GCTGATGGCTTCCCATACGTTGCATTCAAGCCAGGCACCGTGGATCAGATCCGCGCAACC  
CTGAAGATTGCTGATGCAAACCCAGAGACCAAGATCATCATCCAGATCGAGGACGGACAC  
GCTGGTGGCCACCACTCCTGGGTCAACTTGGACGATCTGCTCCTGACCACCTACGCAGAG  
CTGCGTTCCCGCAAGAACGTTGTCTGTCATGATCGGTGGCGGCATCGGAACCCCTGCAAAG  
GCTGCTTACTACCTGACCGGTGAATGGTCCACCGATTGGGCTTCCAGCAATGCCAGTG  
GACGGCATCCTCGTGGGTACCGCTGCCATGGCAACCAAGGAAGCAACCACTTCTCCTCAG  
GTCAAGCAGGCACTGGTGCACACCCAGGTGTTGATCCACACGACGCTGGCGGCTGGGTT  
GGCCGTGGCGATGCTCGTGGTGGCGTGACCTCTGGTCTGTACACCTGCACGCTGACATG  
TACGAGCTGGACAACGATTCTGCTGCAGCTTCCCGCCTGATCTCTTCCATCGATTCTGAT  
GATTACGCAGATCACCGCGAAGAGCTCATCGAGGCTATCAACAAGACCGCTAAGCCTTTC  
TTCGGCGAGGTGGAAGAGATGACTTACGCAGAGTGGATCCAGCGTTGGGTTGAGCTTGCT  
TACCCAACCTCAGGACCAACCTGGGATGATCGTTTCCCTCGATTGGTTTACCGCATTGAA  
GCTCGTCTCAACGAGGCGAGGACGCGGCCATCACCACTGTTCCAGACCATGCGTCT  
GTGAAAATGAGGAAGAGGCGCTCGAAAAGCTTCTTGCTGCTTACCCGCGAGGCCGCGAG  
ATCCAGGTCTCTGCGCGCGACGCCGCGTGGTTTATTGGTCTGTGCGCAAGCACCACAAG  
CCTATGCCTTGGGTTCCAGCAATCGATGCTGACCTAGCACGCTGGTGGGCGCTTGACACC  
CTGTGGCAGTCCCAGAACGAGCGCTACGGCGCGAACTCAGTCCGCGTTATCCCAGGACCA  
GTCTCCGTGCGCGGCATCGACCGTGTGACGAGCCAGTTGCAGAGCTGCTCGGCCGCTTC  
GAAGCTGCCTGCGTTGACGCTCTCGACGGCGAGCCAGAAGAGATCTTCGCTCGCCTCAAT  
GAGTCCAAGAACGAGCGCGAATTCTGCTGGCTACCCACACATCGTGTGGCACGGCAAC  
CTGATCGACAACCCAGCTCACGTCTCAACGAGGGTGCTTTTCGAGCTCATCGAGGAGGAT  
GGCTACTGGGTCTATCCGTATCCTGGCTGATTCTTCTGACGATCTGCCAGTTGAGCAG  
CGCCCATACCTGGTTTCAGCATGTTGACATCCCAGTTGAGCTGGGTGACGCTGGT

>RXN02168-downstream  
TGAACCGGTGGTTTCCCAATTGG

>RXN02233-upstream  
ATCCCCACCAATTGGCCCAAGAGCTGCAGAGTTACGTTGTAGAACCCACCTCTGCCTAA  
CTGTGCGATTTCCTCAAGAGCCCCCTTGGGAGTCGATAATTA

>RXN02233  
GTGCTCGTGACTTCAACATGGGGATGGACCGTCCACGGAGACGGCAAAAAGATCGAACCC  
GGCGCAGTTGTGCTCCTAAAGAGCGCCTGAGCTGGGGGCGCACAATTGGAATCGGTATG  
CAGCACGTGATCGCCATGTTTCGGCGCCACGCTCCTGGTTCCACACTCACCAGGATTTCCG  
GTCAACACCACACTTTTATTCTCTGGTCTGGGAACAATCCTGTTCTGTGATCACCAGA  
AACCGACTACCTCTGTACCTGGGTAGTTCTTTTGTCTTCATTGACCTTTAACCGCAACC  
CAAGTCCATGGCATTGGCGTGCAGATCGGTGGCATTCTTGTGCGAGGTCTCGTGCTCGTC  
GCCATTGGATTTGTGGTGAAAGCAGCGGGCAAACGCGTTATTGATGCTGTCATGCCACCC  
GCTGTCAACCGGTGCGATCGTGGCACTCATCGGCCTGAACCTGGCACCAACCGCGGCAGGA  
AACTTCTCCAGCCAACCACTGGTTGCCACGGCGACCTCTTTGCCATTTTGATCGCTACC  
GTTGCGAGGCCGCGAATGATTGCTCGCCTGGGCATTTGATCGGTGTGGTGATCGGCTGG  
GTTTTGCGAGCTATCACCAGCAACCTCTCAGAAGGCGCAGCAGACACCATCCGTGAAGCA  
GCATGGTTTCGACTGCCACAGTTCCACAAGCCGGAATTCCAGCTCTCTGCCATTTTGGTG  
AACTGCGCAGTCACTCATCGTGTCTCATCGCTGAAAACGTCGGCCACGTCAAAGCAGTCTCA  
GAGATGACAGGGGAGGACCTCGACGACCTCGCCGGCGACGCACTTATCGCAGACGGATT  
GGCACCACCTCGCAGGTGCCTTCGGTGGATCCGGCACCACCACCTACGCAGAAAACATC  
GGCGTCATGGCGGCCACCCGCGTATATTCCACCGCTGCGTACTGGGTTGCCGCGTGCAT  
GCCATCGCCCTTGCCCTTCATCCCCAAATTCGGTGCATGATCTTACCATCCCCGCCGGC  
GTGCTGGGTGGGGCATGTTTGGTTCTTTACGGCCTAATCGGTATGCTCGGCATTCTGATC  
TGGCAAGACAACAAGGTCAACTTCAACAATCCAGTGAATCTGACCATGGCTGCCGTTGCT  
TTGGTTGCAGGCATTGGTAACCTCACCTCACCGTTTTCGGAGTCACTCTTGAAGGCATC  
GCATGGGGCTCTGTAGGCATCATTGTGCTGTACCCAATCATGAAGCGCCTGTACCTTTCC  
ATTGGGGAAGGCAAGAACGCAAAGTTC

>RXN02233-downstream  
TAGTACGCTGCTAAAGTATGCAG

>RXN02309-upstream  
GTGCCTTCCGTCGACTACGGTTAAACAAAAAGCTTTTGTCCATTTCACTGGATTACCG  
AAAGAATGAATCCACACTCGATCACCAAGGTAGCGATGA

>RXN02309  
ATGAGTAGCGGCCGAACCGTTCCAACCCGTTCCACGGGCTCGGAAAAGAAGGTGTATCC  
ACCACAGGAGCATCTCAGGTGCGAGTTTGGTGATCCCGAGCTAACGGCCAGGATCAATGAC  
GCCATGGTGCAGGTAGAAGAACTCCTGCACACTGAACTATCGTCCGGGGAAGACTTCCTC  
GTCGATATCGTCATGCACCTAACACGAGCCGGCGGCAAACGATTCCGCCCCATGTTTGCA  
CTGCTGGCCTCCGAGTTTCGGTGAAAAACCACTCTCCGAAAACGTCATCAAAGCCGCCGTT  
GTCGTAGAGATCACCCACCTGGCCACCCTGTACCACGACGATGTCATGGACGAGGCATCC  
ATGCGCCGCGGCGTCCCAAGTGCTAACGCGCGATGGGACAACCTCCGTAGCCATCCTCGCA  
GGCGACATCCTCCTAGCACATGCATCAGGTCTGATGAGTCAGCTGGGTACCGACACAGTC  
GCCACTTTGCCGAAACATTCCGGCGAAGTAGTCACCGGCCAAATGCGCGAAACAGTCGGG  
CCACGCGACACCGACCCGATCGAGCACTACACCAACGTAATCCGTGAAAAAACTGGTGTC  
CTCATCGCCTCCGCGAGGCTATTTGGGAGCCATGCACGCAGGCGCCGCACCTGAACACATC  
GACGCCCTGAAGAACTTCGGCGCAGCCGTCGGCATGATCTTCCAAATCGTCGACGACATC  
ATCGACATCTTCTCGGAAACCCACGAATCCGGAAAAACGCCCGGCACCGACCTCCGCGAA  
GGTGTATTACCTCCAGTGCTCTACGCACTCCGTGAAGACACCCCGTCGGCGCAGAA  
CTCCGCGACATCCTACCGGCCCTCTAGAAGACGACGAGACCGTCAACCACGTCTCTGAG  
CTCCTCTCCCAATCCGGCGGACGCCAAGCAGCCCTCGACGAGGTCTACCGCTACATGGAC  
ATCGCCAACGCAGAACTCGACCGCTCCGACAGACACCGTCAAGGAAGCCCTCCGCAAC  
CTTGCAACCTTCACAGTCAAGCGCGTCGGA

>RXN02309-downstream  
TAACCCCGTAATCCACCACTTAA

>RXN02321-upstream

TTTAAAACTACCCGCACGCAGCACGAACCTGTTTCAGTGATGTAAATCACCGCGGAAATA  
TTGTGGACGTTACCCCCGCCTACCGCTACGATTTCAAAC

>RXN02321

ATGACCATTTCCTCACCTTTGATTGACGTCGCCAACCTTCCAGACATCAACACCACTGCC  
GGCAAGATCGCCGACCTTAAGGCTCGCCGCGCGGAAGCCATTTCCCCATGGGTGAAAAG  
GCAGTAGAGAAGGTCCACGCTGCTGGACGCCTCACTGCCCCTGAGCGCTTGGATTACTTA  
CTCGATGAGGGCTCCTTCATCGAGACCGATCAGCTGGCTCGCCACCGCACCCGCTTTT  
TGCCTGGGCGCTAAGCGTCCCTGCAACCGACGGTATCGTGACCGGCTGGGGCACCATTTGAT  
GGACGCGAAGTCTGCATCTTCTCGCAGGACGGCACCGTATTCGGTGGCGCGCTTGGTGAG  
GTGTACGGCGAAAAGATGATCAAGATCATGGAGCTGGCAATCGACACCGGCCGCCCATTG  
ATCGGTCTTTACGAAGGCGCTGGCGCTCGTATTAGGACGGCGCTGTCTCCCTGGACTTC  
ATTTCCAGACCTTCTACCAAACATTAGGCTTCTGGCGTTATCCCACAGATCTCCGTC  
ATCATGGGCGCATGTGCAGGTGGCAACGCTTACGGCCAGCTCTGACCGACTTCGTGGTC  
ATGGTGGACAAGACCTCCAAGATGTTTCGTTACCGGCCAGACGTGATCAAGACCGTCACC  
GGCGAGGAAATCACCCAGGAAGAGCTTGGCGGAGCAACACCCACATGGTGACCGCTGGT  
AACTCCCACTACACCGCTGCGACCGATGAGGAAGCACTGGATTGGGTACAGGACCTGGTG  
TCCTTCCTCCCATCCAACAATCGCTCCTACGCACCGATGGAAGACTTCGACGAGGAAGAA  
GGCGGCGTTGAAGAAAACATCACCGCTGACGATCTGAAGCTCGACGAGATCATCCCAGAT  
TCCGCGACCGTTCTTACGACGTCCGCGATGTCATCGAATGCCTCACCGACGATGGCGAA  
TACCTGGAAATCCAGGCAGACCGCGCAGAAAACGTTGTTATTGCATTCGGCCGCATCGAA  
GGCCAGTCCGTTGGCTTTGTTGCCAACCAGCCAACCCAGTTCGCTGGCTGCCTGGACATC  
GACTCCTCTGAGAAGGCAGCTCGCTTCGTCCGCACCTGCGACGCGTTCAACATCCCAATC  
GTCATGCTTGTGACGTCCTCCCGGCTTCCTCCAGGCGCAGGCCAGGAGTACGGTGGCATT  
CTGCGTCGTGGCGCAAAGCTGCTCTACGCATACGGCGAAGCAACCGTTCCAAAGATCACC  
GTACCATGCGCTAAGGCTTACGGCGGAGCGTACTGCGTGATGGGTTCGAAGGGCTGGGC  
TCTGACATCAACCTTGCATGGCCAACCGCACAGATCGCCGTCATGGGCGCTGCTGGCGCA  
GTTGGATTCTATACCGCAAGGAGCTCATGGCAGCTGATGCCAAGGGCCTCGATACCGTA  
GCTCTGGCTAAGTCCTTCGAGCGCGAGTATGAAGACCACATGCTCAACCCGTACCACGCT  
GCAGAACGTGGCCTGATCGACGCCGTGATCCTGCCAAGCGAAACCCGCGGACAGATTTCC  
CGCAACCTTCGCTGCTCAAGCACAAGAACGTCACTCGCCCTGCTCGCAAGCACGGCAAC  
ATGCCACTG

>RXN02321-downstream

TAAATCGGCGAATCCATAAAGGT

>RXN02342-upstream

CAGGTTCTGCTGCGTGCGGGTAGTTTTTAAAGGTAAACTTTTTGGGCGTGTCGCCCTT  
AAAGCGCGCTTTTCGACGCGACCCCACTACATTGGCTTCC

>RXN02342

ATGAACGTTGACATTTACGATCCAGAGAGCCGCTAAACGTTGAGCTCCTGAAGGAAAAA  
TTGTCTCAAACCGGTGACTTTGGCCAGGTCATTTACGAAAAAGTGACAGGCTCCACTAAT  
GCTGACTTGCTGGCACTTGACAGGTTCTGGCGCTCCAAACTGGACGGTGAAAAGTGTGAG  
TTTCAAGATCATGCGCGTGGGCGACTCGGCCGCCCGTGGTCTGCCCCCTGAGGGTTCCCAA  
ACAATCGTGTCTGTGCTCGTTCAACTATCTATTGATCAAGTGGACCGGATTGGCACTATT  
CCACTCGCGCGGGGACTCGCTGTGATGCGTTGAATGACCTCGGTGTGGAAGGTGCC  
GGACTGAAATGGCCCAACGATGTTCAAATCCACGGCAAGAACTCTGCGGCATCCTGGTG  
GAAGCCACCGGCTTTGATTCCACCCCAACAGTTGTCATCGGTTGGGGCACTAATATCAGC  
CTGACTAAAGAGGAGCTTCCTGTTTCCTCATGCAACTTCCTCGCATTTGGAAGGTGTTGAA  
GTCGACAGAACCACATTCTTATTAATATGCTCACACATCTGCATACTCGACTGGACCA  
TGGCAGGTTCCAAAGTGTGGATTGGCTCGATGATTACCGTGCGGTATGTTCCAGTATTGGC  
CAAGATGTTTCGAGTGCTTCTACCTGGGGATAAAGAACTCTTAGGTGAAGCGATCGGTGTC  
GCGACTGGCGGAGAAATTCTGTGTTGCGGATGCTTCGGGCACCGTTACACCCCTCAACGCC  
GGTGAAATTACGCACCTTCGCCTGCAG

>RXN02342-downstream

TAAGGTGACGGTATGGGGAATTC

>RXN02348-upstream

AAAGACCCGAGCCGAAGCCCTGGCCTGCGCATACTTCCTTGTCAACGCTCGCTGGGATTA  
GGTCTTTTCTGAGCGCTAGCATTTCTCCACTCAAAGGAGC

>RXN02348

ATGCTTAACCGCATGAAAAGTGCGCGGCCAAAATCAGTCGCTCCAAAATCCGGACAAGCT  
TTACTCACTCTCGGTGCCCTAGGTGTTGTGTTGGCGACATCGGCACCAGCCCCCTGTAC  
TCACTTCACACTGCATTTCAGCATGCAGCACAACAAAGTCGAAGTCACTCAGGAAAATGTG  
TACGGCATCATCTCCATGGTGTGTTGGACCATCACTTTGATCGTCACCGTCAAATACGTC  
ATGCTGGTCACCCGAGCTGACAACCAAGGACAAGGTGGCATCCTGGCGCTCGTTGCTTTG  
CTGAAAAACCGTGGGCACTGGGAAAATTCTGGCAGTAGCCGGCATGTTGGGCGCCGCA  
TTGTTTTATGGCGATGTGGTGATCACCCCGCGATCTCTGTTCTCAGCGCAACAGAAGGC  
TTGACGGTTATCTCCCCAAGCTTTGAGCGCTTCATTCTGCCCGTATCTCTCGCAGTTCTG  
ATCGCTATTTTTGCAATCCAACCGCTCGGTACAGAAAAAGTCGGCAAAGCCTTCGGCCCC  
ATCATGTTGCTGTGGTTTGTACCCCTTGCAAGATTGGGAATTCGGCAAATCATCGGGCAC  
CCAGAAATCTTGCAGAGCTTGTCTCCACATTGGGCCCTGCGCTTGATTGTGGCTGAGCCT  
TTCCAAGCATTTGTGCTGCTTGGTGCCGTTGTCTGACAGTAACGGGTGCGGAAGCGCTC  
TACGCTGATATGGGCCATTTTGGGGCGAGGCCAATCAGAGTGGCGTGGTTTTGCGTCGTC  
ATGCCTGCTTTAATCTTGACGTATTTGGGGCAGGGCGCCTTGGTGATCAACCAGCCTGAA  
GCGGTGCGCAACCCCATGTTTTATCTCGCGCCGGAAGGTCTGCGGATTCCGTTGGTTATT  
TTGGCGACCATCGCTACGGTGATCGCATCGCAGGCCGTGATTTCTGGTGCGTATTCTATTG  
ACCAAGCAGGCCGTGAATTTGAAACTGCTGCCACGCATGGTGATCCGGCATACCTCCCGC  
AAAGAGGAAGGCCAGATCTATATGCCACTGGTTAATGGATTGCTGTTTGTATCCGTGATG  
GTTGTGGTGCTGGTATTCGGATCCTCTGAAAGCCTCGCCAGCGCGTACGGACTTGCAGTG  
ACCGGAACCTTGGTGCTGGTGACGCTCCTGTATCTGATCTATGTTACACCACATGGTGG  
AAAACAGCGCTGTTTCATTGTGCTCATCGGTATTCAGAAAGTACTTCTATTTCGCTCGAAC  
ACCACGAAAATTCACGACGGTGGCTGGCTTCCACTACTTATTGCGGCCGTGCTCATCGTG  
GTGATGCGGACCTGGGAGTGGGGAAGTGACCGCGTCAATCAGGAACGCGCAGAGCTGGAA  
CTTCCCATGGATAAGTTCTTGGAGAACTCGATCAGCCACACAATATTGGTCTGCGTAAA  
GTTGCCGAAGTGGCAGTATTTCCACATGGCACCAGCGATACGTGCCGTTGTCAATTGGTT  
CGCTGCGTGAAAGACCTCAAGCTTTTATACCGAGAGATCGTGATCGTTTGAATCGTCCAA  
GAACACGTTCCGCACGTGCCACCAGAGGAACGCGCGGAAATGGAAGTGCTCCATCACGCC  
CCGATCAGAGTCGTGCGAGTTGATCTGCACCTTGGTTATTTTGTGAGCAGAACCTGCCT  
GAGCATCTCCATGCCATTGACCAACATGGGATAACGCCACCTACTTCTGTCTGCCCTG  
ACTCTTCGGAGCAGGTTGCCTGGAAAGATTGCTGGCTGGCGTGATCGTTTGTATCTTTTCG  
ATGGAACGTAATCAGGCATCTCGAACTGAGTCTTCAAATTGCAACCAAGCAAAACCATC  
ACGGTTGGAACAGAGCTGCACCTT

>RXN02348-downstream

TAATCAGGCAGTTGCTGGCCAAC

>RXN02372-upstream

GACAATACTGATGGATAAAATTCATATCGAGGACGAAGGGACAACCCCGAACCCGTGAC  
AACATCAACCACAACCCGGGTGAAACATCCGGTAGACCAG

>RXN02372

GTGCCACCCGCACCCAACTTGCAGCCCTAGGGCTCCAACACGTTCTTGCTTTCTACGCA  
GGAGCCGTCATTGTTCCGCTGCTGATTGCACAGTCGCTGAACTTGGACACTGCGACCACC  
ATTACCTGATTAACGCTGACTTGTGACATGTGGCATCGCCACGTTGATTCACTCTGTG  
GGCATTTGGTCGCCACATTGGTGTGCGCTACCGATCGTTCAAGGTGTCACCACTACTGCT  
GTTGCTCCCATCATCGCCATTGGTTTGGGCGTTACTGATGGTCAAGGTGGCGTTGCGTCG  
CTGCCTGCCATTTACGGTGACGTCATTGTCTCCGGCATTTTTCAGTTCTTTGCAGCGCCG  
GTGTTTGCAGCTTTTCTCAAGTTCTTCCACCAGTTGTCACCGGTACTGTGCTGTTGGTT  
ATGGGTGCTTCCCTGCTGTCGGTATCTGCAATGACTTTGTGAACACGCGATGGGGTG  
CCTGCTGCCCAGCATCTTGTACGGTTTGGCACCTTGGCGGTGATCATTTTGGCGCAG  
CGCTTCTTCCGTGGATTTCATGGGCACCTTGGCTGTGTTGATCGGCCTGGTTGGTGGCACC  
GCAGTTGCTCTGATCTTGGGCGATGCCAACTTGGATGAGGTGGGAAATGCTGAAGCGTTC  
GACATCACCACTCCGTTTTATTTTGGTGTTCAGAAATTAACGCTGTTGCCATTTTCTCC  
ATGATTATCGTCATGATCATCACCATGGTGGAGACCACCGGTGATGTGTTGCAACGGGG  
GAAATCGTCGGCAAGCGAACTCGCCGAGTGATGTACCCCGCGCACTGCGCGCTGACGGC  
CTGTCCACCCTGATGGGTGGCGTCATGAACTCCTTCCCGTACACGTGCTTCGCGCAAAAC  
GTTGGCCTGGTGCGCATCACGGGCGTGAAATCTCGCTGGGTGCGGCAGCTGCTGCCGGC



TTCATGATCATCCTCGGTGTGCTGCCAAGGCTGGCGCGATCGTCGCTTCCATCCCTTCC  
CCAGTCCTCGGTGGCGCATCCTTGGCACTGTTGCGCAACGTTGCATGGGTGGGCATCCAG  
ACCATCGCCAAGTCTGACCTCGCTGATAGCCGCAACTCCGTCATCGTGACCTCCGCACTT  
GGCCTAGCCATGCTGGTGTCTTCCGCCCCGATGTTGCTCAGGCGTTCCCTGAGTGGGCG  
CGTATCTTCGTCTCCTCCGGCATGTCCGTGGCGCGATCACCGCGATCCTGCTTAACCTG  
CTGTTCTTCCACGTCCGACGCCAATCCGGTGGACAAGTCGCTACCTCAAAATCCGGTGAG  
CGCATCAATTTGGATGCGGTCAACAAGATGGATCGCACCGACTTCGTAGAAACCTTCGCA  
CCGCTGTTCAACAGCAAGACCTGGCCTTTGGAAACCGCATGGGAATCCCAGCCATTTCGCC  
AACGTACGGAACCTGCGCGAAGCCATCCAAGTCGCTGTGCTCACCGCACCGTTGTCCGAC  
CGCGAAGAGCTCATCCACGACTACCCCGACATGGCACAGCTCATTTTGGCCACCGAAGAG  
GAAGCCGCCACCATCTCTCAAGACCGTGGTTCGATCGGTCTTGATGATCTCGATGACGTG  
GATCAAGAAAAGCTCATCACCGTCACCGAGCAGTACCGCGAACGGTTCAACATGCCGTAT  
GTTGCGTACTTCGACACCATGGATTCTGTGGATACCGTCGTAGCCGCCGGCTTGCGCCGC  
CTCGACAACCTCCGACGAGCAGGAGCACCGCCAAGCGCTATCGGAAATCATTGAGATTGCC  
AATGACCGCTTCGATATATTGCTTGCCGACGCTAACCAGCCCGTTAGCTTTTCGATCGC  
AAGTTTACCGAGACTGACTTCCTCGGC

>RXN02372-downstream  
TAAAACACCAAAACAAATTAAG

>RXN02395-upstream  
AAACAGGAATATTTAACTCGACTTCTTAAAAAGCTCTATACGTAAATATCTTGCCCATC  
CAGCACCACTCATTTGTGGTGCACAATGGAGAGGACACAC

>RXN02395  
ATGTCCACCAACTCTGGCAATAACTTGCCCTGAATCCCAAGAGTCACCCGAGGAACCTCAT  
TATCCTCACGACACCCACCCAGGCCTAGTTCTTGGCATTTTCGGTCGATGCTCAACGCAAC  
AAGTTTCGGACTCGACAAAACCGTTTTTCGGCGTCACCGCAGCATTAATTCTGGCGTTTCATC  
GCCTGGGGCATTTCCAGCCCTGATTTCGGTTTCTTCAGTATCGTCCACGATGTTTCAGTTGG  
GCTATGACGAATACTGGTTGGCTCCTCAACTTTGTCATGCTGATCGGCATTGGCACCATG  
CTCTACATCGCTTTTTTCGCGCTACGGCCGCATCAAGTCGGGCACGGACGAAGACGAACCA  
GAATTCTCTCGCTTTTTCTGGATTGCGATGATGTTTCGGCGCCGGCATCGGTGTGGGTATC  
TTCTTCTTCGGTTCCTTCCGAACCGCTGTGGCATTATCTCAGTCCCCCACCTCACACCGTG  
GAAGGATCTACACCTGAGTCTTGCACCAAGCACTTGCGCAGTCCCACTTCCACTGGGGC  
TTATCCGCCTGGGGCTGTATGCCTTGGTCGGCGGCGGCTTGGCGTACTCCAGTTACCGA  
CGCGGCCGCGTAACCTTGATCAGCTCCACCTTCCGGTCACTTTTCGGTGAGAAAACCGAA  
GGTATCGCGGGTCGCCTCATCGACATGATGGCGATCATCGCCACGCTGTTTGGAACGGCT  
GCAACCTTGGGCCTTTCAGCAATTTCAGGTGGTTCAGGGCGTGCAGATTATTTCTGGCGCT  
TCGGAATACCAACAACATCTTGATCGCCATCATCGCGATCTTGACCATTGGCTTCATC  
ATCTCCTCAGTATCTGGCGTGTCCAAGGGCATTCGTTATCTTTCCAACCTCAATATTTCC  
TTGACGCTTGGATTGGTCTCTGTTGTGTTTCATCACCGGCCCCACCTTGTTCTCTGCTCAAC  
TTGATCCCATCGAGTGTGTTGGAATATGGCAGTGAGTTCTTGTCAATGGCTGGCAAGTCT  
TTGTCGTGGGGTGAGGAACCAATTGAATTCAGCTGGTTGGACGGCGTTCTACTGGGCA  
TGGTGGATCGCATGGACTCCATTTCGTGGGTATGTTTCATCGCGCGTATTTCTCGCGGCCGC  
ACCTTGGGTGAATTTCGCGCTCATCACCATGGCTATCCCCCTCCTTCATTTTGATCCTGGCG  
TTCACCATTTTCGGTGGAACCTGCCATCACGATGAACCGCGAGAACGTAGATGGTTTTGAC  
GGCAGTTCATCCAAGGAACAGGTGCTGTTTGATATGTTTCAGCAACCTTCCGCTGTACTCG  
ATCACACCGTTTCATTTTGATCTTTGTGCTGGCAGTATTCTTTGTTACCTCTGCCGATTCC  
GCCTCCGTGGTGATGGGAACGATGAGCTCCCAAGGTAACCTGCACCAACAAATTAATC  
GTGGTGTCTGGGGACTGTGCATGATGGGCATCGCGGTGGTCATGCTTGCTTACTGGTGGC  
GAATCCGCGCTGACTGGTCTGCAGAACCTCACCATTTTGATCGCCATTCCGTTTTCGCGTG  
GTGTTGATCGTGATGGCTATTGCCTTTATTAAGGACTTATCCACAGACCCAGCCGCTATT  
CGACAACGCTATGCAAGGCACCCATCTCTAACGCGGTGGTTCGTGGCTTGAAGAACAC  
GGCGACGACTTCGAGCTCTCCATCGAACCTGCAGAGGAAGGTCGTGGAGCGGGTGCTACC  
TTCGATTCCACCGCTGATCACATCACCGACTGGTATCAGCGCACCGACGAAGAAGGCAAT  
GATGTTGATTATGACTTCACACCGGCAAATGGGCCGATGGTTGGACACCGGAATCGACC  
GAAGAAGCGCAAGTGGACGCGAAAAAGGAT

>RXN02395-downstream  
TAAAAAATAACGACTGGCTGGGA

>RXN02424-upstream

AGCCAATGCTCAACTGCCCTTCAAAATCGATTTTTGTGCTTCAAAAAATACACCTTCGA  
ACATAGCATCGAACAAGGTGTTTCCGCTAGTCTGAACCA

>RXN02424

ATGACTAACGAGCTCACTCTTACCATATTTCCGTGTCCCAAATGGACAACAATTGCTAC  
CTTTTGGCCGCAAATGGCAACGGTTTACTCATTGATGCTGCAGATGACGCAGCTGCACTA  
CTTAAATTAGCCGAAGATGCCGGTGTGACCATCACCAAAGTGTGACCACCCACCGCCAC  
GCAGACCACGTCCGTGCATTGCCGGAGGTTCTCCAGAAGACCGGAGCAACTCACTACGCG  
CCTTTCCTTGAGGTGCCAGCTTTGCCCTCCGCTGTTGATGTGGAACCTGCATCATGGTGAT  
TCAATTGAATTTGAGGGTCATGTATTCCCTATCAGCATTCTGCGCGGCCACACCCACGGC  
GGTGCAGTACTCACCGCTGAGATCGACGGTAAACTCACCTTTTCGTGGGTGACAGCCTC  
TTCCCCGGCGGTTTGGGCAAACAGCAGCGAAGGCGACTTCGTCCGACTGTTCAACGAT  
GTCAAAGAGCGCATCTTTGACACCTACGACGATGACAGCATCGTGTGGCCAGGTCACGGC  
AAGGAAACCACTTGGAGCCGAGCGTCCACAGCTGGAATCTGGTGGGAGCGTCGCTGG

>RXN02424-downstream

TAAGCGCTTTTCTCAACCAGGCA

>RXN02442-upstream

GCCGTGATGTTGTTGAGCGGATGTGATTGCCGTATGTGCATGTGAGATTCCGGACGCTG  
AGTTCTGCCATTCCCTAATGATAACGGTTATCATTTTCAA

>RXN02442

ATGAAGTTTTTTTACTGACGCCCTCATAGTGCCTTTTGACGTTTCATTCATCTCCCGCGCC  
CTGGTCGCCGGATGCCCTGGCCGCAATTTTATGCTCACTCATTGGAACGTGGGTTATTTTG  
CGCAGGCTAACCTTTTTTCGGCGACGCTATGTGCGACGGCTTGCTCCCGGAGTAGCCACG  
GCATCACTATTGGGCGGAAATCTCATGTTCCGGCGCAGCAATCAGCGCATTAAATCATGTCA  
GCCGGAGTGGTGTGGACCAGCAGAAAATCCAGCCTCTCCCAAGACGTCAGCATTGGCCTG  
CAATTTATTACCATGCTTTCCCTCGGCGTGGTTATTGTGTCCCACTCCGATTCCACGCC  
GTAGACCTCACCAGTTTCCTTTTTGGAGACATTCTTGGCGTGCGACCCTCGGATATATTC  
ATCATCGCCATTGCAACAGTGTGGGTGGATTGACTATTTTCTCTTCCACCGACAGTTC  
ACTGCACTCGCTTTCGACGAGCGTAAAGCTCACACCTTAGGACTCAATCCCGCTTTGCA  
CACCTACTCATGCTGGCACTGATCGCATTAGCTACGGTGGTGTGCTTTCAGGTGGTGGGA  
ACGCTTTTAGTGTTTGGACTTCTCATTGGTCCGCCCCGCCACGGCTGCACTTTTAGTGCAA  
GACAAAGCAAGTATTTCACTGATCATGATCGTCGCGTCGCTTCTTGGATGCGCGGAAATT  
TACCTCGGGCTTTTAATCAGCTGGCACGCAAGCACTGCCGCGGGAGCCACTATCACTTTG  
TTAAGTGCTGCGATATTTTTTGCCACCTTATTGACAAAGAGTGCCATTAGTAGGTTAAAC  
TTCACCGCG

>RXN02442-downstream

TGATACTGAAAGACATTTTCAAT

>RXN02443-upstream

CAAGCACTGCCGCGGGAGCCACTATCACTTTGTTAAGTGCTGCGATATTTTTTGCCACCT  
TATTGACAAAGAGTGCCATTAGTAGGTTAAACTTCACCGC

>RXN02443

GTGATACTGAAAGACATTTTCAATAATGGGGAGCTCTTTGGGGCTTCCTCCGCGAAAAAT  
TTCCGAAAACCTACTAGCTGTTCCAGCCGTTGCCGCTCACTAGCTTTTGGTATCACCGCC  
TGTTCCGCTGTAGATGACACCCCTGACATTGTGGTCACCACCAACATCTGGGTGATGTT  
GTAAGCCATATCGTGGGAGATTCCGCAGATGTCCAAGTACTCATGAAACCCAACGCAGAT  
CCACATTCTTCGGAGTCTCAGCACAAGACGCCGCTGCCATGGAACATGCCGATCTCATC  
GTGGCCAATGGACTAGGACTTGAAGAGGGCCTTCAATCCAATGTGGACAATGCCAAAAGC  
CAAGGGGTTCCTGCTTTGGAAGTCGGCGAACACATCGATGTCATTGACTACTCCCCGGC  
GTTCCAGATCCTCACTTTTGGACAGACCCGGCGCATGATCGCCGCCACGGAAGTTATA  
GAAGCTGAACTGATCAAAGAACTCGATCCTTCCCTGACTGAATCGATCACACAATCAGCC  
CAGCACTACCGTGAGGAACTTGTGGCCCTTGATGAGGAAGTCACCGAATTGCTCAGCGGC  
GTGGCCCCAGAAAACCGCAAGCTGGTAACCAATCACAAATGTTTTTGGATACCTGGCCAGC  
CGGTTTAACTACACCGTCATTGACACCATCATCCAGGTGGAAGCACATTGGCGGCGCCT  
TCAGCATCTGACCTCAATGACATCTCCACCGCCATCGAAGACAACAATGTTCCCGCAATC

TTCACCGATACCTCAAGCCCAACGGTTAGCTGAAGTGTGGCCAGCAACGCTGGCATT  
GATGTTCAAGTGGTGTCCATTTTCACGGAATCACTACCGATGCAGATGGTGAAGCACCC  
ACCTACATCAGCATGCAAAAAATCAATGCCGAGCGCATTGCAAGCACTTTGTCC

>RXN02443-downstream  
TAAACAGTCCTAAACAGTCTTAA

>RXN02447  
ACAGTAGTTCGGGTGTACCTCGCTGAACTCGCACCACTAGAAATCCGCGGCTCCCTGACC  
GGCCGAAACGAGCTTGCTATCGTCACCGGCCAGCTGCTTGCTTCGTGATCAACGCGCTT  
ATCGCCGTCACCTACACGGAGTTATTGATGGAATCTGGCGCATCATGTTCCGCGTCTGT  
GCCCTCCCTGCCGTGCCCTCTTCTCGGCATGCTGCGGATGCCGGAATCACCACGCTGG  
CTGGTCAACCAGGGGCGTTACGACGACGCCCGCGCTCATGGAGACCGTCCGTACCCCT  
GAGCGTGCGAAAGCCGAAATGGATGAAATCATCGCGGTGCACTCTGAAAACAATGCCGCA  
CTTCTGGTGTAAAGCAGTCTTCGGGCCAGGCTTCAGGCCAGGTTTCTAGCAAGCACACC  
CACATGTCCATCGGCGAAGTCCTCAGCAACAAATGGCTGGTTCGTCTGCTCATCGCCGGC  
ATCGGTGTTGCAGTTGCCAGCAGCTACCGGCATCAACGCCATCATGTACTACGGAACC  
CGCTCCTCGAGGAATCCGGCATGAGCGCAGAAATGGCTGTGGTTGCCAACATTGCTTTC  
GGTGCCGTTGCCGTATCGGTGGACTGATCGCACTGCGCAACATGGACCGCCTGGATCGC  
CGCACCACTTCATCATCGGCCTGTCACTGACCACCACCTTCCACCTTTTGATCGCAGCT  
GCCGGCACTCTCTTCCAGAAGGTAACCTCCATTCGACCATTGCCATCATGATCCTTGTT  
GTTGGGTTTCGTGCTCTCCATGCAGACTTCTCAACGTTGCAGTGTGGGTGTGGCTGGCG  
GAAATCTTCCAGTCCGAATGAAGGGTATCGGCACCGGTATTTCCGTATTCTGCGGTTGG  
GGCATCAATGGCGTCTAGCGTTGTCTTCCAGCACTGGTCTCCGGCGTGGGTATCACC  
TTCTCCTTCTTATCTTCGAGTCGTGCGAGTCATTGCCCTGGCGTTTCGTACCAAGTTT  
GTTCTGAAACCCGTGGCCGCTCACTTGAAGAACTCGATCACGCAGCATTACCGGCCAG  
ATCTTCAAGAAGGCT

>RXN02447-downstream  
TAAACCCCTCCGATCTCTTTGG

>RXN02487-upstream  
TCATAGCTACGCGCATGCCCACATTCTAGATCGCCGAAGAAAGCAGCGGGACGTCTCTAT  
ATACTAAAGGGCACTAAAGCAACGCAGTTGAAGGGACACC

>RXN02487  
ATGTCAGCATACGAAACCAAGAATGGCTCCAGCACTACCCAGAGTGGACGCCACACTCG  
CTGGAATATGGCGACACCACCTGCTGGACGTTTACGACAACAACCTGGCCATTAACGCA  
GACAAGCCAGCCACCTACTTTTTCGGTCCGTTACAAACCTACGGTGAAGTGGACAAAGAA  
GTCCGCAAAACTGCCGCTGGCCTGCGCGCACTAGGTGTCCGCCCCGGCGATCACGTAGCG  
ATTATCTTCCCAACTGCCCACAGCACATCGCAGCTTCTACGCAGTGTGAAACTCGGC  
GCAGTAGTCATTGAGCACAACCCGCTCTACACCGCCACGAAGTCTCGAACCCCTTCAA  
GACCACGGTGGCGGTTGCCATCGTCTGGGACAAAGCCTCCCCACCGTCGAACAGTA  
CGTGGACAGACCCAGTTGGAACCATCGTGTGCGTCAACATGATCAACGCGATGCCACCA  
CTCCAGCGCCTAGCACTTCGGCTCCCAATCCCTGCACTGCGCAAGAGCCGCGAATCCCTC  
TCCGGCGCAGCCCCAACACCGTTCCTTTTGAAACCCTGACCAGCGCAGCAATGGGCGGC  
GACGGCGACGACGTAGTTTCAGAACCCACCGTGACCAAAGAATCCGTGCGCTGATCCTC  
TACACCTCCGGCACCAACCGGACGCCCCAAGGTTGCCAGCTCACCCACGGAAACCTGTTC  
TTCAATCTTCTTCAAGGAAAGCACTGGGTTCCAGGTCTCGGAGACAAACCAGAACGCATG  
CTTGACGCCCTACCAATGTTCCACGCATACGGTCTGACCATGGTCGGCACACTGTCCGTG  
TTCATCGGTGGCGAAATGGTGCTACTTCCACCCACGCATCGACCTGATCATGAACGTA  
ATGAAAAGCACACCCCAACCTGGCTACCAGGCGTGCCACCCCTTACGAAAAAATCGTC  
GACGCCTCCGAAAAAGAAGGAATCCCCATCAAGGGAGTCCGCAACGCCTTCTCCGGTGCA  
TCCACACTCTCCAGCGCACCGTTGAACGCTGGGAAAAGCACACCGGCGGACGCCTCGTC  
GAAGGCTACGGCCTACCGAAACCTCCCCATCATCGTGGGTAACCCCATGAGCGATCAC  
CGACGCCAAGGCTACGTAGGAATCCCTTCCCGACACCATCGTGCGCATCGCAACCCCA  
GAAACCTCGACGAAACCATGCCCGACGGCAGCGAAGGCGAAGTCTAGTCAAGGGCCCA  
CAGGTGTTCAAGGGTTACCTCAACCAGGAAGAAGCCACCAAGAACAGCTTCCACGGCGAG  
TGGTACCGCACCGGCGACGTGCGAGTGATGGAAGAAGACGGGTTTCATCCGCTAGTTGCT  
CGCATCAAGGAAGTCATCATCACTGGCGGTTTCAACGTGTACCCAGCTGAGGTTGAAGAA

GTCCTCGCAGAGCACCCAGACATTGAAGATTCCGCAGTCGTTGGTATCCCGCGTGAAGAC  
GGCTCCGAAAACGTCGTTGCTGCCATCACTTTGGTGGAAGGTGCAGCGCTGGATCCGGAT  
GGCCTGAAGGAATTGCCCCGAAGAACCTCACCCGCTACAAGGTTCCGCGCACTTTCTAC  
CACTTTGAGGAGATGCCGCGGGATCAGATGGGCAAGATTAGGCGTCGTGAAGTGCAGGCG  
GAGTTGTTGAAGAAGCTCGGCAAG

>RXN02487-downstream  
TAGACGCCGATTTAAGAGGTCGA

>RXN02512-upstream  
GCTGGAAAGTCCCCATTGGCTAAGGAATTTACCAAGGCACCAGCAGGTGCGAAGGCAGAT  
TACAGCAACACCAATAAAAATTAGCCGAGGGAGCATCGC

>RXN02512  
ATGAAGCCGAAGGATTTCTGCACAGCGGAAAAATTGGGCGGAGAATTTAAGCGCACTGGGC  
TATCTAGCTGGTTGGCGTTTTGTCCGGATGCTCCCTTTGCCTATTGCTCGCCGGGTGTTT  
GACCTTGGGGCGGATCTGGCGTCGAAAAGCGGAAAAGGCATGGGGCAGCTACGCGCTAAT  
CTGGCGCGGGTGGTCGGTGCGGAAAACGTTACGCAGGCGCTGGTGAAGCAAGCAACGCGC  
AGCTATGCGCGGTATTGGCTGGAAGCGTTCCGGCTACCGGCGATCGCGCGAGATCCTGAG  
CTGCTTGC CGGTTGCGTAAGGGAAGTGTGGCCTAGATTTGTTGGATGAATCTTTGGCT  
GCCGGCAAGGGCGTAGTTTTGACGCTCCCACACAGCGGCAACTGGGATATGGCTGGCGCT  
TTTCTGATTAGCCATCATGGGCAATTCACCACCGTTGCAGAAAGGGTCAAGCCGGAACGC  
TTGTTTGAAGCGTTTCGTGGAGTTTCGAGAAAGCCTTGGATTTGAGGTGCTGCCTCTCACC  
GGTGGCGAGCGTCCGCCGTTTGAAGAGCTGAAAGAGCGCCTGACATCTGGAGGTATCGTG  
TGCCTTCTTGGGAGCGTGACCTGCGGCATTCCGGCGTGGAGACCACTTTTTTTGGTGAG  
AAGACCTCCATGCCAGCAGGACCTGCGCAGCTGGCCATTGAAACAGGTGCGGCGCTGCAC  
GTGGTGCAATCCATGGTTTCGATGACGACGCTGGGGTCTCAGCGTATCCGATGCCGTGACC  
GTGGATAATTTATCCGACACGGTGCAGCGGATCGCACATCTTTTATGGCAAATATTACG  
GCGCACCCCGCTGATTGGCATATGCTCCAACCCCTGTGGTTTGGTGATTGGATCCGGAG  
CGTCTCAAGCGCTCTAGGGAGCAGACAAATGTTCAAAACCGGTGGCATTACAGGAGGAC  
AAT

>RXN02512-downstream  
TAGGTGCGAATTGGAATGGTCTG

>RXN02515-upstream  
GTGGCTAAGCACAGTTACTTGGCCAAGCTGGGCGGCAGAAAAACCGGCCAGCTAATACT  
TCAGTTTAAATTCGCTTCAACCCTGAAAGATTGTGACAG

>RXN02515  
ATGAGCACTCTTGAAATCCGTAACTGCACGCACAGGTCCTGCCGTCCGATGAGTCCGCT  
GAGCCTAAGGAAATCCTCAAGGGCGTCAACCTCACCATCAACTCTGGTGAGATCCACGCC  
ATCATGGGCCCTAACGGTTCCGGCAAGTCCACTCTTGCTTACACCCTTGGTGACACCCA  
CGCTACGAGGTAACCGCAGGCGAGGTCCTCCTCGACGGCGAGAACATCCTGGAGATGGAA  
GTTGATGAGCGTGACGCGCTGGTCTCTTCCCTGGCCATGCAGTATCCAAGTAAATCCCT  
GGCGTTTCCGTTGCTAACTTCTGCGTTCCGCAGCGACCGCAATCCGCGGCGAGGCTCCT  
AAGCTTCGCGAGTGGGTAAAGGAAGTCCGCACCGCTCAGGAAGCTCTGGCAATTGACCCT  
GAGTTCTCAACCGCTCAGTCAACGAAGGTTTCTCCGGTGGCGAGAAGAAGCGCCACGAG  
GTTCTGCAGCTTGATCTGCTGAAGCCAAAGTTCGCGATCATGGATGAGACCGACTCCGGC  
CTTGACGTGGATGCACTGCGCATGTTTCCGAGGGCATCAACTCCTACAAGCAGGAGACC  
GAAGGTGGCATCTTGATGATCACCCACTACAAGCGCATCCTCAACTACGTTAAGCCTGAC  
TTATTACAGTTTTTCGCGAATGGCCAGATTGTGACCACCGGTGGCGCTGAGCTTGCTGAC  
AAGCTCGAGGCTGACGGCTACGACCAGTTCATCAAG

>RXN02515-downstream  
TAACATGTCCGATTCCTCAATG

>RXN02547-upstream  
GGGGCCGTGCGATAAGCGAAGAACAATTAGCACTGCGCGCGCTGGTCTGACGCATTGGTTA  
AGGGGCTGGCGGTCCGGCGCCGAATCGGCGGAGGAGCTT

```
>RXN02547
TTGGAGCTCAACAACGCTGCGCGGCTGACCGTGGATGAGTATCCGGCGGCGAGGGGAAGCG
CTTGAATCTGCAGGTGAGAGGAATGTAGAGGACCGAACCCGTGCGGTTGATGAGTTCAAA
GCGGCGGATCAAGAGCTGTCTTCTTTGAGTAAAGGCAGCAGTAATATTGAGTACCGTTTG
CTGCAGGTGCGGGAAAATTTGTGTGAGGATTTGGGCGTGAGCCCGCGGGATATGCCCTTT
GCCGGTGAGCTGATTGATCCGAATAATGCGGAATGGGAACCCGTGTGTGACGCGCATTTTG
GGTGGTTTTGCTGCGGAAATGTTGGTTCTCATGGGTTGTTGCCACGGGTTGCGGATTGG
GTAAATGCCAAACATTTGGCAGCGCTGCTGAAATTCAACGGCGTGGTGACAACGGGGGAG
TACAAAACCTCGCGTTTTCCGGCGGATTCCTGATCCGAAAAGTTGATGTTGTGGAGTCG
CCGTTTTCGCGATTGGGTAAATCAAGAATTAGGCAAGCGTTTTAATATTCCGGTGCCTGCGC
ACTCTGAGGAATTGTGCGCGCTGGGGCCACGCGATCAGGGCGTGACCATTTTGGGTGTG
CGAAAATTTGCGCAGCAGACAGGCGATCCGACGACGCGTTGGGAAAAAGATGATCGCCGA
AAGCTGGGGGATCGTTCCACATACCGTTTGGGTTCCACCAATGATGCCAAGGTGGAAACG
CTTCGGGAAACCGTGAAAGCTGGCAAAGCAGTTGTGACGGCAGCTGATAATCGCATTTGCT
GCAAACCGCGCTGAGCTGCGGGAACTTGAACGGCAGTATCAAGCTTCGCAAGAAATTTTG
AAAGTGTGCTGGGCTCAGATTGATGTGAATCAGCCGACGCGGCGATTGCTGAGCTGGAC
CGATTGCTGGAAGAGCTGAACAACACTCCAGAGGCCACCGAGCTTTCCGCGCGGCATGAG
GCGGCGAAGCAGACGCTCGCGAGGGTTTCTGACTTGCTTGTGCGCAGCTCAGAGTGAGGAA
ACCGTGGCGTCGATGAACCTGAAACGCGCCGAAACTGAATTGAAACGGCTCGAAAGCCTG
CCGTTGCGGAAATTTCTGAGGAAATCGCGCGGGAAGTGAGAAACTATTTCTTGCCAAC
ACCCGCGGGTTTACGCGCGCAACGTGGATGAGCAGACCATTGCGCTGCGCGAGGATCTG
GACAAACAAATCGATGCCAATGAGGCAGAACTTCGACGTTGTGAAAACCAAATTTGTTGGC
ATTTTGGCAGCTATATTGAAACGTGGCTTGCGAACCGCGCTGACTTACAAGCCGAACCT
GAGTTTGTGGTGAGGCCATCAACCGCTTCGGCGAGCTTCGCGAGCGATCGTTTGGCAGAA
TTCACGGCCAAATTCCTAGGGCTCATGAACGAGATGTCCACCCGAAACCTCGGCCAAATC
TCGCGGCGTCTACGTGATGCGCGCCGGGAAATCGAGGAGCGCATCGAGCCGATCAACGCC
TCCTTGGCGCAGTCGGAATTCAACGAAGGTCGTTCTTGACATCGACATCCGTGATCAA
AGTGGTCCGATTGTGAGGGAATTCAGCAGAAACTTGATGCCGCTACCAGCGGTGACCTG
GGAACCAGTACCGAGAAACAAGCCTTCGCCCCGTTATGCGCTGATCGTGAAATCATTTCC
AAACTCGCTCCCACGACTCCGCCGACGCCCGCTGGCGCAACACCGTTCTAGACACCCGC
CGCCACGTTTCGCTTCATCGGCTTCGAGCGGATTCGACGGCGCAACCGTCAACACCTAC
GTGACTCCGCATCACTTTAGGCGGACAAGCCAGAGCTGGTGTTTTTCTGCTCGCC
GCTGCCTTGCCTACCGCTAGCCGAACCCGGCGCCCATTTATCCACCTACGCCACCGTC
ATTCTGGACGAAGCCTTCGACCGCGCCGACCCCGCTTACCCGCCAAACCATGAACGTC
TTCCACAGCTTCGGCTTCCACATGGTGCTCGCGACCCCGCTGAAACTTATCCAAACCTC
GGCGATTATGTGCGCTCCACCATCGTGGTCAGCTACACCGAAAAACCAAACGCCCGGGC
GCAATTCAGGGCAATTCAGTTTCTCTAGGATCGAGAAA
```

```
>RXN02547-downstream
TAACATGCCATTGTTTATCGACG
```

```
>RXN02566-upstream
GACTCCGGATGATCAAGCAGCGAAACCTTTGTCAAGAACATAGCTCCCCACCCTAGACAA
AAGCCCAAATAAATCTGCTCAATAACCTAACCTAAAGTCC
```

```
>RXN02566
ATGCACGCTCGTCGCCCCAACCTCACCTCAGCGCACCCGTGTTCTCAGCGGCTGATT
TTGCCCCAATCATGGTTGGTGCATCCAATGGCGTGACGCTATCGATGGGAAGTTTGCTG
GCAGCACACTTGGCGGGAGCTTCGTGGGGAGGATCAGCCGCCACATTGACCACGATCGGC
GCAGCTATCTTTTCGATTCCCCCTTGGCCGATGGTCTCCACATACGATCGCCGAACCTCA
CTCAGCACGGGCATGTTGCTTGGTTGCGTGGGCGCACTACTGGCGATCCTCGGCGCACAA
TTGCGCTTGTTCAGTAGTACTTTTGGCATTTTTGTTTCTCGGATCCATGTCGGCGGTT
AACCTCCAAGCACGTTTCGCCGCAACCGACGTGGCCAGTGAAGAAACCCGCGGCCGCGAC
CTCTCGATCGTTGTGTGGTCCACCACCATCGGCGCAATCGCCGACCAAATTTATTTGAA
CCAAGCGCCGATTTCAGCGAAACCTGGGGCTCGAACAAATGCCGGCGCATACCTGCTG
TGTTTATTTGGCCAGCTCATCGCCATCGCAGTCTGGCGATTACCCCTCCCCAAAGGCCTC
AAACCCGAAGCCACCCCAAATGCACCAACAGAAAAGAAGCGCTCACCCGAAAGCCCTC
CAAGCCATCATCGGTTGCAACCGCACACTTCTCCATGGTTCGGTCTCATGTCCATGGCC
GCCATCCACATGCAAGGCCACGGCGCCAGCCTCACCATCATCGGCTTCACCATCAGTTTG
CACGTCGCCGAATGTACGCACTCTCACCAGTGTTCGGCCTGCTCACAGACAACTCGGC
```

CGCAATGTCACCATCTATTCCGGCTTCGCCATGCTCGCCACATCCGCAGCATTCTTATC  
 ATTTGGCCCGAACCACAGTGGGCCATGATCACATCCATGATCCTGCTTGGGCTCGGCTGG  
 AACTCTGCCCTCGTCGGTCTTCAACATTGCTTGTGACGCCACCCCATCCACCACCGC  
 ACCTACGCCCAGGGGCGCAGCGACCTAACGATGAATCTTGC GGAGCTTCAGGCGGGTTG  
 ATCGCCGGACCGTTAATTGCCATGGGCGGAATGCCCTTGTGGCAGGCGTCGTTCTTGCA  
 GTTGTGGCGCTTCAAACGGTGCTTAGTTTCAGAACCCGTTCAATTGAAAAGACTCCTGCT  
 TCATGTTTT

>RXN02566-downstream  
 TAGCCTAGGAATTCACGCACGAC

>RXN02571-upstream  
 TGGACAGGCCCGGGCCGCGTACGGTGTTGGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGC  
 ATTGTGCGCTGGTTGTTGCCGCTTTTGGCAGTCGGGATGGC

>RXN02571  
 GTGGTGGCTCTAACTCAAATCGTCGGACCGTCCGGCTCCGGGCTCACGCGGGAATTGGAA  
 AAACGCTACCGGGAACGCCCGAGCGGTGATGCTGACCGCCGACCCGCGCGCATATC  
 ACCTACCTGCGCGGACAGTCGCCGAGGAGCTGGCCTTGGGCTGGAACAACGCGGCATC  
 GTACCCGCGCAGATGTGGGAGCGCGTCCGAAACATCGGGCTCGGCCTCGAGAATCTGCTA  
 GACCGCGCACCCGCGCAACTTTCCGGCGGGCAAACACGGCGGCTGGCGATCGGCACCGTC  
 GCCATCTTAGAGGCGCCAACGATGCTTCTCGACGACCCCTCTCCGGTCTTGATACCTCC  
 TCGCGAGCCCCAACTCATCACAATGTTGGAATCATATGAGGGCGATGTCATCGTCGCTGCG  
 CACAAGCGGTGGCTCGACGCGCCGACTGTGTACTTAGGGGATTGGAGGAGCTGTCCCTG  
 CCTGCGCGGGTGGAATTTCCGGTCCATCGCGAACGTTTCAGCGATTACAGGAACCCGC  
 GGACAACAACGCCGACGCTGGTGGCAATTCAACGAATCCCAACCACAGTTTCAGATCGGC  
 CCCCTGGATATTACTGTTTCTGCAGGTCAAGTGCTGTGGTTGCAGGGTCCCAATGGTTCA  
 GGGAAAGTCCACACTCCTGCGTGGTCTTGCCAATGAACCCGGCACTGAATTGATGCTGCAA  
 AACCTTAGCGATCAAGTCATTGACTCCACTGTTGCTAATTGGGTGCCAGGCAGTAACAGT  
 GAAGAACATCCGCTGGATTTATCGCAACGCGAACTCCGCCTTGCCCAATGCGACGCAGCC  
 CTGGGTAATAACCCGGAAGTTTGTCTGCTGATGAACCCGACGTCGGCCTTGATGTGCGC  
 GGTGCAACGCCATCCACCAGCGCTTTCGGGATTTCTTAGGGAATGGGGGAGCGCTGATC  
 CTGACCTGCGATGATGAAACCTTCGTGGCAGAGGTAGCTGAATACGCGATAGTGAAGGAA  
 ATGGGGCTC

>RXN02571-downstream  
 TAGGTTTCTTTGGACCAAACCAC

>RXN02581-upstream  
 ACGGTCACCTCGCTCAAGTAGTGTTAGTTTGCAAAAGTAATAAAATGTTTCATCTTTGTGCA  
 TGGTCACAATAGTCATTAAAGAATTGTAAGAGGGGTTTAC

>RXN02581  
 ATGGATTTAGATAAAGCGATTGGTTCATTCTTCGATGAGAATGGAGAAATCAACCTTCCT  
 CCATTCCCTAACTTTGGCAGCCATGGGTGAGTTCATGTACCAGGCTGACATCGCTGAAGGC  
 GGCGGGGATAAACCACGCATGCATTTCTGGGACTTCTCCGAAGACCGCGATGGCAAGCTG  
 ATTCAGTACACCCGAAACGAGATCGATACTCGTATCAAGGCTGTAGCAGGCCGTTTGCAG  
 CAGGTCGCCACCCTGGGTGATCGTGCAGCGATCCTGGCTAACAACAGCCCTGAGTACATT  
 TTCAGTTTCCTCGGCGCGATCTACGCTGGCATGGTCCCTGTGCCGCTTTATGATCCAAAC  
 GAGCCAGGACACGCAGACCACCTCAACGCTGTTTTTCGCAGACAGCGAGCCAGTTGTCGTT  
 CTGACCAACTCCAAGTCCGCAGGTGCCGTGCGCAAGCACTTCTCCAGCCTTCCAGCTGCA  
 GAACGCCCCACGCATCCTCTCTGTAGATTCTTGCCTGATTCTCTCGCGGATTCTTACGAG  
 AACCCAATGCTGACCGAAGCCGGCCGCCGCTGGCTGCTCTGCGCCAGTCCGCGCCCAT  
 GATCTGACCGCATTCCTGCAGTACACCTCCGGCTCCACCCGAACCCAGCTGGCGTTGTT  
 CTGACCAACCGCTCCATCCTGACCAACGCTTTCGAGATCTTCAGCGCCGCACAGCTGAAA  
 ACCCCACTGCGCCTGGTTTTATGGCTGCCACTGCACCACGACATGGGCATTATCCTCGCG  
 GCGTTTGTCACTATGCTTGGCCTGGACAACGAGTTCATGAACCCACGCGATTTCGTGCAG  
 CAGCCTTCCCGCTGGATTAAGCAGCTCAACCGTCGCGAAAGCGACGTGGACGTTAACGTC  
 TACACCGTGTTTCCTAACTTCGCCCTCGAGCTTGAGCAGCTACGCAAGCCAGCAGAG  
 GGAGAGACCTGGATCTTTCCGCATTGGATGCCATCATTATCGGTTCCGAGCCAGTCACA  
 GAAACGCTCTGACCACCTTCGCTGAAGCTTTCGAGCCTTACGGCCTGCCGTGTTACAGACC

CTGCGTCCTTCTACGGTCTTGCAGAAAGCATCCCTGCTGGTCACCACCCACAGACCGAA  
AACCGCCCACTGATCTCCTACTTCGACCGCGAGGCCTTGGCCGAAAACCGCGTTGAGCTT  
GTAGAAAAGGGCAATAACAAGGCTGTTGCTTTCGCTCTCCAACGGCCAGGTTGCAGCCCCA  
CAGCAGCTGGTCATCGTTGATTCCGAAACCGGAACCGAGCTGGCAGACGGCCAGATCGGC  
GAAATCTGGACCCACGGCGAAAACACTGCTGCAGGTTACCTCGACCGCGAGGAAGACACC  
GCAGAAACCTTCCGCAACCGTCTGACCACCCGCTTGAAGAAAACCTCCCGCGCAGAAGGT  
GCTGCCGACGACAATACTGGATGGCCACCGGTGACCTCGGCGTCATCGTAGACAACGAG  
CTCTACATCACCGGTCTGCTGAAGGACCTCATCGTTGTCGAGGCCGAAACCACTACCCA  
CAGGACATCGAGTACACCGTCCAGGCTGCTTCCGCACACATCCGTGCAGATTCCGTGCA  
GCATTGCGAGTCCAGGCGATGACATTGAAAAGCTCATCATCCTGGCAGAACGCGACACC  
ACTGCAAACGAAGCCGACGATGCAGCTGCTGAAGAAGCAATCCGCTCCGCCGTTGGCACT  
GCACACGGTGTGTTCCAGAAGAGATCCGTATCCTCGCACCTGACGAGATCGCGCGTTCC  
TCCTCCGGAAGATCGCACGCCGCTCAACCAGCGCAACTACATTCAGGAACAAGCTAAC

>RXN02581-downstream  
TAGTTCTTTGCAGACACCGCAGG

>RXN02595-upstream  
GTGGGTAAAGGGGACTCCGAGGAAGTCCACGTCGTCTTCTTTCGCGGCGCTGAGGATGGT  
TTCGCGGATTTGTGCGGGGAGTGGGTGGGAGAGAAAACG

>RXN02595  
GTGATCGTTGTGGCCATGGCTTCCATTATGGCTTGTTTAAAGCAGCTAGACTGAATAAC  
CCTATGAAGATCCTTTTGTGTGCTGGCGTGATACCACTCATCCTCAAGGTGGCGGAAGT  
GAACGCTATCTGGAGCGGGTGGGTGAGTTTTTGGCGGATCAGGGCCATGAGGTGGTGT  
CGTACTGCTGGGCACACGGATGCGCCACGGCGTTCTTCCGCGATGGTGTGAGGTATTCC  
AGGAGCGGTGGGAAGTTTAGTGTGTATCCCAAGGCGTGGGTGGCCATGATGTTGGGTGCT  
GTGGGGATTGGCACGTTTTTCCAAGGTTGATGTGGTGGTGGATACGCAGAATGGCATTCCG  
TTTTTGGAAAGTTTTTCTCCGGTAAGCCGACTGTGTTGCTCACGCATCATTGCCATAAG  
GAGCAGTGGCCGGTGGTGGGTGCGGTGCTGGCGAAGGTTGGTTGGCTGATTGAGAGCCAG  
ATCGCGCCGCGCGCTTACAAAACCTGCGCCGTATGTGACTGTTTCAGAGCCGAGCGCTGAG  
GAGCTCATTGCGTTGGGTGTGGATCAGCAGCGGATTATATCGTGCAGCAATGGCGTGGAT  
CCCGTGCCGCTGCACACGCCGAAGCTGGATCGCGATGGCCAGCATGCGGTGACGTTGTGCG  
CGCCTGGTTCCGCACAAGCAGATTGAGCATGCGATGGATGTGCTCGCGGCGCTCGACGGC  
GTGGTGTGATGTAGTCGAAAGCGGTGGTGGCAGAAGGAAGTGGTCGATTATGCCCCG  
ACGCTGGGTGTGAGCGATCGCGTGGTTTTCCACGGCCAGGTGCGCGAGGATCACAAGCAC  
GCCCTGTTGGAGCGCGCCACGATTATCTCATGCCTTCGCGCAAGGAAGGCTGGGGCCTG  
GCGGTACAGGAGGCGGCGCAGCACGGCGTTCCGACGATCGGTTACCGAAGCTCAGGCGGC  
CTGCGCGATTCCGTGCTCGACGGCGAAACCGGCCTGCTTGTGCACTCCAAGGCCGAGCTT  
ATTTACGCCACCAAAACCGCTTATCGACGCGCTCCCTCCGCTCCAAGCTCGGCGCCAGC  
GCGAAGCAGCGCGCCGAAAACCTACAAGTGGGACACCGCGGGAGCGCAGTTTCGAGGAAC  
CTTCTTGGTCTTGCCTCGAAAAAG

>RXN02595-downstream  
TAGTCCCAGCGCAACGCCATCC

>RXN02613-upstream  
AGATATCCCCGGCGATCGCCGCACCCACCCCTCCTTTGCCCTCCTACACCGCTCAACTCCT  
TGAGTGGCTCGAAATCACACACCTGCCTAGAAAGAAATC

>RXN02613  
ATGAAATTTAAGAAAATCGCCCTCGTTCTCGCCTTCGGTCTAGGCCTTGCATCCTGCTCA  
TCAGCTTCTGGCGATCCCGCCACCAACGCCGATGGATCCATCGATCTGAGCAAAGTAACC  
CTTAACATCGGTGATCAAATCGCCGGAACAGAACAGTGCTCCAAGCTTCAGGGGAGCTA  
GATGATGTCCCTTATAAAATCGAATGGTCATCATTTACCTCTGGACCACCCCAAATCGAA  
GCATTAAACGAGGTCAAATTGATTTCGCGATCACCGGAAACACCCACCGATCATCGGC  
GGCCCCACCAACACCAAGTGGTCTCCGCCCTACAACAACGATGCTTTAGGTGATGTCATC  
TTGGTTCGCCCCGATTCTTCAATAACCTCGGTGGCTGACCTTGCTGGAAGAAAGTGGCT  
GTCGCCCCGGGATCCAGCGCCACGGACACCTCATCCAACACTAGAAAAAGCAGGCGTG  
AGCGTTGACGACGTAGAAATCAACCTCCTCCAACCCTCCGACGCCAAGCCGCTTTCCAA  
AACGGCCAGGTAGATGCGTGGGCAGTGTGGGATCCCTACAGCTCACAGGCGGAAGTGGAA

GGAGCTCAAGTTTTGGTCAGGGGAGCGGGACTGGTCAGTGGGCATGGATTTGGTGTGCGCA  
AGTGATGAAGCGCTCGATGACCCCGCAAAGGAAGCCGCCTTGGCAGATTTCTCGATCGC  
GTGGCCGACTCTTATGAATGGGCTGAAGACAACACCGATGAATGGGCGACGATTTTCAGC  
CAAGAATCCGGCTTTGATCCGGAGGCCCTCTCAACTGAACACCCGCGAGCCTGCGCCATCAG  
GTGCCGCTCGACGAGTCCGTCAACACCTATCAGAACGCGCTTATCGACGCTTTTCGTCTCC  
GCGGTCTCGTTGAGGACTTTAATTTTCGAGGACACCGTAGACACCCGATTTGAGGGC

>RXN02613-downstream  
TAAGTATGTCTGAGTATGGCAA

>RXN02614-upstream  
TCATTGTATACGCCACCTCGGTCTGCTGTCTGAAGCGCTGATCAGAGCTTGGGAACGTC  
ACACCTTCGCTACCGAAACGCATAAGAAAGTTGCTCGCC

>RXN02614  
ATGACTGCCACATTGTCACTCAAACCCGCGAGCCACTGTCCGTGGATTGCGCAAATCATAC  
GGAATAAAGAAGTCTCCAAGGAATCGACCTCACCATCAACTGCGGCGAAGTAACCGCG  
CTGATCGGACGCTCAGGTTCAAGAAAATCCACCATCCTGCGCGTGTGGCGGGCCTATCT  
AAAGAGCATTCCGGCTCTGTAGAAATTTCCGGAAACCCGGCCGTTGCCTTCCAAGAGCCT  
CGCCTGTTGCCGTGGAAAACGGTGTCTGATAATGTGACCTTTGGCCTCAACCGCACTGAT  
ATTTCTTGGTCAAGAAGCACAAGAACGCGCCTCGGCACCTGCTTGAGAAGTCAAACCTCCC  
GACTCCGACGCGCCTGGCCCCCTCACGCTCTCCGGCGGCCAAGCCAGCGCGTCTCCCTT  
GCGCGAGCGCTCATCTCCGAGCCAGAGCTTTTGCTTCTCGACGAACCCTTCGGCGCCCTC  
GATGCTCTGACAAGACTGACAGCCCCAAGACCTGCTGCTCAAACCGTGAACACCCGAAAC  
TTGGGAGTTCTGCTGGTCACCCATGATGTTTCCGAGGCCATCGCCCTGGCCGACCACGTC  
CTTCTTCTTGACGACGGCGCCATCACACACAGTTTGAAGTGTAGATATCCCCGGCGATCGC  
CGCACCCACCCCTCCTTTGCCCTCTACACCGCTCAACTCCTTGAGTGGCTCGAAATCACC  
ACACCTGCC

>RXN02614-downstream  
TAGAAAGAAATCATGAAATTTAA

>RXN02638-upstream  
CTCTGTTGTTGTTCTTGAGGCGCTTCGTCCATTCTGTGGCAAAGACGTGCTCAAGCCAGT  
GAAACAAGCCGTTAATTAAGCGAAAGCTCGTGGTCGAC

>RXN02638  
ATGGTCAAAGGTTTGGCTTTTTCTGTAGAGGATTCCTGCCTAAGGTTCCGCTGCATCCC  
GAAGAGTCACGGGAGACGTTTTATGGGCGCATCATCATTAGTGCTGTGCGGACGGTGATG  
AAAGCCCAGGATGTGCAGATTTCCATCTTCGGTGCGGAGAACATTCCGACCACCGGCGGC  
GCATTTTTCGCATCAACCACACTGGTTATTATGACTTCATTCTGGGTGGTATCCCCCGCA  
TTCGTGCGGGGTAAGCGCCTGGTTCGATTTCATGGCGAAGAAGGAAATTTTCGACACCCCA  
GTTGTGCGGACCCCTCATGCGCTGGATGAAGCACGTCTCTGTGGACCGCTCCGCGAGGTGCC  
GGTTCCATGGAAGATGCGCGGAAGCGTCTCGACGCGCGCAGCCTCGTCGGTATCTTCCCT  
GAGGCGACGGTGTACGGTCTTTGAAATCAAGGAACTAAAACTGGCGCCGTCCGCATC  
GCCGACAGCGCTAACGTTCCGCTGCTGCCATTATTATTTGGGGCGGCCAGCGCATCATC  
ACCAAAGACATCGAGCGCGACTTCGGCCGCTCCACATCCCCGTATTCATCAGCGTGGGT  
GAACCCGTGACGCCAGCGCGATCCCCGACGAAGCAACGGAACGCCTCTACGAGGCTATG  
AAAAAGCTTCTCGACGAAACCCGCACCGCTACGAACAAAAGTATGGCCCATTTCGAAGGT  
GGAGAATTGTGGGCGCCGAAATCCCTCGGCGGCGGCGCCCCAACGTTGGAGCAGGCGAAA  
ATGTTGGAATCGCCGAACGGGAACGTCGACAAGCAAAACGCGCGGCAAAGGTGCGCAAG  
AAACGCACCACCTTTATAAGGAAAATCTTTAAAAAA

>RXN02638-downstream  
TGATTGCACTGGGTTACGCGCCC

>RXN02662-upstream  
CCAAGGTGTACCCCTACCGTTGCCATCGCCTTCATCATCGTCAATATCGCCGTGGACCT  
GCTCTACGTCTGGTCAATCCACGTATTAGGAGCATCTAG

>RXN02662



ATGCGCCGTAAACTAACCACCACATTAGAAAACAAGCCCGGTGCACGACTTGGTGGCTTC  
CGCGCACTTGACCAACTTCAAAAATCGCGCTGGTTTTCTTCTCCTGATCTTCTCCTC  
GCGATCTTTGCCCCACTGATTGCTAAATACGATCCACTGGCCTCCGGAAGTCCAGTCCAG  
CCTCCAAGCGGTGAGCACTGGTTTGGTACCGACGCCATCGGCCGCGATATTTTCTCCCGC  
GTAGCCACGGCGCCAGAGCCTCCC

>RXN02662-downstream  
TGATCATTTGGTCTTTTCGCTACG

>RXN02794-upstream  
GCGCCCACTCATCGGCGAGCTTCAGGAGATGAGGTTGATGCTCCATTGATAATTTCTTTC  
GCTAATAGTCAAATGATCATTTGAGTGTTAGTGTTTTCTC

>RXN02794  
ATGCTTCTTTCCGCCCCGACACACACGAGTTTCCAAGAACTTGGACTCAATGCTAGTCGG  
CGCAAAGCAATCAACTGGACACTGGCACTCACTGTGGTGCTAATTGCCTCCATGTTTGT  
GGCGTGCTCATCGGTGCATCCGGGACCTCAGTGTTTTCCACGTGGACCGTAATTAGCCAC  
CATCTTTTTGGCACTGAGCTAGGTGGCTCCGACACTGCCGACGCCATCATTGGGTACATC  
CGCACTCCACGCGTCTTGCTCGCTGCCATTGTGGGCGCAGGCCTTGCCCTGGCAGGTGCC  
ATCATGCAAGTACTGGTCCGAAACATGCTGGCAGACCCCTATATCCTCGGGGTGAATCA  
GGTGCCAGTTGCGGTGCGGCCGCTGCCTTACTGTTTCGGAGTGGGCGCTGGATTTGGCGAT  
TACGCCCTCCAAGGCAGCGCTTTCTCGGCGCAATGGCAGCTTCCGGATTGATCTTCTTC  
GTGGCGCGCGCAGCGGGGCGCATCTCCTCGACCCGCTTGTTGATGTCCGGCGTAGCGATC  
GGATACATGCTCTCTGCGGCAACAAGCTTTCTCATCTTCTCCTCCGACTCCGCCGAAGGC  
AGCCGCTCCGTGTTGTTCTGGCTGCTTGGATCCTTAGGACTTGCCGCATGGAATGGGCCG  
ATGGCGATCATCTTCTCATCGTGCGCATTGCCCTGGCGTTGCTCATGGTGTTGGGTCCG  
CAATTGGATGCCCTTAAACTCCGGCGATGAAACCGCACTTACCTTGGGAGTATCCCCGTAT  
CGCCTCCGCATTCTCCTCCTGGTGATCACCTGCCTGCTGGTGGGATCCATGGTTGCCATG  
GCCGGCAGCATCGGATTTCATCGGCCCTTGTCATCCCCACCTGGCCAGGCGTTTTGTTAGT  
GGAAACACCGACTCATGCTGCCTGTATCCGCGTTGATGGGCGCAATTTGCTCATCTGG  
GCTGATATCGCCGCGCCGACCCCTGCTTGCGCCCCAAGAGATTCCCATCGGCATCATCACC  
GCACTCATCGGAGCACCTTCTCCTGATTCTGGTTTCGCCGGATGCACACCTAC

>RXN02794-downstream  
TGATTTTAAAGGAATTATGCGTA

>RXN02809  
AACCTCTCCGTCCAGCAGCACTAACCAACGCCCTTTCTACCTCTCCGCAGAGTGGAAC  
AACCAAGGCTGCAGGCATCGTCTCCTACGGCTCCGCAATGGGCGTTCCGCGCAGCTGAGCAC  
CTCCGCGGCATCCTTTCCGAGCTTCAGATCGCACACGTTCAAAAGACCGGCCTGCTGAGC  
ATCTTCACCGACTTCGAATACCCTAACTTCAAGCCTTCCGAGCAGGGCATCTCCTCTGTG  
GACGCTATGCTTGAGCAGCTTGTTGTCTGGACCAAGGCAATGTCCACCATTCGCGAGTCT  
GCGAACGTCTATCACTTAAGAACCCTCACAAAAGTGGCGAGCTCCCCGACTGGGACTCG  
CCTCTTTTCGTATTC

>RXN02836-upstream  
CCATCACTCGGCTTACCGTCTACGGTGCTGCCCGCAGGACAGAGCGCCCCCAAAGCTC  
GTTTCAGACGGGATCCACCCCTCGAGATGGACGTCACCG

>RXN02836  
ATGACAATCGATGAAGGCCGTCGCCAGTTCGAGGTCAATGTATTTCGGCGCGATGGCCCTC  
ACCCGACTCGTCTGCCCCACATGCAGAAACAAAAGTGGGGGACGATCGTGAACATCACA  
TCGATGGGCGGGAAGATCTACACGCCTCTCGGCGGCTGGTATCACGGCACCAAGTTCGCC  
CTCGAGGCCCTCTCGGACGCCCTCCGCTGGAGGTGCGCCCATTCGGCATCGACGTTGTT  
GTCATCGAACGGGGCGGCATCGCCACCGAGTGGGGAGGAATCGCTGCCGACAATCTCGAC  
GCAGTGTGCAAGACAGCGCATACAAGCGCCAGGCTGACGCAGTATCGAAGTCGTTGCCA  
TCTGAGGCGAACAGCAACCGCAACTCACCACCGTCGGTTGTGCCGATGCGATTGGAAAG  
GCCGTGACGGCAGTCACCCCAAGACCCGCTATGCCATCGGCTTCGGTGCCAAACCGCTG  
ATTGCCTCGCGCAACATCCTACCGATCGCCAGTTCGACCCAGTGATCACTCGAGCGACT  
GGCGTCCCCCGCGAC

>RXN02836-downstream  
TGACCACTCTTCTGCGCCCGTCA

>RXN02922-upstream  
CCCACCGCGGCGCAAGCTACCGCCTAGGCGCTCGGAACTCCACCGCCACTATTGATCTCA  
GTTCCATATCCGCCCAACTAGTTTCCCAGGGAGCCCACTC

>RXN02922  
ATGATCTCACCGCAAACAATCATCGACAATCTTGCTCCAGTCCTCGCGGAGATCGCAGCA  
ACGGGTGCGCAGCGCGAACAGGATCGAGAATTCAGCCGTGATTTGGCAAAGCAGCTTAGT  
GCCGGTGGGTTCACTAAACTCCGCATTCCAGTTGAATTTGGCGGTTTGGGTTTTAGCCTT  
CCAGAAGCATTGAGGTGCTGGTGGCAGCGGCCGCTGCAGATTCAAATATCGCGCAGGGA  
TTGCGGCCTCACTTCTTGGCAGTGGAGAGCTTATTGATCGCTCCTTATTTCAGAGCACCGC  
ACCAAGTGGCTGCGAAAAATCGCTGAGAAAGGCGTGGTCATTGGCAATGCGTTGACTGAA  
GTGGGAAACAAGCCAGGTGAGCTGAAAACCAAGATCCGAAAGGAAGGCGAGTCTTACGTT  
CTCAGCGACACCAAGTTCTATTCCACGGGCGAGTCTTACGCCGACTGGATTCAAGTACAT  
GCGAAAGATGAGGAAGATCAAGATGTTTTCGCCTTTGTTGATCGCGACGCATCAGGCGTT  
GTTTTGGTGGATTACTGGGACGAATTTGGGCAACAATTTTGCTCCGGAACCAGCTTC  
TTTGAAAAAGTCGTGGTAGATCCACTGGACATTGTCAACCCGTGATTACACCGCACCCAGC  
GCTTTCCAGGCGCTGGCGCAGTCACATCATTGTCTACGTTGACTGGTATTTCGCAGGCA  
ATCACCCGTGACATTGTTACCTATGTACAAAACCGCACCCGTATTTTCAGCCACGGAAGT  
GGTGACCTTCCACGCTTTGATCCGCGAGGTGCAACAGGTGGTGGGTGAGGTGAAAGCCAAG  
TCGTATGCAGTCGAGAAAAATCTTTCAGGGTTTCGCACAAGAACTGGATCTTGTGCTCGAT  
AAGGCAAAAGCCGGCACTGCTACGGAGGTGATCTGGCCGCTGTGACCTGAGCGCCTAC  
CAAGCCCAGTTAGCGGTGGCACCTTTGGTGCTGAGCCAGGCCACCCAGGCCCTTTGAGGTT  
GGCGCAGATGCCTTAAACGGCGGCCACGTGGCTGCCCAATACACGATCGGATCCTTGTCAT

>RXN02922-downstream  
TGAGCCAAGAAATTTGAGCCAT

>RXN02923-upstream  
GCATCTACATTGAAGGAATCCACGGAGCGCGCATCGAAGACATCGTTGTGGTGAATGAAG  
ACGTTGTGAAACCTCAACAACCAGCCCCAAGGAACTGCG

>RXN02923  
TTGAGCATTCTTCTCCTAGGCGGAACCTCTGACATTGCCGGTGAGATTGCCACGTTGACG  
TGTCACGGCGAAGACGTTGTTTTGGCTGCTCGTCGACCAGAGGCTGCACAGGGCTTAGCG  
GAAGATCTTCGACAGCGCGGTGCCACATCTGTTTCATGTTTTGAGCTTTGACGCCCAAGTA  
CTAGACACGCACCGAGAACTTGTGAAGAAAACACAAGAGCTAGCTGGCGAGATTTCCCTT  
GCCGTGGTTGCTTTTGGCATCTTGGGAGACCAAGAACGCGCAGAAACCGATGAGACCCAT  
GCGGTAGAGATCGCCACCGTGGATTACACCGCTCAGGTCTCCATGCTCACTGTGCTTGCT  
GATGAGCTCCGCGCACAACTACTCCAGCAGCGATCGTGGCGTTTTCTTCGATTGCTGGG  
TGGCGGGCGCGCCGCCCTAACTATGTCTATGGATCCACCAAGGCTGGTCTCGATGCATTT  
TGCCAAGGGCTTGCAATAGCCTGCATGGGACACACGTGCGATTGATTATTGCGCGTCCT  
GGCTTTGTTATTGGTTCTATGACCACGGGGATGAAGCCTGCTCCGATGTGCGGTGTATCCA  
CGAGATGTTGCCGCGAGCTGTTGTTAGTGCTTATACCTCTAAGAAGAGGAGCACGACCTTG  
TGGATTCCGGGACGTCTGCGGGTTCTCGCCTGGATTATGCGGATGGTTCCCTCGTCCGGTG  
TGGCGGAAGATGCCACGC

>RXN02923-downstream  
TAGATACCCGTTTCAGCCCTCACA

>RXN02929-upstream  
CAGGTGGGGACCTCGCGTATCCCAGCTGGTGGAAAGAAATCGCAGCGCAGTTGAATCAGCT  
TGCTTCTTCTGAAGCTGTGCCGGCCGCTGCTTAAGTTTTT

>RXN02929  
GTGCTGAAGAGAATTTTCTCAACCCCTGGGTGGCTACCGCGTTGTGCGGTAGTCATTTTG  
GGGTTTGTGGTGCTGTTTTAGGTTTTCAGCGGTGTTATTGATTTAAGCCCCACAGCAGTG  
ATTAGACATTTGAGTGGGCAGGACACGCTCACCCCTCGAGATCAGGCCATCTTCTTTGAT  
ATCCGGCTGCCCTCGAATTATCGCTGGTGTCAATTGTGCGAGCAACGCTGGCTATTTCTGGT

GCTTCTTACCAAGCGGTATTTAGAAACCCGCTGGCTGATCCTTATTTGTTGGGTGTGTCC  
GCAGGTTCTGGCCTTGGTGTACGGCAGTGATTGTTGGCGGTACCGTGTGGGATTTTCT  
GCACCGAGCATCGGCGTGATTGGTGCAGCATTGTAGGTGGTGTGCCGAGTACTTGCC  
ACGCTGATGGTGAGTCGGGGAGTAGGACAGGGATCATCAACCACCGTGGTTATTTTGGCG  
GGCGTGGCGGTTGCTGCTTTTGCCAGTTCCATCCAGACCTATATTCAGCAACGACACATC  
GATACGGTGGCGCGCGTATATGTGTGGATGTTGGGCAACCTCAATGTCACCAACTGGATG  
TCGATCTTCATCGTGGCTGTGGTGGCGGGACTATGCGCGGCCGTGATCATGTCCTGCGCC  
AGGTTGTTAGACGTGATGGCTGTTGGTGTGTTGGAAGCCCGCACATTGGGCGTCGATCCA  
GGCCTCGTACGCATTGGCATTGTTCATCGTGGCAACCTTGGTACAGCTGCAGTGGTATCC  
ATTTCCGGTCTCATCGGGTTTGTGGGCATCATTGTTCCGCACGCCCTGCGCCTAATTGTT  
GGCCCGGGGCATCGGATTTTACTGCCACTGTCTTCGTATGGGGTGCCATTTTCTCGTG  
TTGGCAGATACCGCAGGGCGAACATTGATGGCTCCTCAGGAACCTCCCGTGGGTGTGGTG  
ACAGCTGCACTCGGCGCACCGTTCTTCTTATTTATTTTGCAGCAACCAGCAGACAACGA  
GTTCCAAAAAGGAGTGCT

>RXN02929-downstream  
TAAGTGGCGATCATTGAATGCGA

>RXN02933-upstream  
TGATCTGCTGTATCAGGTGGTTGATCCAAGAGTCGGTGCTGTTGGGGTTGCTAGCACTAA  
GGTTCAGGGAGCGTGGCTTAAGTGACAACGATCAAAAAC

>RXN02933  
ATGCCCTTTTTCAGGGAAATCGGCGGCTTCATCGTTGCCGTTGTATTTGTTCTTGCTGCG  
CTGTCTTTTCATTTGGACTCCGTTTGATCCAGTTCAGCTTTCCACAGGAGCGCCTTGAG  
GGAAGTTCTTTAGGACCTGTTGGGAACGGATCGTTATGGTTCGCGATGTTTTATCCCAG  
ATCATGGTTGGTTCCCGCGTCACGTTGTTGGTGGGCATCATTGCGGTGGCGATCGCAGCA  
TTAATCGGCACGCCACTGGGTATTGCTGCGGGAATGCGCCGTGGCATGGTGGAAACCTTT  
GTCATGCGTGGTGCCGATTTAATGTTGGCGTTCCAGCACTGTTGTTGGCGATTATTTCC  
GGCGCCGTTTTCGGCGCCTCCACGTGGTCCGCGATGGTTCGCGATCGGCATCGCAGGCATC  
CCTAGTTTTCGCCGCGTGGCTCGTGACGGCACATTGCAGGTGACCAGTCAGGATTTTCATC  
GCAGCTGCTCGGCTATCAAAAGTAAGTTCGCGCCGATCGCGCTTCGCCATATTTTGCCC  
AACATCACCAGCATGTTGATCGTTTCAGGCATCAGTAGCTTTTGCCCTGGCGATCCTGGCG  
GAAGCCGCATTGAGTTTCTCGGTTTGGGCACCACTCCCCCGGATCCCAGCTGGGGTTCG  
ATGTTGCAAACCGCTCAAGCATCCATCGGCGTCACCCCATGTTGGCGGTGTGGCCCGGT  
GCTGCGATCGCTTTGACGGTCCTTGGTTTAAATCTTTTCGGTGATGGTTTACGCGATGCC  
ATCGATCCAAAGCGGGAGGTTCGGCCGTGCT

>RXN02933-downstream  
TAAAGTTTCTGATTTAACGGTTG

>RXN02947-upstream  
GTATGTTACACAAGAACCCTGCACAACGCCTTCAAAGTACGTGACCACGACCAAGCGC  
ATTATTCACTCTCACCCCTCAGGATTTAGACTAAGAAACC

>RXN02947  
ATGACTGCAGCACAGACCAAACCTGACCTCACCACCACGGCTGGAAAGCTGTCCGATCTT  
CGCTCCCGTCTTGAGAAAGCTCAAGCTCCAATGGGCGAAGCAACTGTAGAAAAAGTGCAC  
GCTGCTGGCAGGAAGACTGCCCGCAACGTATCGAGTATTTGCTCGATGAGGGCTCTTTC  
GTAGAGATCGATGCTCTTGCTCGTCACCGTTCCAAGAACTTCGGCCTGGATGCCAAGCGT  
CCAGTTACTGACGGTGTGTGACTGGTTACGGCACCATCGATGGCCGTAAGGTCTGTGTG  
TTCTCCCAGGACGGCGCTGTATTCGGTGGCGCTTTGGGTGAAGTTTATGGTGAAGAGATC  
GTTAAGGTTATGGATCTTGCGATCAAGACCGGTGTGCCTTTGATCGGAATCAATGAGGGT  
GCTGGTGCAGTATCCAGGAAGGTGTTGTGTCTCTGGGTCTGTACTCACAGATCTTCTAC  
CGCAACACCCAGGCGTCTGGCGTTATCCACAGATCTCTTTGATCATGGGTGCCTGCGCT  
GGTGGTCAGTGTACTCCCTGCTCTGACTGACTTTCATCGTATGGTGGATCAGACTTCC  
AAGATGTTTATCACCGGCCCTGATGTTCATCAAGACTGTACCGGTGAAGATGTCACCCAG  
GAGGAGCTCGGTGGCGCTCACACCCACATGGCTACCTCCGGTACCTCCCATTAATCTGCT  
TCTGATGATTGATGCTTTGGATTGGGTTTCGCGAGCTGACCTCTTATCTTCCATCCAAC  
AACCGTGCAGAACTCCTCGCCAGGAGGCCGACATCATGATCGGTTCCATCCAGGAAAAC  
ATCAACGATGTGGATCTGGAATTGGACACCATCATCCCGGATTCCCCGAACAGCCTTAT

GACATGAAGGAAGTTATTTCCCGCATCGTCGACGACGCCGAGTTCTTCGAGATCCAGGAA  
 GACTACGCAGAGAACATCCTGTGTGGCTTCGCTCGCGTTGAGGTCCGTTCTGTGGCATC  
 GTGGCTAACCAAGCAACCCAGTTTCGCTGGCTGCTTGGATATTAAGGCATCTGAGAAGGCT  
 GCGCGTTTCATCCGCACCTGCGATGCCTTCAACATCCCAATCCTTGAGTTCGTGGACGTT  
 CCAGGCTTCCTGCCTGGCACCAACCAGGAATTCGACGGCATCATCCGCCGCGGCGCAAAG  
 CTGCTTTACGCTTACGCTGAAGCAACCGTCGGCAAGATCACCGTCATCACCCGCAAGTCC  
 TACGGCGGAGCGTACTGCGTGATGGGTTCCAAGGATATGGGCGCTGGCCTGGTA

>RXN02955-upstream

ATGCACTGGCTCCCATCAAAGACGAATTCTTGACCTCAGAATTCCAGCGTGAACCTCTACG  
 AAGCAGTGCGCGCCGCTGATACTTCAGGAGGTGCGGCATC

>RXN02955

ATGATGAATTTTAAAGTCCATCGTGTGCGTCACTGCCTGGCAGGTGTTTAGCCGCCAGGTG  
 CTGCACAGCCCATCAACGTGGTCTGAAGAACTATCCAAGCTGTTGTTCTGTGGCTATCT  
 TTCGCAGGTAGTGCGTTCCCTCTTGGAGAGCGTGGACATATTGCGGTTGATTTTCATCGCG  
 CGCAAACCTGCCTGTTTCTGCGCAGCGGGTCTGCAGGTCAATTGTTTCAATTGTTGATTGTT  
 GTTTTTGCGATCTCGGCATGATCTGGGGTGGCTACTTGGCTGCATCAATCGCGTGGAAT  
 CAGCAGCTCACTGCGCTGCCACTTACCTTGGGATGGGTGTATGTTGTCATCCCGATCGCG  
 GGTGTGTTTCATCGCGTTGTTTCGCGATCATCGATCTCATCGAAGTGCCACAGGCAAGGAA  
 GAGCCTTACCCCTTGTGATGAATCAGAAGAACCTCGAGATTGACGAGCTAGAGGCC  
 CAAAGCGCTATAGATTCTGCAAGTTCAGCGGAAGGTAGGAAC

>RXN02955-downstream

TAATATGTTGTCGCCAGCAGCTG

>RXN02966-upstream

AAATATACCCCGAGGTATCTTGACAGATTAAAGCTCGATGTTTTAGGCTCTACATATA  
 CCCCCACGGGTATCCCCTCAACTTTGATCTAAGGTGTCAC

>RXN02966

ATGCTTTTTGAACGCATCTACGAAGAAGGCCTCGCCCAAGCCAGCTATTTTCATTGGCTGC  
 CAACGCGAAGGCAAAGCGATTGTTGTTGATGCTCGCCGAGATATCCAGACCTATCTGGAC  
 CTTGCAGCAAAAAACAACATGGTCATTAGCGCCGTAACCGAAACCCATATTCATGCCGAT  
 TATCTCTCCGGTACTCGCGAACTTGCACTGCCACCGCGCCGAGATTTTCCTCTCTGGC  
 GAAGGCGGAGCTGATTGGCAATATGGCTTTACAGGCACCACTTGCATGCACAATTCCACC  
 ATCAAGCTGGGAAATATCACCATCACAGCCAAGCACACTCCCGGACACACTCCAGAGCAC  
 CTGTCAATTTTATTGATGATGGTGCGGTCTCAAAGGATCCCGGTTTTATGCTCAGCGGT  
 GACTTCGTCTTCGTAGGTGACGTGGGACGTCCAGATTTACTTGATGAGGCAGCTGGCGGC  
 GTGGACACCCGCTTCGCGGAGCACAGCAACTCTCCATAGCCTAAAAGAGCAGTTCTTT  
 GCACTCCCCGACCACATTACAGGTTTATCCAGGTCATGGTGCTGGCAGCCCTTGTGGCAAG  
 GCATTGGGCGCGATCCCTAGCACCAACCGTGGGATATGAAAAGGCTAATGCGTGGTGGGCT  
 CCATATCTGCGCAGTGATGATGAAGCCGGCTTGTGGAAGAGCTTCTCGACGGCCAGCCA  
 GATGCCACGCTTACTTTGCTCGCATGAAAAAGCAGAACAAGCAGGGACCTGCAGTACTT  
 AGTACATTATCCCCGCTTGTGAAGCTAGAAGCCGAGGAAGTCGTGAAAAGCTTGGTTCT  
 GAAGCAGTATTTGTGGATACCCGCGAGCAAAACCAAGTCCATCTCGGAACCGTTGTTGGG  
 GCATTGAATATTCGCGCGGCGCCAAGGCGTCCAATTTTGCGGCGTGGGTTATTGATCCT  
 CAAAAGGATGCTCAGGACCTTATTGTTTTGGCTCCGGACGCCAATACCGCTGCGGATTTT  
 CGCGACGCTTTGCTGCGGGTTGGCATCGACACTGTGCGTTATTTACCAACAGTATCGAT  
 GGATTGCCCTACCTTTGTGCCAGAACTCATCTCCCCCGCTGAGCTAGCTGAGACCAACTAT  
 GACGCACTGATTGATATCCGTGCAAAGTCCGAATTTGCCGCTGGCAGCATTCCCCGGCGG  
 CAGCAGCTTTCTGGAGGTTCCGGCATGTGGCGCCTCAATGAGCTGCCTGCGGGTGGCACT  
 TTGGTAACCTTCTGCCAATCAGGAGCGCGAAATACCGTGGTAGCCAATGCTTTGCGACGC  
 GCCGGATTACCGTTATCGAGCTCGAGGGCAGCTACGCCGCGTGGGAAAAATCAGCTGCC  
 AATCCTAAAACTTGCACTGCGCTC

>RXN02966-downstream

TAGTTTTAGATCCGGCGCTGTAT

>RXN02979-upstream

CTAGGTCAAGGAACTTCACTCGGCTAGTCCTTAGACTCAAATGTGTTTCAGACAAACACTG  
GCACCGTAAGGCACGAAAGTTACCGAAAGGACTGGTTCCC

>RXN02979

ATGACCGCCCCAAACACTCTCAAGCAAACAACCTCTTCGCTCTGATGAGTTCTCTTGCCCA  
TCCTGTGTCTCCAAGATTGAAAACAAATTGAATGGATTGGATGGCGTCGACAATGCAGAG  
GTGAAGTTCTCTCCGGAAGAATCCTTGTTGATCACGACCCAGCAAGGTCTCTATCAAG  
GATCTAGTCGCTGCAGTCGCAGAGGTTGGCTACACCGCAAAGCCATCAGCAATC

>RXN02979-downstream

TAAAACTCTCAGTTAGACCATTA

>RXN02987-upstream

GTTGTTTGATCCAGGTCAAGGAATTAACCCGGAAAGGACCGTATCTTTAAAGGTGCAAGC  
ACAGGAACATGACGATAAAAGATGAAAGGACCTGGTTACG

>RXN02987

ATGACCGCCCCCGCCACGCTGAAGAACACCACCTTTCGCTCTGATGAGTTACCTGTCCG  
AGCTGTGTCGCCAAGATCGAAAACAAGCTGAATGGTTTGGACGGCGTGGAGAATGCGGAG  
GTGAAGTTCTCTCCGGACGCATCTGATCACCCACGACCCACAGAAGGTCTCCGTACGT  
GACCTGGTCACCGCGGTAGCCGAGGTCGGTTACACCGCCAAGCCGTCGGCGATC

>RXN02987-downstream

TGACGCACTCCCGACCCACAAG

>RXN02991-upstream

TTGTCGTGTTTCGCGATCTTCGCCGTTGGCTTCATGATTCTGACCCTGCCTATGGGCCTTG  
GCTTGGGCAAACCTCTCTGAGCGTTTGGCGGTGAAGAAGTA

>RXN02991

ATGGCTAATACAGTTCGCGCAACAGTCCTCTACGATGCTCCTGGACCAAAGGGCCGTCGA  
TTCAACCTCATAATCACCATTCTCACGGTGGTTCTGGGATTGGCGCTCCTCTTCTGGATT  
GGTCCATGCTTTTCAGGCAACGGCCAACTCGATGCCAACAATGGACTCCGTTTCATCAAT  
TCCCAAACCTGGACCACCTACATTCTTCTGGTTTGTGGGGCACGCTGAAATCTGCCGTG  
TTCTCGGTGATCTTGGCTCTGGTCATGGGTACCGCACTGGGTCTTGGCCGTATCTCTGAA  
ATCAGGATTCTCCGCTGGTTCTGCGCCGTCATCATCGAGACTTTCCGAGCCATTCCGGTT  
CTGATCCTCATGATTTTCGCCTACCAGATGTTTCGCCAGTACAACATCGTGCCGTCGAGC  
CAGCTCGCGTTTCGCCCGCGTGGTATTCCGTCTGACCATGTACAACGGTTCTGTGATCGCA  
GAGATTCTGCGTTCTGGTATCGCTTCCCTGCCTAAGGGGCAGAAGGAAGCAGCGATTGCG  
TTGGGTATGTCTTCTAGGCAAACCACTGGTCAATCTTGTTCCTCAGGCCGTGGCTGCA  
ATGCTCCCAGCGTTG

>RXN02992

ATCGTCCCTTTGGGCAACACACTGATCGCACTGACTAAGAACACCACCATCGCCTCTGTC  
ATTGGAGTTGGCGAAGCCTCCCTGCTGATGAAAGCCACCATCGAAAATCACGCCAACATG  
CTATTTGTCGTGTTTCGCGATCTTCGCCGTTGGCTTCATGATTCTGACCCTGCCTATGGGC  
CTTGGCTTGGGCAAACCTCTCTGAGCGTTTGGCGGTGAAGAAG

>RXN02992-downstream

TAATGGCTAATACAGTTCGCGCA

>RXN02993

GTTGCTGAATACGTAGTCAACTCCATCGCTGATGACAAGGGCTGGGATCACCCACCATC  
GAATGGCGTGAATCCCCTTCTGCGCAGCGTGAAACCCTCATTCAAACGGTGAGGTAGAC  
ATGATCGCAGCAACCTACTCCATCAACGCTGGCCGTTTCAGAGTCCGTCAACTTCGGTGGC  
CCATACCTGCTTACCCACCAGGCTCTGCTTGTTCGCCAAGATGACGATCGCATTGAAACC  
CTCGAGGACTTGGATAACGGTTTGTATCCTGTGCTCCGTTTCCGGATCCACTCCAGCTCAG  
AAGGTCAAGGATGTCTTCCAGGCGTTTCAGCTCCAAGAATACGACACCTACTCTTCTGT  
GTTGAGGCACTGTCCAGGGCAACGTTGACGCCCTGACCACTGACGCCACCATCCTCTTC

GGCTACTCCCAGCAGTACGAAGGCGACTTCCGCGTTGTGGAAATGGAAAAGGACGGCGAG  
CCATTCACCGACGAGTACTACGGCATTGGCCTGAAGAAGGATGACCAGGAAGGCACCGAC  
GCTATCAACGCCGCACTTGAGCGCATGTACGCTGACGGCACCTTCCAGCGACTGCTCACC  
GAGAACCTCGGTGAAGACTCCGTGGTTGTTGAAGAAGGCACCCAGGTGACCTCTCCTTC  
CTCGACGCAAGC

>RXN02993-downstream  
TAGTGTGACGGCTTTTAAAAGCC

>RXN02996-upstream  
TCCTGCCACAGAATCTGCCTGCTGCTCCATTAATAAATAATGCAGGCTAGAATAGAGGG  
TCGATTAGGAGTCGATGAAAAAGTCGGCGCCAACGAGGAG

>RXN02996  
ATGAACAACAACGTGAGTGATCAAAAGCTAAGTGGTAAAGAGCTTGCGGCACTAGAGAAA  
CAAGCCGCAAAACTCTCGAATTGGTGATAAGAAGTGGTATCTCATCGCGGGAGTCGTG  
CTTTTCGCCATCGCACTCGTCCTCCACATATCCGTGGAGTGATGGGCTGGCAGGTTCTG  
ACGCTGTCGAATGTCGCGGAGGATGCCGGCATTACCTTGGTGAGTACGGTTTCTACTGG  
TTGGGCACCATCGGTGTATTCTGCTTTCTTTGGGCACTGTCGTGTTTAAGCGCACGTGG  
ATGGCGTGGATTTTCATGGATTTTCTCCTGCGTCACTCTTGTTGTTTCGCTGTGTTTGCCATC  
TGGATGCGCCAAACAACCACAGCACCAAGTGAATTTTCGTCAACATTGGCATTGATGCTT  
GCTGTGATTGCAGCGATCCTTGCTGTGTGGGGTCTATCTTCGGTGATTTTGGCCCGCAGT  
GATCGCCAAATGGAGATCGCTGAAATGCGCGCCGAGAACCAGACCTTGATGGTGTGCA  
GCTACCCAGCGCGCACTTCTTGAGCAGCAGCAAAGCAACCCAGAAGATAATCCTTTGCTT  
GTCGACGATCGTCGCGCCCGCATCGCCCGCCGCGAGCGTGAACAGGATGCACAAGGG  
GAGCAGGCT

>RXN02996-downstream  
TAAGTTCTAGTTCAAGCGGTTGA

>RXN03060-upstream  
TATGTCCTTTGGCTCCGGTACCCTGGCAGGAGTACCTGGGCTGTTTTTCTAAAATGGCCT  
GACGTTTTCAAGATTGAATTTAAGGAAAGCATCGTAGTTC

>RXN03060  
ATGAGTAACCTGCCGCGAGCACACCTGCCAACAATTCCGACGATGTTGCGAAGGAGAAT  
TGGGACTCTTCTTTTACGCCGAAGACTGACATTGACTCTTCCCAGCCTGTCAATAACTCG  
ACTGGTGAAGCCGCTGCGCGCGCAGTGAACCTGTACAAGGCGTATGGCCAGGGTGATACC  
ACTGTCACCGCGTTGGATCACGTCAACGTGGAGTTTGAGAAGAACAAGTTCACTGCCATC  
ATGGGTCCTTCTGGCTCGGGTAAGTCCACGTTGATGCACTGCATGGCTGGTCTGGATGCT  
GCGACTGGTGGTTCGGCATTCAATTGGTGATACGGATCTGTGCGGTTGAAGGACAAAGAG  
ATGACCTCTTTGCGTCGTGATCGTTGGGATTCAATTTCCAGTCGTTCAACTTGGTTCCT  
ACTCTGACGGCGTCGGAGAACATTACGCTGCCTACCGATATCGCGGGCCGCAAGATTGAT  
CAGTCGTGGTTTCGATGAGATTACCTCTCGTCTGGGTCTGACTGAGCGCCTTAAGCACCGT  
CCTGCAGAGCTCTCTGGTGGTCAGCAGCAGCGTGTGGCGTGTGCTCGTGCGTTGGTGTCT  
CGTCCGGAGATCAATTTTCGGCGACGAGCCAACCGGTAACCTGGATTGCAACTCTTCTAGG  
GAAGTGCTGGATATCCTGCGCACCGCAGTTGATCAGGATGATCAGACCGTTGTGATCGTT  
ACCCACGATGCCAAGGCGCGCTCCTATGCAGATCGTGTCAATTTCTTGGCGGACGGTCGT  
ATCGTGAACCAGTTGTTTGATCCACCATCGAGGAAATCTTGGCCACGATGAACGGAATT  
GAGGATATTGCC

>RXN03060-downstream  
TAATGAATTCCGGTTCCACAATG

>RXN03065-upstream  
GACGGCGCAACTCTGCATTCTTCGCCTCAGCGTGCGTGCGAGTGTTTGCACTGATCGTG  
GGCTTCTTTGTAAAGAGGCCAGCCCGCTAAGCTAGGTCGC

>RXN03065  
ATGATCAGCATTGGAACCGACCTCGTTTACATTTTCGGCGTTTCGCAGAGCAGCTTGCACAG  
CCGGGAAGTTCTTTCATGGAGGTGTTTTCCGCAGGGGAGCGTCGTAAAGCAAATGAACGC

CAGGCAAGCCGCTACGCCGAGCATTGGCGGGGCGGTGGGCGGCAAAAGAATCCTTTATT  
AAGGCCTGGTCACAGGCCATTTATGGCCAGCCACCCGTGATCGCCGAAGAAGCCGTGGTG  
TGGCGGGACATCGAAGTTCGCGCAGACGCGTGGGGGCGCGTCGCGATCGAATTGGCGCCC  
GAATTGGCCGAGTGGTCCGGGAATCCATCGGGGAGTTTTCCAGCAGCTTGAGCATCAGC  
CACGACGGCGACTACGCGGTGGAACGTGCGTGT

>RXN03065-downstream  
TGACTATCCAGTAGCCACGGAGA

>RXN03079-upstream  
GAGCGGGGTTGCTATCGGCCGAAAGTTTAGGGTTTTGTTCAATCTGTTGGTTAGTATTGC  
TTGGGTAAACAAGTCATAACAATTTTCATTAAGGGTCGTT

>RXN03079  
TTGTCGCGCACAGGTGTTTCGAAAAAACCAAGCTCACCGCTCCTGTTGTCATCATCGGC  
ACCCTCGTCTTGTGATCATCGCCTTCACCGCTTCCCTCATGCTGGGTCCCGTGACGGTT  
CCATTGAATGAGCTTGCAACCAACCCCGTTGTACCGATATCCGTGCACCACGCATTATC  
ATCGCAGCATTGGTGGGTGCGGCGCTGGCTGTCTCCGGTGCGATCATGCAGACGGTGT  
CACAACCCGTGGCGGATCCCGGCATTGTGGGTGTGTCTCCGGTGCGCTGTTGCAGCT  
GTCTTGGCGATTGTACCGGTGCGAGTTTCTTTGGCCAATGGACCGTTCCTTTTGGCGCC  
TTCGTGGGCGCATTGGTACCGGTGGCTGTGGTATATTTGATCGCTAGTTCCCGCGCGATG  
GATGGCCGTGGCGCAGATCCGGCCACGTTGGTACTGGTGGCATGGCTATCACTGCCTTT  
TTGGGTGCTGTTATTTCCAGCGCCACTGCGAACGCACCACAAGATTCTGAGCTTCGATCC  
GTGACGTTTGGCTCAACGGCGATCTGGTATCTCGGACGTGGGAACATGTGGGCGTTGCA  
ATAATCCCCATTATCGTTGGGTGATTCTAGCTATCGGCGGTTCCCGCATCTGAACCTG  
TTGCTGCTGGGTGATTCCACAGCGCAAACATCTGGACTCAACGTCAACCGCGCACGCATC  
ATTTTGCTAGCACTTGCGGCACTGCTCACCGCCACAGCTGTTGCGGTCTCCGGCACCAT  
ACGTTTGTGGATTGGTAGTACCCACCTGGTGCGCATTGTTTTAGGTGCCGATCACCGA  
GCGTTACTCCCGGCCGCCGCGATTTTGGGCGCCACGTTTGTATCGTTTCCGACACTGTT  
GCCCCGATGATCTTCTCCCCATCGTCTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGC  
TCACCAATTTTCCTTTATTTACTGCTCAGCATGCGCAAGCGACGCGGATTGGGGCTG

>RXN03079-downstream  
TAAAACTCATGCCTCAATTAGT

>RXN03080-upstream  
CTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGCTCACCAATTTTCCTTTATTTACTGCT  
CAGCATGCGCAAGCGACGCGGATTGGGGCTGTAAAACTC

>RXN03080  
ATGCCTCAATTAGTTGAAATTCGTGATCTCAACGTTGAATTCCCTCTCGCCATGCAGTG  
AAAAACGTGTCTTTTTCTGCACCTGCTGGAAAAAGTCACCGCACTGATTGGCCCAAATGGT  
GCTGGTAAAAGTACTGCCCTTTTCGGCGATTGCAGGATTGGTTGAATCCACCGGCGAGGTA  
ATGGTTGGTGGGAGTGGGGTTGCGTCGAAAAGCGCTAAAGCCCGAGCCCGCTGCTCTCA  
CTCGTGCCGCAAAACACCGAGTTGCGCATTGGTTTTAGTGCACGCGACGTTGTGCGGATG  
GGCCGTACCCGCATCGTGGCCGCTTCGCCGTGGAGACCGACGCAGATCGACGCGCCACC  
GATGACGCCCTGCGCGCCATCAACGCGCTCGACATCGCCGAGCAGCCCGTCAACGAATTA  
TCGGGCGGCCAGCAGCAGCTCATCCACATCGGCCGAGCGCTCGCCCAAGACACCGCCGTC  
GTGTTCTCGACGAGCCCGTCTCCGCCCTTGATCTACGGCACCAAGTTGAAGTCCTTCAA  
CTCCTGCGCGCCCGAGCTAATTCGGCACCAACCGTGATCGTCTGCTTACGATCTCAAC  
CACGTTGCCCGTTGGTGCGACCATGCAGTGTGATGGCCGACGGCGAAGTTGTCTCCCAA  
GGTGACATCCGCGAGGTGCTCGAACCTGCCACACTGTCCACCGTGTACGGACTGCCCAT  
GCGGTGCGCGATGATCCCGAAACAGCTCACTTCGCGTGATCCCGCATCAAATCCCTTT

>RXN03080-downstream  
TGATTGAAAGTTTGACTTAAAAA

>RXN03081-upstream  
ACGGAATGCCATTGCGGTGCGCGATGATCCCGAAACAGCTCACTTCGCGTGATCCCGC  
ATCCAAATCCCTTTTGATTGAAAGTTTGACTTAAAAACCC

>RXN03081

ATGAAAAAATCACTCATCGCCATTGTTGCCAGTGCGCTCGTGTTAAGCGGCTGCACCTCT  
GATTCTTCTGACTCTTCCGGCACTTCCGGAATGTGGAAACCACTTCGATTACAACCAGC  
GTTGCCGCGAGCTGACGGCGCATCCACGACCGTCACACTCGACGATTCTCCATCACC  
TTAGAAATCCAAACCAGAGCGCATCGCCGTACTACCCAGAGGCAGCATCCTTGTTCTC  
CCCATCACAGGCGCCGACCGCGTCGTGATGACCGCGAAATGGACACCGCTGACGAAGAA  
ACCGCAGCTCTGGCCTCCCAAGTGAATACCAAGTCAAAAACGGTGGCAGGCTCGACCCC  
GAACAAGTTGTCGCGGCGACCCAGATTTGGTGATCGTCAGTGCGCGTTTCGATACCGAA  
CAAGGCACCATCGACATTTTGAAGGCCTCAACGTCCCG

>RXN03081-downstream

TAGTTAACTTCGATTCAGACGCT

>RXN03082-upstream

CAGAAAGCAATCGCAGAAATCGATGCAAACCGCATTCGACATTCGACAAGCCTGCCACCTC  
CCCCACTGTGCTCACTTTGATGCAACGCGGACACGCCAA

>RXN03082

ATGGTCATGCCAGAATCTGCCATGCTCACCGGCCTGATCCGCGAAGCCGGCGGCACTCCA  
GTGGTAGATTCTCTCGGCGCGGTAGGCACCATCACTGCAGACCCAGAACAAGTTGTTGCG  
ATGGCACCTGAGATCATCATCATTAGGACTTCCAAGGTAAAGGCCGAGAGAACTTCGCT  
AATTTCTCTCCAACCCAGCGCTAGCCAACGTTCCCGCCATTGAAAACGACAAGATTTTC  
TACGCCGACACTGTCACCACTGGAGTTACTGCAGGTACCGATATCACCACTGGTCTGCAG  
CAAGTGGCAGAAATGCTGAGC

>RXN03082-downstream

TAGTTTTGAGATGTTGAAACTAG

>RXN03084-upstream

CCACCCCCACGTCTAAGTTTTCCCTATTTACACACACCTGACCGAAGCTGTAAGGTTTG  
CCTAATCTTTTTCAATCTAAAGTCAGGATATTCACAGCCC

>RXN03084

ATGTCATCTCGCAGAAAATCTCCTCCGCACTGATCGTGCTTCTCGCAGCAGCACTACCT  
CTTACTGCTTGTTCTCCAGCTCAGAAGAGGAAGCATCCACCAGCTCTGCGACTCGCGAA  
TTCACAGACGCTCACGGAACAACCGAAGTTCCCGAAAATCCTCAGCGCGTCGTTGTCTC  
GAGCCACTTGAGCTAGACACCGCAATCGCCCTCGGAATCACCCAGTGCGTGCAGCTGTC  
GCCAACAACGTCACTGGTATTCTGCATATCTCGGCGTCGATGGAATCGAGCCTGTGCGC  
ACCGTTTTCTGAGCCAAATATCGAAGCGATCGCTGCTCTCGAGCCCGACCTGATCCTGGGC  
ACCGATTCCCGCCACGCCGAAATCTACGACCGCCTCGAATCCATCGCCCCAACCGTGTTT  
ATGACAACCCATGTTGATCCGTGGAAAGACAATGTCGTCTTCATCGGCGATGCATTGGGC  
AAGAAGCAGGAATCCGAGGATCTCATCCAAGGCTTTAATGACAAGTGCGAAGAGATCAAG  
TCCGAGCATGATGTGCAAGGTAAGACCGTCAACATGATTCTCGTCCCGCGACGAGCAAAC  
ATGAGCCTATACGGCCCGACCTCATTTGCCGGCAGCTCTTTGGAGTGCGCAGGACTCACC  
ATTCCTGATCAGGAATGGAAGGATGACCTCCAGGCCGACATCGCTCCTGAGAACTTCATG  
CTCGCCACCGCCGACTACGTCTTTGTACCGCAACTGATGTCACCGATGAAAATGAGCTC  
CCCGAAGTAATCCGAGAAAACCGCGAACAGTTCCCATCACTACCCTTGTCGATACCAAGC  
TACTGGGTATCTGGCGTCGGTCCACTTGCGGCGCAGCAAAGTCTTGGAAGACATCGATGCC  
TTCCTCGACGCACAGCAA

>RXN03084-downstream

TAATGTCCACAGCTCTCCCGAT

>RXN03095-upstream

AACGCCTCAATTAGTGCCAGACCTTGCCGACCGCAGACCAAACCTTACCATTTCAAACCA  
TCCCTAGCCACAACAACGGCAGTTGTGCAATGATCTGCGT

>RXN03095

ATGAATGCAGATAAGAAAATGTGCGGAATGAACCCGGATAGCCAATACGTGGAACCTTGCC  
GTCGAAGTTTTTCGGAATCTCGCGGACGCCACTCGAGTTGCGATCATCTTGGCACTTCGA  
AACAGTGGTGAACCTTCCGTAAACCACCTCGCGGACATCGTCGATAAATCCCCCGCAGCA



GTTTCCCAACACCTCGCCCGGCTGCGCATGGCCGAATCGTGTCCACCCGTCAAGAAGGT  
CAACGAGTTTTCTACAACTCACCAATGAACACGCATCACAGCTAGTCTCCGACGCTATT  
TTTCAGGCGGAACACACCATTTGCGGACGGCCAGACTCCCCACACCACCGAGAACGA  
GAACAATCA

>RXN03095-downstream  
TGACCACCCACAGTCACCAAGAA

>RXN03097  
ATTTTCAGCCAGTGCAGGTGCTATAGGTTGGTTAATTTTAGAATATATTTTTAAAAAGACG  
ACAAGTTTACTTGGACTTTTACTCGGTGCATTAGCAGGATTAGTTGTTATTACTCCTGCA  
GCAGGATATGTAACATATCTTAGTGCAACAATAATGGCTTAAATAGGAGGTATCTGTTGT  
TATATTGTCATTAATTACATCAAGGTAAACTAAAATATCATGATGCATTAGATGCATTT  
GGTATTCATGGTGTGGTGGTATTATTGGTGCTGTTTTAACAGCAGTTTCCAAAGTAAA  
AAAGCCAATCCTGACATTGAGAATGGCTTTATTTATACTGGTGACATACATATTATACTT  
GTACAAATATTATGTGTAACAGCAGTTGTAATTTTTAGTATCGTCATGACGTTTATTATT  
GCGAAAGTAATTAAATTAATTACACCATTATCTGTTACGGAACAAGAAACGAATATAGGA  
TTAGACAAGATTGTTACGGTGAACATGCTTACTTTGAAGGTGAGCTAAATAGATTCAAT  
AAACATATTTCGATAT

>RXN03097-downstream  
TAGAATATATTTACATAGAATAT

>RXN03103-upstream  
ATCTTCAGAGTCACTTCTTTCAGTGTCAATTTTTCTCGGCCCTAATCCCCCGCTGGAGTTC  
AATCAGCGATTGCAACCTTTTAGATATATAAGGAGACAAC

>RXN03103  
ATGTCTGCAAAGCGTACTTTTACCCGTATCGGTGCGATTCTTGGAGCAACTGCATTGCC  
GGAGTTACCTCACC GCCTGTGGTGATTCAAGCGGTGGCGACGGATTCCCTCGCAGCCATT  
GAAAATGGTTCTGTCAATGTGCGGCACCAAATACGATCAGCCTGGTCTTGGCCTCCGCAAC  
CCAGACAACTCCATGAGCGGTCTCGACGTGGATGTTGCTGAATACGTAATTCAACTCCAT  
CGC

>RXN03103-downstream  
TGATGACAAG

>RXN03109-upstream  
ACTGGCGCTTCCCGATGGTCAATCATTGGCCTTTGGTGCCCAAACCTGGCGAGTTGTTGCT  
CCGCGCATCCGCGCAACTGTATGTGCAGGGCGGCGAGTAG

>RXN03109  
ATGGTTGTGAAGGAGGTTGACGTGCAAAAAGCAAAAAGCTGGCCGGGTGCCTGGTGCTATA  
GCTAAGCGTCGGACCGTGCGGATTGTGCTGTTTGTGCGCGTGGGCGCGATCGTGATTGCG  
GCGTCGCTGTGGTCGATTCTGGTCGGCCAATACACCATCCCGATTGCGGATCTACCTGCG  
ATTTTAGCCTCCGGTCCGACCGGTGCGCAGACGATGGCGGAACAAGTCGTGTGGCAAATC  
CGCATGCCGCGCATCGTGCTGGGACTGCTCGTGGGTGCCGCTTTGGGCGTGGCCGGCGCG  
CTGTTGCAGGCGGTGTTTTCCAACCCGCTGGCGGAACCGTCGATCATCGGCGTGACCTCC  
GGCGCGGGCGTGGGTGCTGCTGCGGTGATCGTGTTAACCTGACATTTTGGGCACATCC  
ACCGTCGCAGTCGGCGCGTATTATTACCGCGGTGATCACCACGATTTTGGTATATCAGCTG  
GCCAGAAGCCGTGGACGTGTGCAAGTGATCAACCTGATCCTGACAGGCATAGCCATTAAT  
GCAGTATCCGGCGCGCTGACCTCAGTTCTTGATCTACATCGCGCCGACGAGCTCCCGCGA  
AGAAATATTTTCTGCAGATGGGTTCCCTCACGGCTCGCATGGCGCACGTCAACGT

>RXN03110-upstream  
AATGAGTGAACCTGCGCTTGAACCTATACCCCTGGGGTATTACTGTAGATTCTCAATACC  
CCGAGGGGTATCTAGTTTTTACGTTGAGAAGGAGAGCTCA

>RXN03110  
GTGCTTATTGAACGCATCTACGACGAAGACCTTGCGCAGGCCAGCTATTTTCATTGGCTGC  
CAAGCCCACAACACCGCAGTCGTGGTTGATCCGCGTCGCGATATTGCCGTCTATCTGGAC

ATGGCCAAGAAAAACGGAATGGAGATTGTTGGAGTTACCGAAAACCCATATCCATGCGGAC  
TATTTGTCAGGAACCCGTGAGTTAGCTGCTGCAACTAATGCCACCATGTACGTCTCAGGG  
GAGGGCGGCGCCGATTGGCAGTATGAATTCGACGCCGAGCGAATATGCGACGGCAGCGAG  
ATTGCGCTGGGAAATCTGGTGCTCACAGCTGTTACACCCCCAGGCCATACCCCGGAACAC  
TTATCGTTTCTGCTGAAGGACGGCGCGTTTCGAGATGAGCCAGGATTTCATGCTCACTGGC  
GATTTGCTTTTCGCGGGTGATCTTGGCCGACCAGATTTGCTCGATGAAGCAGCTGGGGGA  
GTGGACACTCGTTTTGAGGGGGCTCGCCAAATGTTCAAGAGCTTGAAGGAAAAATTCCTG  
ACATTGCCTGATCACATCCAGATCTTCCCTGGTCATGGTTCCGGTTCCGCGTGTGGCAAA  
GCCTTGGGTTTCGTTCCCTTCAACAACACTTGGATATGAACGTCATTTGCGTGGTGGGGA  
AAGTATCTGGAGGCAGATGATGAACAAGGATTTCATTGATGAGCTTCTGGAAGGCCAACCT  
GATGCACCTGCATACTTCGGCAGGATGAAGAGGCCAAAATAGGCAAGGGCCCGCAATTATG  
GGCGCTCGCGAGCTGTTGCCACAGCTGGAAGCTTCTGATCTGCACGACGTCATTGTTGTT  
GATACCCGCTCAGCCGATGAAGTTACCCAGGGCACTGTAGCTGGTGCAGTGAATATTCCT  
GCGGGCAATTCGATGGCGAAATTTGGCTCGTGGACCGTTGATCCCGAGAAGGATTCCCGA  
GCTTTGGTTCTGCTCGCGGCAAGCCAAATTTGGTGCATGGAGATGTGGGACCACATGGTT  
CGCGTGGGAATCGATAATGTTGCTGGTTTTATCACCAACTTTGATGGGGTGGACCTAGTT  
GCACCGCAAACTGTGTCCCGAGATCAGCTGGATGAATTGGAATACGATCTACTTCTTGAT  
GTCCGCAACCCGAGTGAAGTCAAGAAGGCTACATCCAGGAGCACTCCATATTAATGGT  
GCATCCGTGCTGTGGAATCTGGAGAACTGCCACGTGACGGAAAGATCGTGAGCTACTGC  
AAGAGTGGAACACGCAGCTCAATCGCCGCAAGCACCTGCGTAATGCTGGTTTTGATGTG  
GTGGAATTCAGGATCCTATGACAACCTGGGTCCGGCACAAC

>RXN03111-upstream

CGTGACCGAATTGAGCAGGAACCTTCGGGGCCAGCCGACTGATTAACCGCTTTGGCCAGGA  
GCCTTTTGCTTCGCTTTTCGCCGGCCAAGGATATGACTGG

>RXN03111

TTGAAGACCCCTTCGTGCCGCGGTTGCCGAGGTGCAGGCACCAATGTTAGTGACATCGTC  
GAGCGCGCAAATGCGCTGCTTGCACTAGTTGCAGATGATCTCATTGGCACCCTTCCATTT  
GGTTTCGATCCAGTGGCTTGGGCTAACAACCTCCGAAGATCCAGCTTTCGATACTGCACAA  
TCTGCAGTGAGCGTGCCGGGTATCTTTGTCTCCAGATCGCAACCCTGGATTCCCTTGAG  
GCGCAGCGCCTTGATGTGGATCAGGCTGTGTCCAGCATTGGTCATTCCAGGGCGTATTG  
GGCGTGCACTGCTCAATGATGCGACTCGTGCTGATGAACCTCGTTGCCATTGCGCAGTTG  
ATCGGTGCAGCGATCACCCGCACCGCACGCATGACGGGCTGATCGCGCAGGGCGACAAC  
ATGCCGATGCTGTGATCGCCGGAATTTCCCGCGAACAGCTTCAGCAAGCTATCGACGCG  
GCCTGCGCCGAAGTCCCTGCGGAGATCCGCCCGGTTATCGGTCTGCGCAACTCACGCGAT  
TCTTATGTTTTGGTTGGCCGCCAGACGACAACGCTCGCGTTGTTAAGGTCATTGAGGCA  
ATGGCTGCCAAGGATAAGAAGGCCATTGAAGATAAGCTGCGCGGCGGTTCCGCGTTCAGC  
CCCCGTATTACTCCGCTGAAGGTGCAGGCTGCTTTCCATCACCCAGCTATGAACATGGCT  
GTGGAGCAGACCGTGGCGTGGGCAACCACTGCTGGTTTGGATGTGGAACCTACCCGCGAG  
ATCGCCGCTGATGTTTTGGTTAAACCTGTGATTTGGGTAGCACGCGTCAACGAAGCGTAT  
GAGGTGGCGCTGCTGCTTCCCTCGACGTTGGACCAGATGGTGGCATCGTTAAGCTGACT  
GCCAACATCCTTGAGGGCCGCGGCGCGGATTCCCTTCTATGTTGGTGACGCCGAGGCCAG  
GCCAAGATATTTGATGCTGGCATGGCACCTGAACCTCCAGTGGATTACCAGGAGTTCGCA  
CCACGCGTTGAGCACGTTGATGGAACCCACGCTGGTTACCAAGTTCAGTGAGCTGACC  
GGCCGCACCCCAATGATGCTGGCTGGCATGACCCCAACCACCGTTGACCCTGCCATTGTT  
GCAGCCGCTGCAAACGGTGGACACTGGGCTGAGCTCGCTGGTGGCGGACAGGTTACCCCA  
GAGCTGCTGGAAACCCACATCGCACAGCTCACCGACATGCTTGAGCCAGGTATCAACGCC  
CAGTTCAACTCCATGTTCTTGGATCCATACCTGTGGAAGATGCAGATTGGTGGCAAGCGC  
CTTGTTCCTAAGGCCCCGCGCTAATGGTGCATCCATCGACGGCATCGTCATCACCGCCGCG  
ATTCCCTGAAAAGGATGAAGCTGTTGCATTGGTCAAGGAACTGATGCGTGATGGTTTTCCCT  
TGGATCGCATTCAAGCCAGGTGCCATCAAGCAGGTTAACTCTGTGTTGGCTATCGCTAAG  
GAAGTTCCAGAACTCCCCATCATCATTCAGATTGAGGGTGGCGTTGCAGGTGGACACCAC  
TCTTGGGAAGACCTCGATGAGCTGCTGATCGCCACCTACGGCAAGGTCCGCGCACTGGAT  
AACGTGGTGCTGTGTGTCGGCGGTGGCATTTGGCTCACCTGAGCGCGCTGCTGATTACGTC  
ACCGGTTCCCTGGTCCACTTCCCTACGGCCTGCCAGCTATGCCTGTTGATGGCATCTTGGTG  
GGTACCGCTGCGATGGCAACCAAGGAAGCAACCACCTCCCAGGCCGTCAAGGAACCTCTT  
GTTTCCACCCAGGGCTCTGATGAATGGGTTCCCTGCTGGTGGCGCAAAGAACGGAATGGCA  
TCTGGCCGTTCCAGCTTGGCGCAGACATCCACGAGATCGACAACCTCTTGTCTAAGGCT  
GGACGCCTTCTTGATGAGGTTGCAGGCGATGAGACGGCTGTGCAGGCGCGCCGGGATGAG  
ATCATTGAAGCGATTGGCAAGACCGCCAAGGTGTACTTCGGTGACATCGGATCCATGACT

TACGAGCAGTGGCTCAACCGCTACCTCGAGCTGTCTGGCCCTGTTGATGGTCAGTGGATT  
GATGCTTCTGGGCTGCACGTTTTGCCCAGATGCTGGAGCGTGCCGAGGCGCGTTTGATC  
GAGCAGGATCATGGCCAATTTGAGCCAAGCCTGACGGTGGAGGATGGCGTCGACAAGCTT  
GTTGCTGCTTACCCGCATGCCGCAACCGACCTGCTCACCCCGGCTGATGTCGCCTGGTTC  
TTGGGCTGTGCCGCACGCCGGGCAAGCCTGTGAACCTTTGTGCCCGTCATTGATAAGGAC  
GTGCGTCGCTGGTGGCGCTCGGACTCCCTGTGGCAGTCCCACGATGATCGCTACACCGCT  
GATCAGGTGGCTATTATCCCTGGTGTGCTCGCCGTTGCTGGCATCACCAAGGCCAACGAA  
CCTGTGCTGACCTGCTTGATCGCTTTGTGACGCCACCATCGAGCGCATCGATGAGCAC  
GATTCCTCGCTCCCGCGACATCATGGGCAAAGTGCTTCTCACCTGGCACATTCTGGGCT  
GGCCGCAACATCCCATCGGTGATCCACAGCCTTGGGCATGCTGACAAGTGGTCCCGCTCC  
GAATTCGAAGCAATTCATAGCCCCAACCGCGCCAACCTGGGTGTACGAAGACGCCGAGCAC  
GCGATGCTGACTGTGCCCTTTGGCGGGTTCCACCGCATTTCGGCACCAACCGCTGAGCTGAAA  
ATCCGTTTCACCGACCCCATCGACGCTCTGCCAAGCGCTGTCCCACTGGTCACCCAGGAA  
GACGCTGAAGCCGCGATGGGTGAAGTACCCGCGCATCGCAGCTGGCGGCACCCCTGGCAACT  
GTGAACAATGGCACCGCTACCTGGGAAACCTCCGTCGATGCCGCGCTCATCGCTGACTAC  
AACAACGTACCCGAGGCTACCTGCCAGCATCCGTTGTTCTGTCACACACCCGACCTGAC  
GTGCTGGTTGGCCGCGCATGGCCAGCAGTTTTGCTGCGCTAAAGTCCGCGAGTCATCCCA  
GGCACCGATTCCGCATCCGTTGTGGAAGGCATGCTGTCCCTGGTTCACCTGGAGCACCAC  
ATTGTGCTCAAGTCCGATGTCCCAACCGACCGCGCGCTGAAGGTTTCCGCGACTGCCGAT  
GAGGTAGTCGATACCGACCTGGGTGCGCTCGTGATCGTGCGCGCAGAAATCGCCGACGCA  
GAAGGCAACCTGATTGCTACGTTGGCTGAGCGTTTCGCGATCCGCGGACGCAAGGGCAAC  
GCTGTGCGACGCACCAACACCTCCGCACTGCCAACCACCGTGGACACCCACGCTCAGCT  
CGCGCAGTGGCAACCGTTGTTGCACCTGAATCCATGCGCCCATTCGCTGTGATCTCCGGT  
GACCGCAACCCAAATTCACGTCTCTGATGTTGCGGCTTCCCTGGCTGGTCTGCCAGGTGTG  
ATCGTGACGGCATGTGGACCTCTGCCATCGGTGAAGTATCGCCGGTGCAGCATTC AAC  
GATGAGCAGATCCAACTCCCGCAGCCAAGGTGCTGGAATACACCGCAACCATGCTGGCA  
CCAGTCTTCCAGGTGAAGAAATTGAGTTACGCGTTGAGCGCTCCGCGAGTGGACAACCGC  
CCAGGAATGGGAGAGGTCCGCACCGTTACCGCAACCGTCAACGGCAACTTAGTGCTTACC  
GCCACCGCTGTTGTGGCAGCTCCATCTACTTTCTACGCATTCCCAGGCCAGGGCATTCAG  
TCCCAGGGCATGGGTATGGAAGCACGCCGTAACCTCAGGCAGCTCGCGCTATCTGGGAC  
CGCGCCGATGCACACACCCGCAATAAGCTGGGCTTCTCCATCGTGGAATCGTGGA AAC  
AACCACGCGAAGTAACCGTGGCAGGGGAGAAGTTCTTCCACCCAGACGGCGTTTTGTAC  
CTCACCCAGTTACCCAGGTGGGCATGGCAACTCTGGGCGTTGCTCAGATCGCTGAAATG  
CGTGAAGCACATGCCTTGAACCAGCGTGCATACTTTGCTGGACACTCCGTTGGTGAGTAC  
AACCGCTTGTGTCATATGCTGGTGTGCTGTCCCTGGAATCCGTTCTGGAGATCGCTTAC  
CGTCGTGGCTTGACCATGCACCGCTTGGTGGATCGCGATGAAAACGGTCTGTCCAATAC  
GCGCTCGCAGCTCTTCGCCCCAACAAAGATGGGTCTGACCGCAGACAACGTTTTCGATTAC  
GTTGCGTCTGTTTCCGAAGCTTCCGGTGAATTCCTGGAGATCGTTAACTACAACCTTGGCT  
GGCCTGCAGTACGCGATTGCTGGAACCCAGGCTGGTCTTGCCGCCCTTCGTGCCGATGTT  
GAGAACCGTGCACCGAGTACGCGTGCCTTCATTTGATCCCTGGCATTGACGTGCCATTC  
CACTCCTCCAAGCTGCGCGACGGTGTGGGCGCGTTCCGTGAGCACCTTGATTCCTGATC  
CCAGCTGAGCTGGATCTGGATGTGCTGGTTGGCCGCTACATTCCAAACCTTGGTGGCTCGC  
CCATTCCGAACCTACTGAAGAGTTCTGTGGCATCCATGGCAGAAGTGGTGGAGTCCACCTAT  
GTCAATGAGATCTTGGCTGATTTCAAGGCTGCTTCCGCCGATAAGCAGAAGCTTCCCGC  
ACGTTGCTTATTGAGCTGCTTGATGGCAGTTTCGCATCACCTGTGCGCTGGATCGAGACT  
CAGGATCTGTTGATCAAGGGCCTTCAAGCTGAGCGTTTCGTGGAGGTGGTGTGGCTCT  
GCTCCAACGCTTGCCAACATGATGGGCCAGACCCTGCGCCTTCTCAGTACGCGGACGCC  
ACCATTGAGGTGTTAAACATTGAGCGCGATCGCCAGTTGTGTTGCTACCGATGAGGTT  
GTGCGTGAAGTGGCGGTTGAAGAGACCCAGCAGCTCCTGCAGAAACCACTGAAACCCCA  
GCAACCCAGCAACCCAGCCCTGTTGCAGCTGCAGCCCTGCCACCGGCGGCCCTCGC  
CCAGATGACATCAGCTTCACTCCTTCTGATGCCACTGAAATGCTCATCGCTATCTGGACC  
AAGGTTCCGCCAGATCAGATGGGTGCCACTGATTCCATCGAGACCCTGGTTGAGGCGGTG  
TCCTCTCGCCGTAACCACTCCTGCTGGATCTTGGTGTGGAGTTTCGGCCTCGGCGCAATT  
GACGGAGCAGCCGATGCTGAGCTCGGTGATCTAAAGGTCACCGTGTCCAAGATGGCTAAG  
GGCTACAAGGCGTTTGGCCCTGTGCTCTCCGATGCTGCAGCTGATGCCCTGCGTGCCTC  
ACTGGTCTTACCGGTAAGCGCCCGGGATACATCGCAGAGCGGTCACCGGCACGTGGGAA  
TTGGGCCAGGGCTGGGCTGACCACGTGGTCTGATGAAGTTGTGATCGGCGCCCGCGAAGGC  
GCATCCCTGCGCGGCGGCGACCTGGCGTCACTGTCTCCTGCAAGCCAGCGTCTGCATCA  
GATCTTGATTGCTTATCGACGCAGCCGTCCAGGCCGTAGCCTCCCGCCGCGGCGTTGCG  
GTCTCCCTGCCTTACAGAGGCGGCGCTGCCGGTGGCGTGGTTGATTCCGCAGCTCTTGGC  
GAGTTTGCAGAGCAGGTACCCGACACGATGGTGTGCTTGTCTCAGGCAGCCCGCACCATC

TTGACCCAGTTGGGTCTTGATAAGCCAGCAACCGTTTCCGTGGAAGACACCGCAGAGGAA  
GACCTCTACGAGTTGGTCTCCAAGGAACTCGGTTCTGATTGGCCACGTCAGGTTGCACCA  
AGCTTCGATGAAGAAAAGGTTGTTCTGCTTGATGACCGTTGGGCTTCTGCGCGTGAGGAT  
CTCTCCGCGTTGCTCTTGGCGAACTCGCAGCAACTGATATCGATGTCACAGGCGCAGGCG  
AAGCTGTTGCAGCACAAGCTGAATTCTTTGGACTTGATGATCTCGCAGCTAGGCTCGCGA  
ACAAAGCTTCTTGACTACGCCGACAATGTTGCGGC

>RXN03126-upstream  
TCTTGGACAACATTACCCACACACGGGACACTCAAACGTGCATGAATTCACCTGTCTGTC  
GATACCCAAAAATCACTCCACCACCACTAGGGTGTCTTAT

>RXN03126  
GTGCAGGAACAATCGAAGCAGAAAGACCTCCAGGCTGATATCGCCAGAATCACTGCCGTG  
AAATCGGACACAGTTCCGAATTCAGTCAATGACCTTTGGCGCTGCCTGGAACGATATC  
GTCCGCGGATTCAAGCAACATGAGTTGTGGCTGCAACTCGGCTGGCAAGACATTAAGCAA  
CGCTACCGGCGATCCGTCTTGGGCCCCCTGTGGATCACCATCGCCACCGGTGTCATGGCG  
CTCGCCCTCGGCTTGCTGTACTCCGTGCTGTTCAAAATCCCCATCGCGGAATTTCTGCCC  
CACGTACCGTCGGCTGATCATTGGAACCTTCATCTCCGGATGCATCAAAGAAGGCTCC  
GACATCTTCATAGATAACGAGGGACTCATCAAACAGCTCCCCCTCGGCGCTGTCCGTCCAC  
GTGTACAGACTCGTGTGGAACAAGCCCTCTTCTCGCCCAACCTGGTCATCTGGGTC  
ATTCTCATGATGATCTTCCCCGACCCCTCGGCTGGGACGTCTCCTGATCATCCCCGCA  
ATGTTCTCTCTGGTGATCAACGGCGTGTGGGTAGTCATGTTCTTCGGCATCATCGCCACC  
CGCTACCGCGACGTCTCCCCGTTGCTAGAAGCCGGAACCCAACTCCTCTTCTACGTACC  
CCCATCGTCTGGATGACTTCCACCCTGCAATCCAGAGCGCAGAAATCGGCAACCGCGCA  
CGCTCGCCGAACTCAACCCGCTCTACCACTACCTCGAAATGTCCGCGCCCCCATGGTC  
GGCGCCGACCTCCCCGCCTACCACTGGTGGATCGTCTCGCCTTCACATTGTCGGCCCTT  
GGCCTTGCTCTCCTCGCGATGAAGCAATGGCGATTCCGCGTCAGCTACTGGGTA

>RXN03126-downstream  
TAAGGAGCACCACATGGTATCCA

>RXN03132-upstream  
TAACTTATTTATACATAAAAAACACAATAAAAAACCGCACACGCGGCGAACTTCAATAAAT  
CCCTAGACTGCAAAAAATGGTTAGGCTAACCTTATTTCCA

>RXN03132  
ATGAATGTGAATCAACAGTTGGGAGCCCGCACCGCCATGAACCACCCTGAGACCGCAACC  
GTCCTTCGCTCCATCTCTGACATGGTTAGCACCGAAACCAATCCGCGCCGTAAAAGCCGC  
CTCGAGCAGCTCATTTACGCCACCGCCAGCGCTGGCCCCACTACCCCATTTGCCACGCA  
GCCCAGGCCGCGGTGCAATTAGCCAGGCCAATGCGGGTTTTTGAGCTCCAGAGCTTTGAA  
GGCGTCAAGCACGCACTCCACCACATCGATCTTCGCCCCGCCCTCGAATGGGACATCATG  
GGATTTCCCGAATCCCCGACACGCTGCCCATTTTGCTCAGTGACCTGCGCGACCCCCCT  
TACGCCACCACTGCTGTGCCACCTCAATCCACGCCACGCTCCGCTCACCGATCCACACAT

>RXN03132-downstream  
TGACGCTTCAGGCGCCACCGCG

>RXN03157  
GGCCACCTCGACATCGTGACCCGCGCCGCGCGCAATTTAGCGAAGTCACCATCTTGGTC  
ACCGCCAACCCCAACAAAACCTCAGGACTGTTACCGTCGCAGAACGCATGGATCTCATC  
CGCGAATCCACCGCACACCTGGACAACGTAAAAGTAGACACTTGGGCCTCACTGCTCGTG  
GATTACACCACCGAATCGGCATCGGCGCCCTAGTCAAAGGCCTGCGAAGCTCCCTCGAC  
TACGAATACGAGCTCCCATGGCACAGATGAACAGGCGACTCACGGGCGTAGACACCTTC  
TTCTCTCTACCGACGAGAAATACGGCTACGTGAGCTCCACACTGTGCAAAGAAGTTGCC  
CGCTTCGGTGGCGATGTCTCCGGCCTCTACCTGAGGTAGTGGCAAAGCCGTGACAGAA  
AAATACAGCAACCAGCAC

>RXN03157-downstream  
TAGTTTCTTTTGATCAAGCGTC

>RXN03160-upstream

GAGCATATGGTGC GCGCGGCCGATATGCTGATCAATTCCAACCCCGATCCGCACGCTTAA  
CTTCTGCCAAAAAGTCGTTTTGACCATAAGCTAAGCGATT

>RXN03160

GTGAATCGAATTGCAGAAATCGCACGCAGTTTCGGCGTGCTGGGCTTCAGCGCTTTCGGC  
GGCCCCACCGCGCACCTCGGATATTTCCGCACGGAATTCGTGGAGCGGCGGCGCTGGCTG  
GATGATCGCCAATATTCCGAGATCGTAGCGCTCAGCCAATACTTCCCGGACCTGGATCG  
TCGCAGGTCCGGTATGATGCTGGGCTACCACCGCGCCGGTTTTTCCGGCATGGCGATCGCC  
TGGCTCATGTTTACCTGGCCCTCATTTGGCGCTCATGGCGGCGTTCCGCCCTGCTTTTGAT  
GCGACCTCCGCCAGCTGGACGCTCGGCCTGCTCGCCGACGCGGTCCCGCTCGTTTTCAAA  
CGAGTCAACCGGGCATGGCGCGGTTCAATGGCTTCCACGCCGGGGCGCCGGCCACCATCG  
GGGGTCGGCTCGGGGCATCGCGGTGCTCGGCCCTCCCCAACGGGGT

>RXN03160-downstream

TAACACACCTTGGGGTTCAATCA

>RXN03164-upstream

CTTTTTTGCATCCAGATGCACAAAGCCGTGGCACAACGAGACAACTGAGCACAATGGC  
TGTCATGGCATATCAACCAGCAGACAATCGCTATGACGAC

>RXN03164

ATGATCTACCGCAGGGTGGGAAATTCTGGGCTGAAGCTTCCGGCAATTTTCGCTTGGGCTG  
TGGCACAACCTTCGGTGATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCG  
TTTGATAGGGGAGTCACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTCC  
GCAGAGACCAACTTTGGCAGGATTTTGGCTGAGGATCTCAAAGCCACCGCGATGAGTTG  
ATCATTTCTTCCAAGGCGGGTTGGGATATGTGGCTGGACCTTATGGTTTGGTGGTTCC  
CGAAAGTATCTAGTAGTTCCCTTGATCAGTCCCTGACTCGCTCGGCTTGGATTACGTG  
GATATTTTCTATCATCACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCA  
TTGCGTGACATTGTTGCGTCTGGAAGGCTCTTTACGTGGGTATTTCTTCTACGGTCCA  
GAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGGAGGCTGCCCGCTTCTGATTAT  
CAGCCAAGCTATTCCATCATTAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAAC  
TTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCATTGCTTTCTCACCCTTGGCGAG  
GGCTGCTCACGGACAAATATCTCGATGGAATTCAGAGGGTTCCCGCGCCAGCCAGGGT  
AAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAAT  
GACATCGCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCGC  
GAGCAAAGAGAGTACGGCGCCGGATTACCG

>RXN03164-downstream

TGACCAGTGCATTGATTGGTGCT

>RXN03183

GAAGCCGAAGCAACCGCAGGCAAATTCGAAGTACAGCCCCTCGTAGGTAAAGACGGCGTC  
GGCGTATCCACCCTTGGTGGCTACAACAACGGCATCAACGTCAACTCCGAAAACAAGGCA  
ACCGCCCGCGACTTCATCGAATTCATCATCAACGAAGAGAACCACAACTGGTTTCGCGGAC  
AACTCCTTCCCACAGTTCTGGCATCCATCTACGATGATGAGTCCCTTGTTGAGCAGTAC  
CCATACCTGCCAGCACTGAAGGAATCCCTGGAAAACGCAGCACCACGCCAGTGTCTCCT  
TTCTACCCAGCCATCTCCAAGGCAATCCAGGACAACGCCTACGCAGCGCTTAACGGCAAC  
GTCGACGTTGACCAGGCAACACCGATATGAAGGCAGCGATCGAAAACGCTTCCAGC

>RXN03183-downstream

TAGTTCGGTAATTTAGTTTCATTC

RXC00354 - 5'-Region

GGCTTGTCGGTAAGGCTGCAGGGTAGCGGGAGTTTCCTTCAGATTGGAAGTTCTTTAATTTTCTCGATT  
ATGTACCTCATTTACGCGTAAAGTTTGGGGC

RXC00354 - coding Region

ATGGGAAAGTTACTTTTCGTAGACATCGGTGGCACACTGCTGGATTACTCAAATGAAGTTCCGCGTTCCG  
GCCGTTGACGCGATCCGTAAGGCACGCGCCAAAGGACACCGCGTGTACTTGAGCTCTGGTTCGAAGCAGC  
GCTGAGGTGACTTCTCAGTTGTGGGATATCGGAGTGGATGGCCTCATTTGGCGCAAATGGTGGATATGTG  
GAAAGCGCACAGGAGTCTGTGTTCCACCGCCGTTTGTGGGTGAGGAGACCCGCCACATTGTGGAGTGG

CTCTACAACCGTGGTTTGGAGTTTTATCTCGAGTCCAACAACGGTTTGTATGCAAGCCGTGGTTTCCGT  
GAGGCTTCTAAGCCAGTGTCTCGCCTTTCGGAGAAGACCGAGTGCAGTGCATGTACCCG  
GATATGTTCTGGGGCGCGAGCCTTGATCGTGACGATGTGAACAAGATCAGTTACATCTTCAATTCTCAG  
GAAGATTTGGACGCGAGCGCGTGAGGCGTTCCCTAACCTGGAGCACACCACGTGGGGTGGTCAGACGGGT  
GCGTTGTTCCGCGACGATCGGTGTGTCTGTCAACAAGAAGATCGGCGTGATCGCCTGCTGAAGTACCTG  
AACGCAGATCGCGCAAACACCATTGCGTTCGGCGACAGCGATGAGGATCTCTCCCTATTTGAGGCGAGC  
GCTTACGGCGTTCGCGATGGGCGAGGCCACCGAATCGCTCAAGGCTGCTGCTGACCTGGTCACGGATGCT  
GTTGGGACAGGACGGCTTGCGCAATGCGTTTTTAAAGCTTGAGCTTATCGACGCC

RXC00354 - 3'-Region  
TGACCCCATCAAAGAACTTCCCA

RXC01748 - 5'-Region  
ATCACCAAATGTGGCGGTTTTGCGTCGAAAAGCGTGCTCTTTCTACACCTCTTTGAGGTTCATTTTCGC  
GGTTTCTCACAATCGCCTATTGTTAAGTAC

RXC01748 - coding Region  
ATGGCAGACGCGAAAAAGCAGGCGGATAAAGCCGCCAAGAAGCAGGTAAGAGCAGCCAAGAAGGCACAG  
CGCAAGGAGACTCGCTCACAAATGTGGCAGGTCTTCAACATGCAACGCAAGCAGGATAAGGCTCTTATT  
CCGCTTCTGTTGCTCGCTATTCTTGGTATCCCGCTGGTCTTTTCTCATCGGTTTGATTTGGGGTGGT  
CAGTGGTGGATGCTTCCGATCGGCATTGCTGCAGGTGTTGTAGCTGCAATGTTTATTTTACCCGCTCGC  
GTTGAGCGTGACGTGTACAAGCGCGCCGAAGGTGAGCAGGGTGCTGCTGGTTGGGCTGTGGAGAACCCTC  
CGCTCTGGCGTGGGCATGACCTGGCGCACCAAGACCGCTGTTGCAGTGACCACTCAGATGGATGCAGTG  
CACCGCGTCATTGGTCTGTGTGGTGTGTGCTGGTGGCGAGGGCTCCCCCTCACCGCCTGAAGCCAATG  
CTTGGCGAGCAAAGAAGCGCCTGAACCGCGTGGCACCTGGTGTTCAGTGTATGAAATCATCACGGGC  
AACGGCGAAGGCCAGACCCCTATCGCGAAGCTGCAGCGTGAACCTGGTCAAGCTGCCTCGCAACTACAAG  
AAGAACGACGTCGCTGCCCTGGCCGCTCGCATTGAGGCTATGGACAATGTGCGAAACGCTCCTGGCGGA  
TCTTTGCCTAAGGGTCCATTGCCAAAGGGCGCAAGCATGTCCGGTATGAACCGCCGCGCTCGCCGACAG  
GCTGAACGCAAGGGCGAGGCT

RXC01748 - 3'-Region  
TAAAGCCTTTTCGCTTTTCGCGTC

RXC01749 - 5'-Region  
GGTTTTTTCGCTGCTCTGGTTTAGGGACTGGTTTTGGGAACGTGCCAGTTCCACATCAAATAACGCTGA  
GGTCGTACTTAATCCATGAGATCATGAATGG

RXC01749 - coding Region  
GTGAGCTTCCTTGTAGAAAAATCAATTACTCGCGTTGGTTGTTCATCATGACGGTCCGACTATTGCTCGGC  
CGCATCAAAATTTTCGGGTTCGGTCTCGGCGTCGCGCTGTACTGTTGTAGGTCTAGCGCTATCCACC  
ATTGAGCCGGATATTTCCGTCCCATCCCTCATTTACGTGGTTGGACTGTCGCTTTTTGTCTACACGATC  
GGTCTGGAAGCCGGCCCTGGATTCTTCACCTCCATGAAAACCACTGGTCTGCGCAACAACGCACTGACC  
TTGGGCGCCATCATCGCCACCACGGCACTCGCATGGGCACTCATCACAGTTTTGAACATCGATGCCGCC  
TCCGGCGCCGGCATGCTCACCGGCGCGCTACCAACACCCAGCCATGGCCGCAGTTGTTGACGCACTT  
CCTTCGCTTATCGACGACACCGGCCAGCTTCACCTCATCGCCGAGCTGCCCGTCTGCTCGCATATTCCTTG  
GCATACCCCTCGGTGTGCTCATCGTTATTCTCTCCATCGCCATCTTCAGCTCTGTGTTCAAAGTCGAC  
CACAACAAAGAAGCCGAAGAAGCGGGCGTTGCGGTCCAGGAACTCAAAGGCCGTCGCATCCGCGTCACC  
GTCGCTGATCTTCCAGCCCTGGAGAACATCCCAGAGCTGCTCAACCTCCACGTCAATTGTGTCCCGAGTG  
GAACGAGACGGTGAGCAATTCATCCCGCTTTATGGCGAACACGCACGCATCGGCGATGTCTTAACAGTG  
GTGGGTGCCGATGAAGAACTCAACCGCGCGGAAAAAGCCATCGGTGAACTCATTGACGGCGACCCCTAC  
AGCAATGTGGAACCTTGATTACCGACGCATCTTCGTCTCAAACACAGCAGTCGTGGGCACTCCCTATCC  
AAGCTCCAGCCACTGTTTAAAGACATGCTGATCACCCGCATCAGGCGCGGCGACACAGATTTGGTGGCC  
TCCTCCGACATGACTTTGCAGCTCGGTGACCGTGTCCGCGTTGTGCGACCAGCAGAAAACTCCGCGAA  
GCAACCAATTGCTCGGCGATTCTTACAAGAACTCTCCGATTTCAACCTGCTCCCACTCGCTGCCGGC  
CTCATAGTCCGTTGCTTGTGCGCATGGTGGAGTTCCTACTACCAGGTGGAAGTCCCTGAAACTCGGTT  
AACGAGGTGGACCGCTAGTTGTTGCGCTGCTGCTCGGCATGATCAATCGCACAGGCAAGTTCGTCTGG  
CAAATCCCTACGGAGCAAACCTTGCCCTTCGCCAACTGGGCATCACACTATTTTGGCTGCCATCGGT  
ACCTCAGCGGGCGCAGGATTTGATCAGCGATCAGCGACCCCAATCACTACCATCATCGGCTTCGGT  
GCGCTGCTCACTTTGTTTCATCTCCATCACGGTGTGTTGTTGGCCACAACTGATGAAAATCCCTTC  
GGTGAAACCGCTGGCATCCTCGCCGTACGCAAACCCACCCTGCTGTGCTGAGTTATGTGTCAGATGCC

TCCCGCAACGAGCTCCCTGCCATGGGTTATACCTCTGTGTATCCGCTGGCGATGATCGCAAAGATCCTG  
GCCGCCCCAACGTTGTTGTTCTACTTATC

RXC01749 - 3'-Region  
TAGCATTGACCCCTTAAGCGCAG

RXC01971 - 5'-Region  
AGGTCTTGTATTATTCGGCTACTGATTAGCTAGCTGCGCTCCGATAGGATTCTTAGTTTTTCAGTTCAGT  
ATCTTTGAGCCACGGCTAGAATGTGAATCCT

RXC01971 - coding Region  
ATGTCTAAGAAGAAGCCTCGCCCCATTCCGGTTCCTGCCCAATTTATCCCTGGTCTCATTGATGCGCAT  
ACACATTTGGCATCGTGTGGAGGAGATCTTGAGGGTTGGTGGAAAGGGCCAAGGAGGCGGGCGTCGAA  
AAGCTTTGTACCGTCGGTGATGGTTTGGCTGAGGCCGAGCTTGCCTGGAGGCCGCGCAACAGTTTGGC  
AATGTGTTTGTGCTGCGTGTGCGATTTCATCCGACGAAGGCTGATCAGTTGGATGGGGCTGCGCGTGC  
CTGACGCAGATGGCGGCGGATCCGAATTGTGTGGCCATTGGTGAGACTGGTTTGGATTTCGTATTGGATC  
AAGCACGATCCAGAGGACACGGCGGCGTTGGATGTGCAAGAGGAGGCGCTGCGCTGGCATATTGATTTG  
GCAATTAGTGCAGATAAGCCGTTGATGATTACCAATCGTGAGGCGGATGCTGATTTGATGCGAGTGTTG  
GCGGATGCTCCACCTCCAAAAGATACGATTCTGCATTGTTTTCTTCGCGCTTGGACGTGGCGAAGGAA  
GCGTTGGATCGTGGATATGTGTTGAGTTTTGCGGGCAATGTGACGTTAAGCGTAATGAGGAGTTGCGG  
GAGGCTGCTCGTATTGCGCCGATTTCCAGATTTTGATTGAAACCGATGCGCCGTATATGACGCCGGAG  
CCGTTTCGGGGGAGTAGGAATGAGCCGTCGTTGATTGGTCATACGGCGCTATGCATTGCGGAGGTTGCG  
GGGATGGCTGTGGAGGATGTTGCGGCGGCTTTGAATGAGAATTTTGATCGCGTTTATGGGGTCACAAAT  
CTA

RXC01971 - 3'-Region  
TAACGTGAGGTAGCTCACAGTCA

RXC02697 - 5'-Region  
TTTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACTGGCTATCCG  
CTCAACCGAACGTGCGATGTAGTAGACGCT

RXC02697 - coding Region  
ATGACACTTTTTCAACGTTTAACCAACCCGTAGTGCTCGGCGGCCCTAGCAGGTGTTTTGCTTCTGCTC  
GGCTCTTTCCGGTGGCGGTGCCATTCCGTACCGTGCGGAGTGCTCGATGCGTTGGGGCTTAACCTTCCTT  
GCTTTTGGCCACGCGCAGGGTATTTCCAATACCGTGTTGTGGGTGGGCGAGCTGCTGCTGATTGGCGCG  
TGGGTTACCTTGGACGTCGGTTGTTCAAGAAAAAGTCGCTGATGACACCGCAGACGCTGCTGACTTA  
GGTCTTGTAAGCGCACGTTGTATGCCATGGTGGTGGCCCTCATTTTTGCGGCACCAATGATGTGCGGT  
GATGTTTTATTCCTATCTCATGCAGGGCGCGATGCTGCGTGATGGCTTCGATCCCTACACTGAGGGCGCT  
GCGGTAAACCCCTGGCCCCATGTTGCTTGAGGTCTCTCATGATTGGCGCAACACCACGACCGCTATGGT  
CCACTACACCTGTGGATTGGAGACATGATCACCACGTTGTGGGCGATAATGTCACCTTGGGCGTCGTC  
GCTTACAAGATCTTGTGATCATTTGGCCTTGCTGTGACAGGCTGGAGCATTGTCCGCATTGCACAACAT  
TTTGGAGCCAACCCAGCAATTGCATTGTGGATTGGTGTGGCCAATCCTGTGATGATCATCCACATGATC  
GGCGGCATGCACAATGAATCCCTCATGGTGGGATTGGTCAGCGTCGGCTTGTTGCTAGCACTGAAGAAG  
CGTTTCGTGGCAGGTGTGGCACTCATTCAGTGGCTGTGTGCTGAAAGCTACAGCGGCGATTGCACTT  
CCTTTTGTGGTGTGGATCGGCATGCATCATTTGCGCAGGATTCTTAGCCACCAAAAAGGGCAAAGACTCC  
CCTACCCTTAAGCAACAGGTCCCCGCGTTCTTTGCCACTGGAGCTGCAGGTGTTGCTGTCACTGGTGT  
GTTGTCACTGCGATCACTTGGGCGTCTGGCGCTTCGTGGGGCTGGATCAGTGAGATCAGTGGCAACAGC  
AAGGTAATCAACCCGCTGGCTTCCCTTCTTTGGTGGCCAGTGTGATCACCATGGTGGCTGAAGTGTTT  
GTTGACGATTTTCGACTACAACGCAGTGGTTAATGTTGTGCGCTCAATCTCCATGCTGATCATGCTTGGC  
GGGTTGGTTCGATGTTGGTGGCTGTTCCGCCAGAACGAACGCAGGGCGGTCACTGGTACAGCAGCGGCT  
TATGCCGTGGCTTTTGTGTTCAATTCTGTGACCTTGCCGTGGTACTACGCCAGCTTGATCTCTTTGCTC  
GGCACATTTAAACCACCGATGTGGTTGATTGCTTTCGAGCGGGTGCTTCGGTGTATTCGCGCTGATG  
TTTACCGGAAGTGGAACACCAGCTGTACAACATCGTTACGGTGATCATCGCAGCAATTATCGCGTGG  
CTTGCCACCGTGGTGATCTTTGATGACACTGACCCTGCAACAACGGCCACGGAGAAACCTCCCCGCAT  
ACCGTTTCC

RXC02697 - 3'-Region  
TAGTTGCATAAGGTAAACCGCCA

RXS00148 - 5'-Region

CTTTGAGGGCAGCGCGCATGCGCCCGATGGTTATTTGAACATGACAATTGATGCCGCGGCGACGCTGGC  
TGACCTGCTAGATGCTTTGGGAGCTTAAATC

RXS00148 - coding Region

ATGACGTCGATCCCTAATTTTTTCAGACATCCCATTTGACTGCTGAGACACGTGCATCGGAGTCACACAAC  
GTTGACGCCGGCAAGGTGTGGAACACTCCCGAAGGCATTGATGTCAAGCGCGTATTCACGCAGGCTGAC  
CGCGACGAGGCGCAAGCGGCGGGACATCCGGTGGATTCTTTGCCAGGTCAAAAGCCATTTATGCGCGGG  
CCGTACCCAACTATGTACACCAATCAGCCGTGGACGATTTCGCCAGTACGCAGGCTTTTCAACCGCCGCG  
GAATCCAATGCGTTTTATCGGAGGAACCTTGCTGCGGGTCAAAAAGGTTTGTCCGTTGCGTTCGATCTA  
GCGACCCACGCGGTTATGACTCGGATAATGAGCGCGTGGTTCGGCGATGTGGGTATGGCCGGCGTGGCG  
ATTGATTCGATTTTGGATATGCGTCAGCTGTTTGTGATGGCATTGATTTGTCCAGCGTGTCCGTGTCGATG  
ACCATGAATGGCGCTGTGCTGCCGATTCTTGCGTTCTATATCGTGGCGGCTGAGGAACAAGGTGTGGGT  
CCGGAGCAGCTTGCGGGCAGATCCAGAATGACATCTTGAAAGAATTTATGGTGCACAACACCTATATT  
TATCCGCCGAAGCCGTGATGCGCATCATTTCCAACATCTTTGAGTACACCTCCTTGAAGATGCCACGT  
TTTAACTCCATTTGATTTCTGGCTATCACATCCAGGAAGCGGGAGCGACTGCCGATTTGGAGCTGGCC  
TACACTCTGGCGGATGGTATTGAATACATCCGTGCAGGTAAAGAGGTAGGCCTTGACGTGGATAAGTTC  
GCGCCTCGTCTGCTCTTCTTCTGGGGTATTTCTATGTACACCTTCATGGAGATCGCAAAGCTGCGTGGC  
GGACGACTGCTGTGGAGCGAGTTGGTGGCAAAATTCGATCCGAAAAACGCCAAGTCCAGTCCGCTGCGC  
ACGCACTCGCAGACCTCTGGTTGGTTCGTTGACCGCGCAGGATGTGTACAACAACGTGCCCCGACCGCG  
ATTGAGGCGATGGCTGCAACCCAGGGCCACACCCAGTCGCTGCACACCAATGCACTTGATGAGGCGTTG  
GCGCTGCCACCGATTTCTCTGCTCGTATCGCCCGAAACACCCAGCTGTTGCTGCAGCAGGAATCTGGC  
ACGGTGCCTCAGTTGATCCATGGGCGGGCTCCTATTACGTGGAGTGGTTGACCAATGAGCTGGCTAAC  
CGCGCGCGCAAGCACATCGATGAGGTGGAGGAAGCCGGCGGAATGGCGCAGGCCACCGCGCAGGGAATT  
CCTAAGCTGCGCATTGAGGAATCAGCGGCACGCACCCAGGCTCGCATTGATTCCGGCCGCCAGGCGCTG  
ATCGGCGTGAATCGCTACGTGGCGGAAGAAGATGAGGAAATTGAAGTCTCAAGGTTGACAACACCAAG  
GTTTCGCGCAGAACAGTTGGCTAACTCGCGCAACTGAAAGCAGAGCGCAACGATGCGGAAGTCAAGGCT  
GCGCTGGATGCGTTGACAGCTGCTGCCCCGAACGAGCATAAAGAGCCAGGGGATTTGGATCAGAACCTG  
CTCAAACCTTGCCGTCGATGCTGCGCGCGCAAAAGCTACCATTGGAGAGATCTCCGATGCTTTGGAAGTT  
GTCTTTGGCCGCCACGAAGCAGAAATCAGGACGCTGTCTGGCGTGTACAAGGATGAGGTTGGAAAGGAA  
GGCACAGTGAGCAACGTGCAACGCGCGATCGCCCTGGCTGACGCCTTTGAGGCTGAGGAAGGCCGCCGC  
CCACGTATCTTTATTGCCAAGATGGGCCAGGATGGACATGACCGTGGACAGAAGGTTGTCGCGTCTGCC  
TATGCTGACCTGGGCATGGACGTGGATGTTGGACCGCTGTTTCAAACCTCCAGCCGAAGCTGCCCGCGCC  
GCCGTGGACGCCGATGTTACGTGGTGGGTATGTCTTCGCTGGCAGCAGGCCACCTCACCTTGCTGCCC  
GAGCTGAAGAAAGAACTTGACGCTCTTGCCCGCGATGACATTCTGGTCACCGTGGGCGGCGTCATTCCG  
CCGGGCGATTTCCAGGATCTCTACGATATGGGTGCCGCCGCGATTTACCTTCAGGAACCGTCATCGCG  
GAGTCGGCGATCGATCTGATCACCCGACTCGCCGCACACCTGGGCTTTGACCTGGATGTGGATGTGAAT  
GAA

RXS00148 - 3'-Region  
TGATCACGGTTTCCTAGAAGACA

RXS00149 - 5'-Region  
TTTTCGTAGGTAAACACAGGTGAAGGCTTTACAAGCTTGTGAACTCCCTACACAAAAGCAATCCAATAG  
CTATCCATAAGCAAGAGAAAGTAAGTCTACG

RXS00149 - coding Region

TTGACTGATCTCACAAAGACTGCGGTGCCCGAGGAACCTTCAGAGAACCTCGAAAACCTTGGTACAAGGCT  
GTGGCCGGTGTTTTCGCGCGCACACAGAAAAAGACATCGGCGACATTGCCGTAGATGTGTGGAAGAAA  
CTCATCGTCACTACACCGGATGGTGTGATATCAATCCGCTGTACACCAGAGCAGATGAGTCCCAGAGG  
AAATTCAGTGAAGTTCTGGTGAAGTTCCCTTCACTAGGGGAACCACTGTTGATGGTGAACGCGTTGGT  
TGGGGTGTACTGAGACTTTTCGGACATGACAGCCCCGAAGAATATCAACGCTGCGGTGCTGAATGCTCTG  
AATTCTGGCACCACCACTTGGGTTTTGAGTTCTCTGAGGAATTCACGGCAGCTGATCTTAAAGTTGCT  
CTCGAAGGCGTGTATCTCAACATGGCTCCGTTGCTGATTCATGCGGGTGGATCCACGTCAGAGGTTGCA  
GCGCGTTGTATACGTTGGCGGAGGAACCGGAACGTTTTTGTGCTGCGTTGACCTTGGGTTCTCGTCTC  
TTGACGGCGCAGGTTGATGGTTTCGCACAGTGACACCATTTGAAGAAGCAGTTCAAGTTGGCAGTGAATGCT  
TCCAAGCGTGCAATGTGCGCGCTATCTTGGTGGATGGTTCCAGTTTTTCCAACAGGGCGCGTCGGAT  
GCTCAAGAAATTGGTCTAAGTATCGCCGCCGGTGTGGATTATGTCCGTCGCTTGGTCGATGCAGGCCTT  
TCCACGGAAGCTGCACTTAAGCAGGTGGCGTTCCGTTTTGCGGTCACCGATGAGCAGTTCGCGCAGATT  
TCTAAGCTGCGTGTGGCTCGACGTCTGTGGGCCAGGGTGTGTGAGGTGCTTGGTTTTCCAGAGCTGGCC  
GTAGCACCACAGCATGCGGTGACTGCACGAGCGATGTTTAGCCAGCGTGATCCGTGGGTGAATATGCTG  
CGCAGTACTGTTGCAGCTTTGCTGCGAGGCGTGGTGGAGCAACCGATGTGGAGGTTCTGACTTTTGAT



GATGCGATCCCAGATGGAGTTCCTGGAGTGTGCGAGGAATTTGCTCACCGCATCGCGCGCAATACTAAT  
TTGTTGTTGCTAGAAGAGTCACATCTTGGTCACGTGGTTGATCCTGCTGGTGGATCATATTTCTGTTGGAG  
AGCTTCACCGATGATCTAGCGGAGAAGGCGTGGGCTGTGTTTCAAGTGGCATCGAAGCTGAGGGCGGATAC  
AGTGCAGCTTGTGCATCCGGCACGGTGAAGTGCATGCTTGTATCAGACGTGGGAGCAGACTCGCGCTGAT  
GTGGCGTGCAGAAAGAAGCTCACTGGAATTAATGAGTTCCTGAACTTGGCGGAGTCTCCGCTGCCA  
GCTGATCGTCGGGTAGAACCCTGCAGGTGTGCGTCGATGGGACGCGGATTTTGAAGCGCTGCCAATCGT  
TCGGATGCTTTCTTGGAAAAGAACGGCGCGAGGCCACAGATCAGATGATTCTCTGGGACCGTTGTCC  
AAGCACAATATTTCGCACTGGTTTTACTTCCAACCTGTTGGCTTCCGGTGGCATTGAAGCAATCAACCCG  
GGTCAACTTGTTCCTGGCACTGACGCTTTTGCAGAAGCTGCACAGGCCGAGGCATTGTAGTGGTGTGT  
GGAACGGACCAAGAGTATGCCGAAACGGGGGAGGGAGCCGTCGAAAAGCTCCGCGAAGCGGGCGTTGAG  
CGCATCCTGCTTGTGTCGGCGCGCCGAAGAGCTTTGAGGGCAGCGCGCATGCGCCCGATGGTTATTTGAAC  
ATGACAATTGATGCCGCGGCGACGCTGGCTGACCTGCTAGATGCTTTGGGAGCT

RXS00149 - 3'-Region  
TAAATCATGACGTGATCCCTAA

RXS00948 - 5'-Region  
ACACCTCCAAATGATCTCGTAAACAGTATTGAATTTAGGTACGACTCTAATCGTACCTTGCCCTCAA  
GCCAAGCTAGTTGTACGATCAAACCTCGTTGT

RXS00948 - coding Region  
ATGGCAAACGTCGTACTAGTCGATCGAATGGAGCCTTTGGTGTCCAAGCTGTTTACCCCAATTCAAATC  
CGCGACATCACCATCCCCAACCGCGTGTGGATGTCACCGATGTGCACCTACTCTGCAGCCACCGGTTCA  
GGTCTTTCCACCGATTTTACCAGGCTCATTACGCAGCTCGCGCAGCAGGTGGTGTGCGATTAGTCATG  
GTTGAAGCAACTGGAGTGAACCCGTAGCTCCCATCTCCCCAGTCGACCTTGGACTTTGGAGCCATGAC  
CAAATTGAACCATTTCTCCCGAGTGACAGCAGCTATTTCGCGCCGGTGGGGCAGTACCGGCCGTTCAATTA  
GCCCATGCTGGCCGAAGGCATCCACCGATGCTCCGTGGAATGGTGGCGGATATGTTGGACCAGAAACC  
AATGGATGGGAGACTGTGCGCCCCAGCCCTCTGGCATTCCCAGGTTTGCCTGCTCCGCGCGAGCTGACG  
GTTTTAGAAATCCAAGAGGTTGTGACAGGTTTCGCTGGCGCCGCCGTTTCGTGCCGATCAGGCTGGTTTT  
GATGTCGTGGAAATTCACGCAGCACACGGCTACCTTTTGCATAACTTCCTTTCTCCGATCTCCAACAAG  
CGCACCGATTCATACGGCGGATCTTTAGAAAACCGCGCTCGCATCGTGTCTGAAGTCATTGATGCAATC  
CGCGCAGTGTGGCCAGAGGAAAAGCCTGTATTTCATGCGCATTTCCACCACCGACTGGGTGGAGGAAAAC  
CCACAGGATGATCGCGAGTCTTGACGCTGAGCCAAAAGCAGGCAGCTGGCTTTGTGGGCATCCGAGCAC  
GGAGTTGATTTGATCGATGCCTCTTCTGGTGGCCTCGACATCGTCCCCATTCCGCATGACCGCGATTAC  
CAAACCGCGAAGGCCGCGAGATCTTACGCAAGTACCGGAGTGACAGTCGCTGCTGTGGGGCGCATTTGAT  
GACGCCCAAACGCGCACAATTTGGTTGATTCTGGCGATGTCAATGCAGTTTTCTCGGCCGTCCACTG  
CTCAAGGATCCTTCTGGGCAAACCAAGCAGCCCTCGCACTAGGTGCGGAACCCAGGTATGTTACCAA  
TACGACTACGTACTT

RXS00948 - 3'-Region  
TAAAGGAGAGTTGACATGAAGGT

RXS01166 - 5'-Region  
ACCGTACCCACAGACACACCAGAATTAACAGAAACAGACTGAAAAACAACATCGCTCGACATGCGCGTA  
ATCCTAACCCGCGCACACTAATGTGGCCGAT

RXS01166 - coding Region  
ATGGGCTACACCAACCTCAACGACACACGGGTCTTGCAGCGCCGGGTCATGTGATGCCTGGTGGCGCACG  
ATGTCTCCGCTAGTGCAGCAGGGAAGTGAGGCAGTCTTTTCGGCGCATCATGGGTCTCTCGCGCGCTCCT  
GATCGGAAACCTGGCTTTGACGATGTCCACATTTTCGGCGCAGCTGTTTCGAGTTCCCGGTCTAAAAAC  
GGCACGTTGGTCAATGCTGCACCCCTTGAAGTTTTGGGCGCACGGGGCGAGCCCAACCCCGCAGTTTCG  
TACCGTTTTGAATACATCACCGGTGATTCCGCAGGTCGAGCCATCACTGCGACCGGCGCTGTCTCTTT  
TCCACACGCCCTTGGACAACCGGCCCGCTCCCGCGATCGCCATGGCTCCATCCACCAAGGCGTCGCA  
CAGCACTGCGATCCCTCCACACCTGCGCCATCGGACTCAACGCATTCTATGACAAACCTTCGACGCA  
ATCATTGCTTACGAACTCCCCGTCATCCTCTGGTTTTCTAGCTCACGGACTTGACGTTGTGTTTCATCGAT  
TACCCCGCGACCCCGCAACCGGCGTCCAATACTATTGCGATTCCATCGCTGCAGCTAAATCGCTTCTC  
GACGCCGTCTCGCTCCAGACAACCTCGGCTTTACCGGAAGCAGGCTTGGCCTGTGGGGATTCTCC  
CAAGGAGGCGGCGCCACTGGCTGGGCTGCACAATTGCAGGATTACGCACCTGATGTCCGCCCCAAGGCA  
GCGGTCTGGGCGCTCCACCAAGTGGATCTCTTCGCGCTTGGACACTGTGACGGCGGATTGCTCACC  
GGAGTGATTGCCTACGCCATCGCGGGACTTGCAGTGAACCTTTCAGAGATGTTTGGAGAAATCATGTGCG  
GTGTTAAATGAACGCGGAGTCAGTGATGTGCTGAAAAATATCACCAGCTGCGCGGGAGGTTCTTGTG

GCCAGTGGCTACTCGTCTTCCCGCGGGTGGACACATCAGGGCACGCCGCTGGCAGACATTCTGGACGAT  
CTGCCACTTGTGTGCTGAGTTTGGGAAGCAAAAGCTGGGTCGTGTGGCGCCAGAAATCCCAGTGCTG  
TTGTGGGGCTCTAAAAATGATGATGTCATTCCCATTGATCCCATTAGGGAATTGCGTGATAGCTGGGCG  
GACAAGGGTACGCCATTGACCTGGCATGAATCCCAAGCGCCGCGTGTGCCAGGACGCACAGGTCTCAAC  
CATTTGCGGGCCCTATTTTAGAAACCTGGAAAAGTACTCGGGATGGCTCATAGATCATCTTGTC

RXS01166 - 3'-Region  
TGAGTGCCGTTTTAAAGGCTCGG

RXS01746 - 5'-Region  
AAACCGCCACTCCCCTTTCACTGGGGAGTGGCGGTTTTGTGCTTTCATGCATGCAGTGTGTGACTTATC  
AACCTTGTTAGGGCTAGGGTGGATATCTATC

RXS01746 - coding Region  
ATGACTGCACCAAGAGATCCTTTTTTCCCCGCAGATCTTCTATCCGCGCGTCTGCAGAGCCCATTGAA  
ATTCAGCGGTTGGGTTTGATCGATTATCAAGAGGCTGGGATTATCAAGCAGAGCTTGCTACCCGTAAGCGC  
GCTAATGATGAAATCCCTGATCAGCTGCTTATTTTGGAGCACCCGTCGGTGTATACCCGAGGTAAGCGC  
ACCCAGCCGGAAGATCTTCCCACCAACGGACTGCCGGTGATCAATGCTGATCGTGGTGGTTCGCATCACG  
TGGCATGGTCTGGCCAATTGGTGATCTATCCGATCATCAAATTAGCCGATCCGATCGATGTGGTTGAT  
TACGTAAGACGCCTCGAGGAAGCGCTCATCCAAGTTGTCGGCGATATGGGTGTTGCCGGCGCTGGGCGC  
ATTGATGGGCGTTCGGGTGTGTGGGTGCCAGCTCATGATGGTTGGGTGGACAGCAAGGTTGCCGCCATC  
GGCATTCCAATAACTCGTGGTGTGCAATGCACGGTGTGGCCATCAACTGCAACAACACGTTGGATTTC  
TATGAGCACATCATTCGCTGTGGCATTGCTGATGCAGGCTTGAGCACACTCTCGAGGGAAGTAAAAAGG  
GACGTTTCAGTTGAGGAATTAGTCGAGCCATCGATCCGCGCATTGGATGATGCTTTGGCTGGTCCGGCTG  
GTTGTTTCTGATCATTTCTTTCGGCAGCGCGCCCGACCCAACCTAAGAATCTCCCTAAACGGGGG

RXS01746 - 3'-Region  
TAGTACGAGGAATTTTGTGCGTG

RXS01747 - 5'-Region  
CGAAGTAGAGCCGATTGCAGAATCGGCGGAATGAGACGTCGAAAAGCGTTTAAGCTTTCCTAAAAATA  
TCACTAACTCGAAAGATGTAAGGTTGCATTT

RXS01747 - coding Region  
GTGACTATCGCACCTGAAGGACGACGACTGCTACGCGTCGAAGCTCGAAACTCAGAAACCCCGATTGAG  
ACGAAGCCTCGATGGATTAGAAACCAGGTCAAAAACGGACCTGAGTATCAGGATATGAAGGAACGTGTC  
GCTGGCGCATCACTACACACTGTGTGTGTCAGGAGGCTGGCTGTCTAATATCCATGAGTGTGGGAATCC  
CGTGAGGCAACCTTCCTCATTTGGTGGCGCCAACCTGCTCTCGCCGCTGTGATTTCTGCATGATCAACTCG  
GCTCGCCCTGAGCCACTCGACCGCGGTGAGCCACTGCGTGTGCTGAGTCTGTTCTGAGATGCAGCTG  
AATTACTCCACCATCACCGGTGTTACCCGTGATGATCTGGATGATGAAGGCGCATGGCTGTACTCAGAA  
GTGGTTCGTAAGATCCACGAGCTGAACCCACACACCGGTGTGGAAAACCTGGTGCCTGATTTCTCCGGC  
AAGAAGGATCTGCTGCAGGAAGTTTTTGAATCCCGCCAGAGGTTTTCGCTCACAACGTGGAAACTGTG  
CCACGTATTTTCAAGCGCATTTCGCCAGCATTCCGCTACGAGCGTTCACCTGATGTGATCCGTACGGCT  
CGCGATTTTCGGTCTGGTGACCAAGTCCAACCTGATTTTGGGCATGGGTGAAACCAAGGAAGAAATCACC  
GAGGCGCTGCAGGATCTGCACGACGCTGGCTGTGACATCATCACCATCACCAGTACCTGCGTCCTGGT  
CCTTTGTTCCACCCCATCGAGCGTTGGGTGAAGCCTGAGGAGTTCCCTCGAGCACGCTGATGCTGCAAG  
GAAATGGGCTTCGCTGCTGTTATGTCCGGCCCATTTGGTTCGTTCTTACCGTGCAGGCCGTCTGTAC  
GCGCAGGCCATGGAGTTCCGTGGCGAGGAAATCCCAGCACACCTCGCGCACCTGAAGGATACTTCCGGA  
GGATCCACCGCCAGGAAGCATCTACACTTCTGGAGCGTTACGGTGCTTCCGAAGACACCCAGTGGTG  
TCCTTCAAC

RXS01747 - 3'-Region  
TAAGCCCGAAGTTTTTTAACCGC

RXS01879 - 5'-Region  
CTTTGCGGGCCGCTGATATTGATCCAACGCTTCGTGGCGAAAAGCTTGATGTCACTGACTATGTGCGCC  
TAGCTGGGGTGTTGCAGCAAAAGGATGAGAA

RXS01879 - coding Region  
GTGAAAATTACCGCTAAGGCGTGGGCGAAAACCAACCTGCATTTAGGTGTGGGACCGGCTCACGACGAT  
GGATTTACAGAGCTCATGACGGTGTTCCTCAACCATTTGATCTGTTTGACACCGTCACCTTAACCAACCTC

GATGAGGAGTTGGTGGAGGAGGGAGCGTCGTCAAGCAATTATCTGTGACCGGTGCCCGTGGCGTGCCT  
GAGGACGCCAGCAATCTTGGCTGGCGCGCTGTGGATGCGTTGGTTAAGCGGCGCGCGGAAAAGACGCCG  
CTGTCTGCAGTTTCGCTGCATATTTCCAAGGGGATTCCGGTGGCTGGCGGCATGGCTGGCGGCTCTGCG  
GATGCGGCTGCGACACTGCGCGCAGTGGATGCGTGGATTGGGCCCTTTCGGCGAGGACACATTGCTGGAG  
GTTGCCCGGAGCTCGGCTCAGATGTGCCGTTTTGCGTGGTGGTGGCACCATGCGCGGTACCGGTGCG  
GGCGAGCAGCTGGTAGATATGTTGACGCGCGGCAAGCTACATTGGGTGGTGGCCGCGATGGCGCATGGC  
CTGTCCACGCTGAGGTATTCAAAAAGCATGATGAGCTGAATCCGGAATCGCATATGGATATCAGCGAC  
CTCAGCGCCGCACTTCTCACCGGCAACACCGCCGAGGTGGGGCAGTGGCTGCACAATGATCTGACCAGC  
GCCGCACTCAGTTTGGCGCCCTGAACTGCGCAGCGTCTCCAAGAAGGCATCCGCTCCGGCGCGCATGCA  
GGAATTGTCTCCGGCTCCGGCCCCGACCACGGTATTCTTGTGCGAATCGGAGCACAAAGCGCAAGACGTT  
AAAGAGGCGCTAATCGACGCCGCGCAGGTGTACGCTGCTTACACCGCCACCGGCCCTGCGGCCTCAACC  
GCCGACCAGCGCGGCGCACACATTTTGAAGTGTTC

RXS01879 - 3'-Region  
TAATAAAGACAACTTAAGTATC

RXS02023 - 5'-Region  
GATGTGGCAGCAATTTTGAAGCAGTACCTGAGCGAGTAACCGCATTCGGGGTTATCGTGGGACTTCCGA  
AATGTAAGTACGAGTACGAGGAGGAAACACG

RXS02023 - coding Region  
ATGGCTCCTAAACAACTCCCAGCCCAGAGAAGAATCGAAACCTGGTGGGACCAGTTCTGCAACGTCGG  
CAGCAGAGGGTACTTTTGATCAACGCTTGCTAGAAATGCGCGCTGATCACAATTGGAAGCACGCCGAT  
CCATGGCGTGTACTGCGTATTGAGTCTGAGTTTGTGGCGGGTTTGTATGCCCTCCACGAGATGCCAAAG  
GCCGTAACCGTCTTTGGTTCCGCACGCATTAAAGAGGATCACCCGTACTACAAGGCGGGTGTAGAACTT  
GGTGAAGGCTCGTTGCAGCGGACTACGCAGTTGTACCCGGTGGCGGTCCAGGTCTGATGGAAGCCCC  
AATAAGGGGGCAAGCGAGGCCAATGGTTTATCAGTTGGTCTGGGCATTGAGTTGCCACATGAACAGCAT  
CTGAACCCCTTATGTGGATTTGGGTCTGAACTTCCGGTACTTCTTCGCACGCAAGACCATGTTCTCTGAAA  
TACTCCAGGCTTTTGTGTGTCTGCCTGGTGGTTTCGGCACGCTCGATGAGCTTTTCGAGGTCTCTGTC  
ATGGTACAAACCGGCAAGGTACCCAACTTTCCCATCGTGCTGATCGGCACTGAGTTCTGGGCAGGTTTG  
GTGGATTGGATCCGTCACCGCCTGGTAGAGGAAGGCATGATCGATGAGAAGGATGTTGACCGGATGTTG  
GTCACTGATGACCTGGATCAGGCCGTCAAATTCATCGTCGATGCACACGCTGGATTGGACGTAGCGCGT  
CTCCACAAT

RXS02023 - 3'-Region  
TAAGCAGTGGCTACATTAGGTGT

RXS02106 - 5'-Region  
GGTCGCCGCTTTTCGACGCCCGCTGCGGCGGGATGACTGTGATGGAGGGGCGCGTCGACAAGCAAAAT  
CTCTTTAGCAAATTCGGTTACTGTGGGGCGC

RXS02106 - coding Region  
ATGAATAACCATTTTGAGCTCAAAGTACCTGGTGGAAAGCTTGTCGTCGTTGATGTGACCACCGATCTG  
GATTCCATTGCTGACGTGAAGATTTCCGGCGATTCTTCCCTCGAACCCGATGAGGCATTCTTCGCCCTT  
GGCCGGGCGCTGCAGGGGCGTCGGTGGGTGATAACACTGATCGTTTGCAGGCAAAGTTGGATGCAGCG  
TTGGCGGAATATGATGACGTTGAGCTACACGGCTTTAGCACTGCGGATATTGCTTTAGCTGTGCGTCGG  
GCAGTCACCGGCGCGCAAGATTTACCGGATTATGAATGGGAAATCCTGCACCCAGGGGTGCTTCCCTACC  
CCACTTAACGTTGCGTTGGATGAGCTCCTTTTGGACCAAGTTGCCAGTGGTCAGCGTGGCCCCGACGATG  
CGCATTTGGGATTGGGATGATCGCGCCACAGTATCGGTAGTTTCCAGTCATATGTCAATGAAATCAAC  
CAAGAAGGCGTTAATGAACATGGTGTGACCGTGGTACGACGCATGTCTGGTGGCGGTGCAATGTTTATG  
GAGGGCGGCAACTGCATCACCTATTCCCTGTATGCACCGGAATCTCTCGTTGCTGGTTTGAAGTATGAG  
CAGTCCTATGAATATTTGGATCGTTGGGTGATTGCTGCGCTGAAGACACACGATGTTGACGCTTGGTAC  
GTGCCTATCAATGACATCACCTCCACCGGCGGAAAAATCGGTGGCGCTGCACAGAAACGTGCGAGTGGC  
GCAGTCTCCACCACGTGACCATGTCTATGACATCGATGCGGACATGATGACCCAGGTGTTGCGCATTT  
GGAAAGGTGAAGATTTCCGACAAGGGTCTTCGACGCGCAAAGAAGCGGTTGATCCTCTGCGCCGCGCAA  
ACAGGTGCATCACGTGAGCAAATCATCGACACCCCTAAAGTCCACATTCAAGTGTAGGTACGGCGCGCAA  
GAAGTAGAGCTCAGCGATGAAGATTTTCGCGGCGAGGCCACGACCTAGTAAAAACCAATACGCCACCGAG  
GAGTGGACTAAGCGAGTTCAA

RXS02106 - 3'-Region  
TAGTTTCTATGGATCTGCACAAG

RXS02228 - 5'-Region

ACAGAAGCGTCAACTGCTCAACTTCTCGACAGCGACGACACACACGGCGTGGGACGCTACGTTGCTCGC  
TGGACTTTTTAACTTAAGGGAGATCTAGATC

RXS02228 - coding Region

GTGGTAACACCGATCGCAGTGGTTGGACCCACTGCATCTGGAAAATCAGCTTTGGGAATTGCTCTAGCC  
CACAAGCTTGACGGTGAAGTAGTCAATGTGGATTCCATGCAGCTGTACAAAGGCATGGACATCGGCACG  
GCAAAGCTGACTGTGCAAGAACGCGAAGGCATTGCGCATCATCAGCTCGATGTCTGGGACGTTACCGAA  
ACTGCGTCAGTGGCGAGGTTTCAATCCGACGCCGTTGCCGATGTGGAAGATATTATGTCCCGTGGCAAA  
ACCCCATCTTGGTTGGCGGCTCCATGTTGTACGTCCAATCTTGGTCGATGATTGGCAATTCCACCT  
ACCGACAGCGCTGTTGCGCGACGCTTTGAGGCCCGCTTGGCAGACATCGGTGTGCAAGCACTACACGCT  
GAACTTACTCAGCTTGACCCAGAAGCAGCAGCCGTCATCGAAAGCAATGATCCCCGACGCACCGTCCGA  
GCATTAGAAGTCATTGAACCTAACCGGCCAGCCCTTCCAAGCAAGCCAACCGCCCAAGACGCGCCACCT  
CGCTGGGGAACCTCGAATCATTGGCCTGAAACACCACTCCAGAATGGCTAAATCCACGCATCGAGCAGCGC  
ACCGCCAGGATGTTTGAACAAGGCTTTGTGCGCCGAAGTGGAACACCTTGTGCAGCAAGGACTCATCGCT  
GACTCCACCGCGGGACGAGCAATCGGCTACTCCCAAGTACTGGCAGCCATGGCAGGGGAGATGACCTGG  
GAAGACGCCTTCGAACGCACGGTCACCGGAACCAGACGCTATGTGAGGCGCAACGCAGCTGGTTCAAC  
AGAGACCACCGCTGTCCTGGGTCGACGCCTCTGGCGATCCACCGCACAAGCCTTGGAGATTTGGGT  
CTACAA

RXS02228 - 3'-Region

TAGCGAGGGTGAATTTGACCATC

RXS03212 - coding Region

GCCTCACTTAACTGGTCAGTCATCGTTCCAGCCCTAGTCATTGTCCTAGCGACAGTGGTGTGGGGTATC  
GGATTCAAAGATAGCTTTACCAACTTTGCTAGTTCTGCGTTGTCAGCAGTAGTTGACAATCTCGGCTGG  
GCCTTCATTTTGTGTTGGCACAGTCTTTGTATTTTTATCGTTGTTATCGCCGCTAGTAAATTCGGCAGC  
ATTCGCTTAGGCCGCATTGATGAAGCACCAGAGTTTCGCACGGTGTGATGGATTTCCATGATGTTTGCT  
GCAGGTATGGGTATTGGTTTGATGTTCTACGGAACCACAGAACCTTTAACCTTCTACCGCAATGGTGTA  
CCTGGACATGATGAACACAATGTTGGCGTTGCTATGTCCACGACAATGTTCCACTGGACCTTGCATCCA  
TGGGCTATCTACGCAATTGTGGGCCTAGCCATTGCCATTTCGACCTCCGAGTGGGCGCTAAACAGCTT  
CTAAGCTCTGCATTCTGCCACTCATTGGTGAAAAAGGTGCAGAAGGATGGTTGGGCAAGCTCATCGAC  
ATCCTGGCGATTATCGCCACCGTATTCCGGCACGGCATGTTCCCTTGGCCTTGGTGCCCTGCAGATTGGT  
GCAGGCCTGTCCGCAGCAAACATCATTGAAGATCCAAGCGATTGGACCATCGTTGGCATGTTTCTGTT  
TTGACCCTGGCATTATCTTCTCCGCTATTTCTGGTGTGGGCAAGGGAATCCAGTACCTCTCCAACGCC  
AACATGGTTCTGGCAGCTCTGCTCGCGATTTTCGTGTTCTGTTGTGCGACCAACCGTGTGATTTTGAAC  
CTGCTGCCAGGTTCTATTGGCAACTACCTGTCCAACCTCTTTCAAATGGCAGGCCGCACTGCCATGAGT  
GCCGACGGCACAGCAGGTGAGTGGCTAGGTAGCTGGACCATCTTCTACTGGGCATGGTGGATCTCTTGG  
TCACCATCTGTAGGAATGTTCTTGGCACGTATTTCCCGTGGCCGCTCCATCCGTGAGTTCATCCTGGGC  
GTGTTGCTCGTCCAGCAGGTGTGTCCACCGTATGGTTCTCCATTTTTTGGTGGCACTGCGATTGTCTTC  
GAACAAAATGGGGAATCCATTTGGGGTGATGGTGCAGCAGAAGAGCAGCTTTTGGATTGCTTCATGCA  
CTTCCAGGTGGGCAAATCATGGGCATCATCGCCATGATTTTGTGTTGCTGGTACTTCTTCTATTACCTCTGCT  
GACTCTGCTTCCACCGTCATGGGCACCATGAGTCAGCACGGCCAGCTGGAAGCCAACAAGTGGGTGACA  
GCTGCCTGGGGTGTGCTACCGCAGCTATTGGACTAACGCTATTGCTTTCTGGTGGTGACAATGCCTTG  
AGCAACTTGCAAACGTCACCATCGTGGCTGCAACACCATCTTGTGTTGTGGTTATTGGATTGATGTTT  
GCG

RXS03220 - coding Region

ATGGGCTTAAGGGAAATTTTGTCCAGCAAGTGGCTTGTGCGCATCCTCCTGGTAGGTATCGGATTGGGT  
GTCGCACAGCAGCTGACCGGCATCAACTCCATCATGTACTACGGCCAGGTGTTCTCATTGAGGCTGGT  
TTCTCCGAGAATGCAGCTCTGATCGCCAACGTGGCGCCAGGAGTGATCGCAGTTGTGGTGCATTTCATC  
GCACTGTGGATGATGGATGGTATCAACCGCCGTACCACCTCATTACCGGTTATTCTCTACCACCAT  
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTCCCAGTCGGCGATCCTCTTCGCCCTACGTTATC  
TTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCCTCAACGTAGCTACCTGGGTTATGCTC  
TCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCTTCTCTGGATCGCA  
AACGCGTTCTCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTAGGACTAACCGGAACCTTCTTCATG  
TTGCGCGGAATCGGTGTGGTTGCCTTGATCTTCTACACCCAGGTTCTGAAACTCGTGGACGTACC  
TTGGAGGAGATTGATGAGGATGTTACTTCCGGTGTGATTTTCAACAAGGACATCCGAAAAGGAAAGGTG  
CAC

RXS03220 - 3'-Region  
TAAAAACCCAGACACTGCATAGATAACACG

## APPENDIX B: AMINO ACID SEQUENCES

> RXA00051 (1-1404, translated) 468 residues  
 MNASPAPTRS FKGLRARHIH FIALGSAIGT GLFYGSAGAI QAAGPSVLLV YLLGGAVVYF  
 MLRALGEMAV HHPVRGSFAV YTRAHLGGWA GYITGWMFAF EMLIVCLADL TAIGIYMFW  
 FPGTPQWTWV VATLLIVGGA NLASVRWFGE LEFIFTIIVK TAVVAMIVGG AAILAFGLGA  
 NAEVAGVSNL WEHGGFFPNG VEGMIAAFIL VLFAFGGTEI IGVAAGSEAD PEKSIKAVN  
 TVPVRILLFY VGAILVILAL NPWPSITGEE SPFVQIFDTL GVNWAAGLLN AVVITAALSA  
 INADLFGAGR VLTGLAKENL APKAMGKIAK NGVPVMTTTI MIIVLIVGVI LNAVLPERVF  
 EIVASLATFA TVYVWLMILL AQVGSRRNMP ADEVKSLKFP VPFYFPGQYF AILFIAFTFG  
 IMVWYDNYHL PLAVGVGFLV LMTILYYATG RPKAIAPIDY EELDPRRD

> RXA00091 (1-753, translated) 251 residues  
 VITLTNVRKE YSSDVAIGPV NLEIPAGGIT ALVGPNGAGK STLLTMIGRL LGIDEGNITV  
 ASYDVTSTAS KDLAKIISIL RQENHFVTKL TVRQLVGFGR FPYSKGRLTE EDEGIISRYI  
 DFFNLTELED RYLDQLSGGQ RQRAYVAMVL CQETDYVLLD EPLNNLDIAH SVMEMKHLEN  
 AAAQFGRTHI VVLHDINFAA RYADYIVAVK HGMIEKEGTP EQIMKNEILS EIFNTEIEVI  
 EGPHGKIACY H

> RXA00092 (1-204, translated) 68 residues  
 IARALIGPRK ILLADEPTGA LDTSTGDAVL RVLQRIDSG AAGLLVTHEP RFAAWADRTI  
 MLRDGEIQ

> RXA00104 (1-756, translated) 252 residues  
 MTAQIDDSIL THRLAQGTGE ILKGVNRVGV LRGRNLGDAG DELAQSWIAR VLEQHRPNNG  
 FLSEEAADNP DRLSKDRVWI IDPLDGTKEF ATGRQDWAVH IALVENGVPPT HAAVGLPDLG  
 VVFHSADARA VTGPYSKVIA ISHNRPPKVA LSCAEQLGFE TKALGSAGAK AMHVLLGDYD  
 AYIHAGGQYE WDSAAPVGVC KAAGLHCSRL DGSELTYNK DTYMPDILIC RPELADELLE  
 MCAKFYEENG TY

> RXA00113 (1-3294, translated) 1098 residues  
 ASGGGVVDSA ALDAYASTVT GEEGVLANVA RGILSQLGLD TKDEVEGA EI DTELYDAVEA  
 ELGTGWLKLV TPVFSADRAI LFDDRWARAS EDLARLANGE DIAVERFAGT GETVVKQAAW  
 WAEHVEDTAL AATLKQVSEV AAKPANEPHI DDVALVTGAA PESIAGAVAA RLLSQGATVI  
 LTASNVSQAR KEYARKLYAA NATPNAKLWI VPANMSSYRD VDAVIDWIGN EQRVTVGSTV  
 TVTKPALTPT LAYPFAAPSV SGTLDAGPQ AENQARLLLW SVERTIAGLA DLASRGVDGR  
 VHVLPGPSN RGMFGGDGAY GEVKAAFDAL LAKWGSETGW PQFVSLAQAR IGWVAGTGLM  
 GRNDVLIPAA EKLGIHVYTP EEISSELLGL ASAESREKAL EAPIDYDLTG GLSGGVSI AA  
 LAASLESDAV ETTSAAEDTI KALPSPKHPE QPVGTPVGEV KTDLEDMMVM VGVGEVSSWG  
 SGRTRFEAEY GIQRDGSVDL TAAGVLELAW MMGLISWSED PKPAWYDADG TEVPEEEIYE  
 RFRDEVIARC GVRELVDDAF LVDGGS LDAA EVFLDRDISF SVTSAAEEAQA YVDADASVTV  
 EEADGEWIVT KKKGSTSFVP RKATLTRSVA GQLPTDFDPA KWGIPAS MID ALDNIAAWN L  
 VTAVDAFLSS GFSPAELLQS IHPADVSTQ GTGIGGMQSL RKLFVNRF LG QDRPSDILQE  
 TLPNVVAAHT MQSYVGGYGQ MIHPVAACAT AAVSVEEGVD KIRLNKADFV VAGGIDDIQV  
 ESLTGFGDMN ATADTQAMLD KGIDPRFISR ANDRRRAGFL EAAGGGTVLL ARASVAAELG  
 LPVLAVVAHA QSYADGAHTS IPAPGLGALG AARGGKSVL ARELNKLGLT PDDVRVVS KH  
 DTSTNANDPN ESELHNLWK TIGREADNPM FVVSQKSLTG HSKGGAALFQ IGGILVSILET  
 GKLPQNASLD CVDPEMEAKG ENFVWLRKPL DLGAGSIKAG VLTSLGFGHV AAVVVLATSG  
 IFEQAMRNAG LDVEAWRARA TQRLRTGANR LEAGMVGRAP LFEQVDGRRL PEHGAHQAEI  
 NLLIDADARL GADGIYQG

> RXA00158 (1-2085, translated) 695 residues  
 VTELSRNFGA SRLINRFQGE PFAFAFAGQG YDWLKLTRAA VAAGAGTNVS DIVERANALL  
 ALVADDLIGT LPFGFDPVAW ANNSDPAFD TAQSAVSVPG IFVSQIATLD SLEAQRLDVD  
 QAVSSIGHSQ GVLGVHLLND ATRADELVAI AQLIGAAITR TARMTG LIAQ GDNMPMLSIA  
 GISAREQLQA IDAACAEVPA EIRPVIGLRN SRDSYVLVGR PDDNARVVKV IEAMAAKDKK  
 AIEDKLRGGS AFSPRITPLK VQA AFHPAM NMAVEQTVAV ATTAGLDVEL TREIAADVLV  
 NPVDWVARVN EAYEAGARWF LDVGP DGGIV KLTANILEGR GADSFYVGDA AGQAKIFDAG  
 MAPELPVDYQ EFAPRVEHVD GTPRLVTKFT ELTGRT PMML AGMTPTTVDP AIVAAAANGG  
 HWAELAGGGQ VTPELLETHI AQLTDMLEPG INAQFNSMFL DPLYLWKMQIG GKRLVPKARA  
 NGASIDGIVI TAGIPEKDEA VALVKELMRD GFPWIAFKPG AIKQVNSVLA IAKEVPELPI

IIQIEGGVAG GHHSWEDLDE LLIATYGKVR ALDNNVLCVG GGIGSPERAA DYVTGSWSTS  
YGLPAMPVDG ILVGTAAMAT KEATTSQAVK ELLVSTQGS D EWVPAGGAKN GMAYGRSOLG  
ADIHEIDNSF AKAGRLLDEV AGHETDLQAR PDEII

> RXA00164 (1-1689, translated) 563 residues

VGRIPRAKWW FLGALVLLSA GAYASVLVPQ VLGRIVDLVS DGAQMRDFVE LSVILIAVAI  
AGAVLSACGF YVVSRISEKI IANLREDMVG TALGLPTHQV EDAGSGDLVS RSTDDVSELS  
AAVTETVPIL SSSLFTIAAT IIALFSLDWQ FVLIPVVVAP VYYFASKHYL SKAPDRYAAE  
RAAMAERARK VLEAIRGRAT VRAYSMEDAM HNQIDQASWS VVVKGIRART TMLILNMWML  
FAEFLMLAVA LVIGYKLVID NALTIGAVTG AVLMIIRLRG PMNMFMRVLD TIQSGYASLA  
RIVGVVADPP IPVPDSGVKA PQGKVELRNV SFSYGDSWAV KDIDITINSG ETVALVGASG  
AGKTTVAALL AGLRVPDQGG VLVDDFPVSH LSDRERIARL AMVSQEVHVF SGTLRQDLTL  
AKPDASDEEL AHALGQVNAL DWLESLEPEGL DTVVGARGIQ LEPVVAQQLA LARVLLLNPA  
IVIMDEATAE AGSAGASALE EAADAVSKNR SALVVAHRLD QASRADQILV MDKGEVVESG  
THQELLDHGG IYQRLWTAW S VGR

> RXA00181 (1-1572, translated) 524 residues

MSDNTWFIIA IVIYMLVMVL IGYWSYRKTE KYDDYMLAGR GLNPFVAAMS AGASDMSGWL  
LMGLPGALFV TGMSELWIAV GLTIGAWANW MWVAPRLRSY SEISANSITL PSFFENRLRD  
KSRLRIIAA LIIIVFFTFY ISSGMVAGGV YWESTFGGDY LLGMAIVAGV TVLYTFIGGF  
LAVSYTDAVQ GTIMFFSLII VPMAYFALA NPMDIWSFAN SNDYGPHTDG IGNPTYFSMI  
SGISAAAIIG NLGWGLGYFG QPHIVVRFMA LRTPAEAKQG RRIGISWMII CLIGATFTAI  
ISTVFFAQNP DANITDTRAY ESIFLDLARM LFHPLIAGLI LTAVLAAIMS TMSSQLLVTA  
SSLIEDLLKV VKKDSLERT LIMLSRATVI ILAIIAAAMA INPSDSLGL VGFAGWAGFGS  
AFGPILASL YWKRLNAAGA ISGMITGAIV SIAWGMSPLS DTLYEIIPGF ALATIVMVVV  
SLLTKEPSEE ILNEFETAKD LAAAVESNED VDFADAAQKL SKES

> RXA00186 (1-747, translated) 249 residues

MGEKTSVAYV HDVLIKGVPV RIYNPHPNDG PLPVFIYFHG GGWVLGDLES VDSTVRDIAV  
ASGALCISVD YRRAPEHPFL AALDDCQVVT EAVLNGELAS ANQHLVAVGG DSAGGNIAAV  
IAQQLRDQIT HQVLVYPVMD VILLVICSH TTGFALLMHP KSKDKTETIS DEFLAEIQAG  
SEKISILRST PAEKANASRW IMYFVGGIGL LYSVFSLWTG GVTGLTLNSF NFLFLSLGMV  
LTANYGPEY

> RXA00187 (1-351, translated) 117 residues

VISGFFTSIS TATTWPVIAF LYSGLLNIAV PSGGSKFIIE APYIIPTPVD LGADMGLVLQ  
AYQMSDGATN LLIPFFALPY LANFKIKFSQ VVGTVPPVL VVIAVICIYL FLRASII

> RXA00201 (1-186, translated) 62 residues

VADCGPIPE HVEIIDLALV FGIPTFEQVL NALKPEVVVE GAVIAEGAPQ RIREMVDTDV  
EV

> RXA00228 (1-591, translated) 197 residues

MRDLRSMIGV SSSALGNRIP SEEKVSDLVI SAGYAILGRW REDYDEMDFG QATEILEQVG  
AMHLADRTWG TLSEGERKRV LVARALMTNP ELLILDEPTA GMDLGGREDL VGYLGE LAMD  
PDAPAIVMIT HHVEEIPAGF THAMLLDEGE IVAQGLINTV MTNENLSKAF HQPIQVDRIG  
ERYFARRVRT ARSHRAQ

> RXA00243 (1-927, translated) 309 residues

VTSEQALDPI HPGQFRLSRI QLINWGTFHG TVDIPVTREG ILVTGGSGSG KSTLIDAITA  
VLLPQGKLRV NSAAQANTPR NKGRSLVTYI RGAWRAQEDP LQDQIVSTYL RPRATYSLVG  
LTYSNGEGVE HTLVAIIFYLK SGHNLTSDIS SYYGVPVVDQ DINALLDFLK EGIDKRQIRA  
AFKEAIFSEQ HSVFSGRFRS RLGISSEAL LLLHRAQSAK DLQSLDDLFR DYMLVEPDTF  
SIAKTAVEQF QDLEGAYEQV EDIKRQIHTL DPLVQLKNRR EKAQQSKDHA NALKKALPTV  
GNRIKKEEQ

> RXA00259 (1-2202, translated) 734 residues

MSGLFTPFSD AAKNNTVKTD GDSVSGRDLP ITKISED RFE RSAYS AQLAN IICDVAPWGA  
STVFSLTGQW GSGKTSLVNL IRSEESLSNE KWTIVDFNPW VASDPQSLIE EFYRVIVGT  
PDDKTGQKIK TVLQKTFSTI GSIAGGVGGF GVLEALALSK GVDAANAVYK TWKQEQDSWP  
TLYTRAANHF KDLNKRILIV VDDIDRLHTD ELALLMKVIR LLGRFPQVNY LLVYEEESLL

TTLARSTAVG GSEDDALRFM EKIVQYPFDV PPLTSFQIEK ELSALFDKLF QGVSLSGDPE  
 DFALVKSRMF DVWEKTLVTP RLLHRFAALL TNWTRIYGSG EVNGVDLTIL ATIRIVFPSV  
 YKRLSRAKEV LLQGGRTTGS QKPGWEKQLC EGMNNEQMDL LKTMLLFLFP RLSDHPSTRM  
 HRERGISTEV YFDTYLMFQR PGHVISDEQL DKYLSNADDA MGFVDLINS DNDMVASVMK  
 KLPLAIDRLD GEGVRHMAVE VLFTAANGMH DKGRQVRMSG IFSDLYSHAC SILGALPQLP  
 VEQLYEKFFS EMTLNEAAFW LNQVGERARA CGNDVSGLEL FRKVNKTEA RILSVLKNQD  
 PSDWDLGPYS LGILAKSSNF SSVLKSLSQS IEEHQFDVID IGVLFLLTVY SSRQGPSGGA  
 WIDSFQHSLE SRYVPDSLRA ITKSEVDVEL GKIQFTDFSW EGKRKVVAYA LETGRSDFTR  
 ERLGGYSIAD SIVD

> RXA00269 (1-789, translated) 263 residues  
 MLSINGISKT FFPGTVNERR ALQQLKLDMA EGDFVTVIGS NGAGKSTLLN AVSGRLLVDS  
 GEISIDGNKV NKMSEHKRAR YIGRVFQDPL AGTAPNLTIE ENLAIALLRG KRRGLGFALT  
 SKRREQFKQE LERLELGLEN RLTAQVGLLS GGQRQALSLL MAGFTQPKIM LLDEHTAALD  
 PQRAELVTTL TEKIVADGNL TTLMVTHNME QAIRLGNRLI MMHEGQIVYQ ADQATKSKLT  
 VRDLLQEFAN IKGATLSDKA FLG

> RXA00281 (1-684, translated) 228 residues  
 MINVEGLTKQ YGQVRAVDDL SFEVKPGIVT GFLGPNGAGK STTMRLILGL DNPTAGHATI  
 EGQPYRSLKN PLTKVGALLD AKATHPNRTA ENHLKWIARA NGLSTKRVDL VTLVGLTGV  
 GSKKTGGFSL GMGQRLGLAA ALLGDPEYLI LDEPVNGLDP EGIHWVRTLL QNIAKQGRV  
 LVSSHLLSEM AQTAEHLIVI GRGKLVADMP MHEFVRSHSA STVVVRAA

> RXA00298 (1-1845, translated) 863 residues  
 MSSNIAITTE PEGKNKKGLK SDPFIFSISV GFIVVFVIAT IALGEKARTT FSAIAGWLLE  
 NLGWMYIGGV SLVFIFLMGI FASRYGRVKL GDDDDDDPEHT LIVWFCMLFA GGVGAVLMFW  
 GVAEPINHAFF NVPMA NEESM SEAAIVQAF YTFYHFGIHM WVIMALPGLS LGYFIYKRKL  
 PPRLSSVFSF ILGKHIYSTP GKLIDVLAIV GTTFGIAVSV GLGVLQINAG MNKLWSTPQV  
 SWVQLLIILI ITAVACISVA SGLDKGIKLL SNINIAMAVA LMFFILEFTGP TLTLRLFLVE  
 SFGIYASWMP NLMFWTDSFQ DNPWGQGWKT VFYWAWTICW SPYVGMFVAR ISRGRTVREF  
 IGGVIALPAI FGVVWFSIFG RAGIEVELSN PGFLTQPTVV EGDVPAALFN VLQEYPLTGI  
 VSFAFALVIV IFFITSIDSA ALVNDMFATG AENQTPTSYP VMWACTIGAV AGSLLIISPS  
 SGIATLQEVV IIVAFPFLLV QFVMMFSLK GMSDAAAVR RVQTRQWEKT DTPEKLEHS  
 SQPAPGYDDE GNPLPMPALE HDDEGNIVIP GNVVIEGDLG VVGDVVDDE EAQEMGSRFK  
 IVEQTRPQSR DEYDI

> RXA00346 (1-690, translated) 230 residues  
 MLLTFNDAV DPLWRGLNLE LRQGEFLAVL GPNGVGKSTL IGTILGTRKL THGSVKTDAR  
 VGYIPQQRIF DVPLRARDMV SLSAAHGVS KRGPAKGDVD KLLARVGASG IADRRVGELS  
 GGQQQLVRQA QALATRPQLL LADEPLLSLD PGVAQRTVSL FGELKAEGV VVVVTHDVNP  
 LMGLVDRILY LAPNGHTIGT VGDVMQSEKL SELYNAPVTV ARINDRIVV

> RXA00368 (1-579, translated) 193 residues  
 SLMLSLGAAL ICGVLGWLIG VLITRTQHFA NVPLTLTVLL PTALPGMIIG VGWLILGRYT  
 GIYNTWPVIL GAYVCAFTAL VVQAVRGPLS QAPEAIEEAA RISGAGRLRS IMDTTGAMAI  
 PAAFAGAVLV AVTAVRELTV SILLIAPGTT TLGVQVFNLO QAGNYNQASA LSLMFAIIGI  
 VALALTVRSQ KEF

> RXA00369 (1-717, translated) 239 residues  
 VSSIKLRDLS VSFRDGTFLG QDINLKIEPE EFVVLLIGPSG SGKTTMLGTI AGFVEPSSGS  
 VLIAGEEMTH VPPERRRMGM VFQQHAWPH MSVAKNVGYP LARSGQKGAS ISKRVERTLA  
 LVGLEGFGRS RPASLSGGQR QRVALARAI ADPTVLLLE ALSALDEPLR DALRRELVS  
 TRREGLTTVH VTHDRAEAI IADRIVVLGN GRIQQVATPT ELLSAPATAD VARFIVDAT

> RXA00370 (1-798, translated) 266 residues  
 GKALWNSAYT TVLSAVGATI IGTIMALTLD RTDVFGRAL RLFLLSPLLI PPFIGAIWL  
 QLEFGKNQGIN RFFGTEVWDI YGADGVTFLL IVHSYPTVYI IVSAAALRQLP SDLEQAARIA  
 GADTFTVLRIT LPLLLKPAL LSAFTLTVA NLADFGIPAL LGSPARFETL ATMIYRFMES  
 GTVSNPLQV STIGIVLLFL GIAAVTADYL VSLYAASKLO DAGTPHRFTL NKSRIPVSVI  
 TWIIALIITA APLLGLAYRA LLPAPG



> RXA00410 (1-666, translated) 222 residues  
MMIYGKGSTE VRALDGISVQ IQSDKWTSIM QSGSGKTTL LQCLSGLAQP TSGRVTLNKN  
NITLSSLSSEN KRAKLRRTHI SMVFQDFNLV PILSVKDNIL LPLRLAHRV DKQWFEHITS  
VLKIDNMRMH LPGELSGGQQ QRAAIARALM SRPDIVIADE PTGSLDSVTS DAVLNLFRSI  
VDDFGQSLVF VTHDKDAAHR GDVLITMRDG KIIDTADLRV GR

> RXA00419 (1-462, translated) 154 residues  
DNEAQWRDQA LAVEATTVNY TAGVSVGVLL GQKFEQQGHG TIVALSSVAG QVRRRSNEFVY  
GSAKAGFDGF YTQLGEALRG SGANVLVVRP GQVRTKMSAD GGEAPLTVNR EDVADAVYDA  
VVNKKDIIIFV HPLFQYVSFA FQFIPRAIFR KLPF

> RXA00421 (1-159, translated) 53 residues  
MLNAVKGAKQN ILLGGTSEI GISIVSRFLK QGPSHVTLAA RKDSRPVDAA VAE

> RXA00432 (1-891, translated) 297 residues  
LSALVIFGGV QRIANVTQWM VPFMAGAYII VGVVVIVINI QQVPTMINDI IAGAFGFRPV  
ATASVWGAFF LAFMNGMRRG LFSNEAGEGS VPNAATATV SHPVKQGLVQ TLGVYFDLTL  
VCSITAFVIL LSGVEYATGD IQSSSLTQSA LASVVGWGT HFITVVMFFL AFSSVLGNYY  
LAQANIQYFT DSKTVMTVFR LLVLLSVFSG AVASVPLIWA LGDTFAGIMV LINLAAIPL  
GGVAVKLLKN YTIQKKAGLD PVFHRDMMPE VRNIACWNGK DAATSNYHEA MEVIKKS

> RXA00436 (1-525, translated) 175 residues  
MELLETFITD VINDNLWMIL PFLLVAGLY FGGRTLLVQI RMIPEMFKAV VEKPAKDGEF  
ADKQDISAFK AFTISAASRV GTANVAGVAL AITLGGPGAV FWMWIIALVG GATSFIESTL  
GQLWKVKDGD SYRGGPAYYM TLGLNARWLA VVFGVAITLT FGFVYNALQS NAVVE

> RXA00449 (1-1005, translated) 335 residues  
LALTAETVGG MKNQKKFATG LMLSIAYSAS IGSIGTLIGT PPNALLAAYM SESHDIHIGF  
GQWMILGVPI AVVFTIIAWL VLTTVFKPEM KEIPGGRELI KREIAEMGPW TAPQVTVGVI  
FAAAALAWVF IPLTLDWTGS QLSINDSLIG IAAGLLMFIV PANFKTGERI LDWRTAGELP  
WDVLLLFGGG LSLSAMFTST GLSLWIGELA KGLDALPIFI LIFAIAVLVL FLTEFTSNTA  
TAATFLPIMG GVAVGIGLTA GGEQNVLLLT IPVALSATCA FMLPVATPPN AIAFGSGYIK  
IGEMVKGGLW LNIIAVILIT IFTYFVAIPL FGIML

> RXA00456 (1-312, translated) 104 residues  
VLQALLAIMV SLSVAAILEG NRALVGLLLA TTLGLGVAQW IQKVVAEDLG QHYVHEVRRE  
LVGAALVPGN TASLGVTVTR ASNDLTAVRN WVALGIVPMV TGLP

> RXA00459 (1-987, translated) 329 residues  
VCTRAAGGGA VTLKRARELR KKRGRMAARI ADSVMAGELL HATGAIDREL NAVTRDSDRV  
VIAAVRRSWA TGFSRALMAM AASLGTVSIV ISGHLEVSEV AGIMMLLGVL ATPVAELGRV  
VEYRQNYKAA TRILIPLLQR GSEFKHSQQK LPGLQATEGI PGVYVKGISA LPERIYLHG  
SADATRKWVT SLSAMEEGTD VIVNGQRLSQ LPLKQRRALI GIASAHHHLS RGSVSRVLGL  
RVPDATVEEI EQALEQVGLN NTGKQRLKNG GHPWSTSQIN KLKIASATLR TPPLLVEGI  
TPENLLNYPG VIISTVQENP SETWRQVNI

> RXA00477 (1-1644, translated) 548 residues  
MKVSTKTPRS SGTAVVIGAG VAGLATSALL ARDGWQVTVL EKNTDVGGRA GSLEISGFPG  
FRWDTGPSWY LMPEAFDHEF ALFGACTSDY LDLVELTPGY RVFSGTHDAV DVPTGREEAI  
ALFESIEPGA GAKLGNLYDS AADAYDIAID RFLYNNFSTL GPLLHRDVL T RAGRLFSLLT  
RSLQKYVNSQ FSSPVLRLQIL TYPVFLSSR PTTTPSMYHL MSHTDLVQGV KYPIGGFTAV  
VNALHQLALE NGVEFQLDSE VISINTASSR GNTSATGVSL LHNKRVQNL ADLVVSAGDL  
HHTENNLLPR ELRTYPERYV SNRNPIGAV LILLGVKGEL PQLDHNNLFF SEDWTDFAV  
VFDGPQLTRP HNASNSIYVS KPSTSEDGVA PAGYENLFVL IPTKASSSIG HGDAYMQSAS  
ASVETIASHA INQIATQAGI PDLTDRIVVK RTIGPADFEH RYHSWVGSAL GPAHTLRQSA  
FLRGRNSSRK VNNLFYSGAT TVPGVGIPMC LISAENIIR LHADTSAGPL PEPLPPKTPP  
SQKTSYDH

> RXA00478 (1-831, translated) 277 residues  
VIEEYSTSFS LSTWLLSPRI RNDIRNLYAV VRIADEIVDG TAHAAGCSTA KIEEILDAYE  
IAVLAAPQQR FNTDLVLQAY GETARRCDFE QEHVIAFFAS MRKDLKANTH DPDSFTTYVY

GSAEVIIGLLC LSVFNQGRIT SKKRLEIMQN GARS LGAAFO KINFLRDLAE DQONLGRFYF  
PKTSQGTTLTK EQKEDLIADI RQDLAIAHDA FPEIPVQARI GVISAYLLFQ KLTDRIEATP  
TADLLRERIR VPLHIKLSL ARATMKGLSM SIYRKNS

> RXA00480 (1-1116, translated) 372 residues  
MDNGMTITTE HSTHPDLDFN DEIYRELNRI CASLSQQCST YQPEFRTCLD AAFQALRGGK  
LIRPRMLLGL YNTLVDDIE VKLNTVLQVA VALELLHFSL LVHDDVIDGD LYRRGKLNFI  
GQILMHRTPE SFAQIQRDPE HLDWAQSNGL LMGNLFLAAT HQIFARLDLP HHQVRLLDL  
LNHTINDTIV GEFLDVGLSS KAISPNDIA LEMSRLKTAT YTFELPMRAA AILAEPLQEI  
ETKIGEIGTN LGIAYQLQDD YLSTFGDAE HGKDAFSDLR EGKETTIIAF ARDTAKWTDI  
QDNFGSADLS TSQAERIQHL LIQCGAKNHS LNAISDHLNI CRSMIKTLSP QVDPKAQNLL  
LKQVEQLASR KS

> RXA00524 (1-333, translated) 111 residues  
VTTNHQLSAE EISLAYGERT IIDSLSVDIV PGKITSIVGP NGCGKSTLLR AFARLLKPSA  
GQALIDAHPL PSLPGKELAR MLGLLPQSPT GPEGIVVADL VGRGRHPHQG L

> RXA00526 (1-690, translated) 230 residues  
MSLIEMRNIV KTYNIGSEGE LTVLHGVDFH VDRGEFVSUV GTSGSGKSTM MNIIGLLDKP  
TDGTYTLDG VDLDISDDAL ASHRAKSIGF VFQNFNLIGR IDALKNVEMP MMYAGIPAKQ  
RRSRVELLE MVGMGERLNH EPNELSGGQK QRVAIARALA NDPEIILADE PTGALDSATG  
RMVMDIFHQL NKEQGKTIVF ITHNPELADE SDRVVTMVDG RIIGSEVKHS

> RXA00559 (1-213, translated) 71 residues  
MSDNPHENPR ENPHRSPEVV LRFMAAPT DV LMAGSHGVGG GRVLEWIDKA AYACATHGSG  
TYCVTAYVGH I

> RXA00570 (1-498, translated) 166 residues  
PTIVMAMVAG IFLRFGDLI DASVTDPLIA LPMVIVFVAL SMSPRLASIA PPVAVAAVVG  
TIVAIASGKL ASGILDNGII SRPVFTAPEF SFAAIMELVV PLAIVVIVQ NGQGVAVLKA  
AGHRPGVNL AASGLWSLP MALIGNITTC LTGPTNALIV AGAKSH

> RXA00571 (1-1185, translated) 395 residues  
QIGALSPA V GTLGSYAMIG VMIGALSAGA VGDRLGRRKV MLTAIVWFSV GMALTAFASS  
IALFGFLRFL TGLGVGMIVA TGGAIIEFA PANRRNLFNA IVYSGVPAGG VLASILALLF  
EDVIGWRGLF LIGGSPLLFL LPLAYFFLPE SPRWLTSRGR AADAKALCAR YGLPTEEFVV  
EKQKETKGTG FAGIFSSKYL MGTILIGAMS FIGLLSTYGL NTWLPKIMES NGATSHDSL  
SLLFLNGGAV FGGLIASWFA DRIGAKTVIT STFALAAICL GVLPNISSWP MMYTAIAFAG  
VGVLGTQVLT YGLTSNFFGT ECRAAGVAWC AGFGRLGIV GPAIGGLIIG AGFGPSSAFL  
IFAAAAAIGA VCTLLIPRSP AEVEVKVAQE PLARV

> RXA00572 (1-3831, translated) 1277 residues  
QWLNRYLELS GPVDGQWIDA SWAARFAQML ERAEARLIEQ DHGQFEPSLT VEDGVDKLVA  
AYPHAATDLL TPADVAVFLG LCRTPGKPVN FVPVIDKDVR RWRSDSLWQ SHDDRYTADQ  
VAIIPGVAV AGITKANEPV ADLLDRFVDA TIERIDEHDS RSRDIMGKVL SSPGTFWAGR  
NIPSVIHLG HADKWSRSEF EAFHSPTGAN LVYEDAEHAM LTVPLAGSTA FGTTAELKIR  
FTSPIDALPS AVPLVTQEDA EAAMGELTRI AAGGTLATVN NGTATWETS V DAGVIADYNN  
VTAGYLPASV VPAHTAPDVL VGRAWPVFA AVKSAVIPGT DSASVVEGML SLVHLEHHIV  
LKSDVPTDGA LKVSATADEV VDTDLGRLVI VRAEIADAEG NLIATLAERF AIRGRKGNV  
ARTNTSALPT TVDTPRSARA VATVVAPESM RPFAVISGDR NPIHVS DVAA SLAGLPGVIV  
HGMWTS AIGE LIAGAAFNDE QIQTAAKV EYTATMLAPV LPGEEIEFSV ERSVNDNRPG  
MGEVRTVTAT VNGNLVLTAT AVVAAPSTFY AFPGQGIQSQ GMGMEARRNS QAARAIWDRA  
DAHTRNKLGF SIVEIVENNP REVTVAGEKF FHPDGVLYLT QFTQVGMATL GVAQIAEMRE  
AHALNQRAYF AGHSVGEYNA LAAYAGVLSL ESVLEIVYRR GLTMHRLVDR DENGLSNYAL  
AALRPNMGL TADNVFDYVA SVSEASGEFL EIVNYNLAGL QYAVAGTQAG LAALRADVEN  
RAPGQAFIL IPGIDVPFHS SKLRDGVGAF REHLDSLIPA ELDLDVLVGR YIPNLVARPF  
ELTEEFVASM AEVVESTYVN EILADFKAAS ADKQKLARTL LIELLAWQFA SPVRWIETQD  
LLIKGLQAER FVEVGVGSAP TLANMMGQTL RLPQYADATI EVLNIERDRP VVFATDEVVR  
EVAVEETPAA PAETTETPAT PATPAPVAAA APATGGPRPD DISFTPSDAT EMLIAIWTKV  
RPDQMGATDS IETLVEGVSS RRNQLLLDLG VEFGLGAIDG AADAELGDLK VTVSKMAKGY  
KAFGPVLSDA AADALRRLTG PTGKRPGYIA ERVTGTWELG QGWADHVVAE VVIGAREGAS

LRGGDLASLS PASPASASDL DSLIDAAVQA VASRRGVAVS LPSAGGAAGG VVDSAALGEF  
 AEQVTGHDGV LAQAARTILT QLGLDKPATV SVEDTAEEDL YELVSKELGS DWPRQVAPSF  
 DEEKVVLLDD RWASARE

> RXA00590 (1-387, translated) 129 residues  
 MRVVFLAVL GVVAGGVTLT TTGNPAAEAF QHAAGDIGLR IFGAVLWAAS ISSVIGASYT  
 SATFLVENKP EKKRLQNWVT IIFILISCSV FIMLGTAPAI LLVFAGAFNG LVLPVGFTLM  
 IYVAIFRQK

> RXA00591 (1-1353, translated) 451 residues  
 MTTSSSTASPI AELQNLSPKQ RKSESRRRAII SSYLGSTIEF YDFLLYAAAS ATVFPAVFFT  
 NLDPLAGTIA AYGTFGAAGYL ARPLGGAIFG HFGDRLGRKK MLVLSMLIMG VASTCIGLVP  
 SAEMIGSMGA VILIMLRICQ GIAVGGEWGG AALMALEHSD SKKRGFAASF TNAGAPTGAA  
 LGTFALGTAS AVLTQEQFLS WGWRIPFLLS FVLLIVGLVI RAKVSESPLF AAAAAAEKAK  
 PTERKVPLLQ VLRRPKALIL TMLGGASGFG LQVLLSTFSI SYATQSGIER SSVLYAFAVA  
 SVFSVFFVIL FGRVSDLFGR RPVMIIALVL FVAYLPAFFR MLTSDNWFIL LSAFTIALAL  
 HAMLYGPLAA FISEQFGTSA RYTGASLGYQ LATLIGAGFT PTILASLYAG PGGGTSVTPV  
 IVFLATMSLV SIIAIAITRE SKDHDLSTYE H

> RXA00596 (1-453, translated) 151 residues  
 MLNALKFIPW LIGQIFLSGF SVITAAVKKD TGFNPVVIRY PLRVTTDFQI AALSTCITAT  
 PSTLSLGLRE PRKPGDPTIL LIQAVFGSDP VEVFESIADM EQRLVPSVAS IDHGVPGQGP  
 YKEIRPSDAE WPSREIADTA QNTVSQDKRE F

> RXA00607 (1-381, translated) 127 residues  
 MILALTVAIL FGGGVYLIQQ RGMVRIVFGM SLIGHAANLT ILYAGVPTWR GEAFPDRTPL  
 TDAADPLPQA FVLTAIVIAM ATTTIMLALA ALGRSDDTRS IEPDDDQSPL TTSARSVTNP  
 TDQEDKA

> RXA00623 (1-1338, translated) 446 residues  
 MDSNTESSSV EVKNEHIKQV KPPKKDRTHW LYIAVIALI GGITLGLISP ELGKEFKILG  
 TMEVSLIKMI IAPVIFCTIV IGIGSVKAAA TVGRAGGIAL AYFITMSTFA LAVGLLVGNF  
 IQPGSGLNIS VDEESSFAST ESSPEGLLGF IHSIIPETFF SAFTDGSVLQ VLFIAILVGF  
 AAQSMGEKGQ PILDFVSHLQ KLIFKILNWI LWLAPVGAFG AMAGVVGETG FDAVVQLGIL  
 ILAFYVTCVI FIFGVLGAVL KVFTGVNIFK LVKYLAKFL LIFATSSSES ALPNLMRKME  
 HIGVAKPTVG IVVPTGYSFN LDGTAIYLTM ASIFIADAMN MPMSLGEQVG LLVFMIIASK  
 GAAGVSGAGI ATLAAGLSSH RPELLHGVDV IVGIDKFMSE ARALTNFAGN SVATLLVGKW  
 TGTVDMNQVH DVLNGKSPFV ELEEDH

> RXA00660 (1-1023, translated) 341 residues  
 PGHTPEHLSF LLKDGAFAHE PGFMLTGDFV FAGDLGRPDL LDEAAGGVDT RFEGARQMFK  
 SLKEKFLTLF DHIQIFPGHG SGSACGKALG SVPSTTLGYE RQFAWWGKYL EADDEQGFID  
 ELLEGQPDAP AYFGRMKRQN RQGPAIMGAR ELLPQLEASD LHDVIVVDTR SADEVHQGT  
 AGAVNIPAGN SMAKFGSWTV DPEKDSRALV LLAASQIGAM EMWDHMRVVG IDNVAGFITN  
 FDGVDLVAPQ TVSPDQLDEL EYDLLLDVRN RSEVEEGYIP GALHINGASV LWNLEKLPRD  
 GKIVSYCKSG TRSSIAASTL RNAGFDVVEL QGSYDNWVRH N

> RXA00681 (1-744, translated) 248 residues  
 MPSPRTVLIT GAAGGLGRAF AEGFAAQGDR IAVADINLDG AQETVDKLKA LGADAAAFEV  
 DVTSLESTEA LAAGAAEFGG GRIDVLINNA AIYATVTRSP FEDIDPAEWD LVMGVNLKGP  
 WLTVRSVSPF LSDNARVVNL SSATVFGSGA HWAHYVASKG GVIALTRVLA KELGGRGITV  
 NAVAPGFTLT EASLGLMDSA ETYGVDRGSI KRASQPKDIV GTTMFLASPE AEYITGQTLI  
 VDGGRQFI

> RXA00690 (1-1146, translated) 382 residues  
 VKWIERYVLS RRMVHPWAWW VWALGIAGCA SMTNNPYILA LTFATLCFVV FNRRGSSPWS  
 RAFFIYLMIA GWLVVYRLVM HIVVGAKIGT IELFRIPPVQ LPEWAAGIHF FGTVYLEGLI  
 IATTQGLTLG TMIVAVGAAN SLADPKLLK SLPGALGELG TAVVIGISIA PQMAESAFRI  
 NRATTLRGDD AKGVRGFARI LMPVFQDTLD RSLALANSMD ARGYGRQAHV SKFQQRVTSI  
 FGAFGILGVT VGLFVVLDAS SPMFVAVPVF ITGVGFLIIS LVVASHRKTS TTFDQLPWGA  
 AEWLVCITGV IPLLMAALTR YLDPGSMITT WVPLHMPDTV PLLVVAGLVV ATMPGFLTFR

LPKNKVRVKR RKAINSPERA EV

> RXA00733 (1-408, translated) 136 residues  
MSNTAGPRGR SHQADAAPNQ KAQNFGPSAK RLEFGILGHDR NTLIFVIFLA VLSVGLTVLG  
PWLLGKATNV VFEGFLSKRM PAGASKEDII AQLQAAGKHN QASMMEDMNL VPGSGIDFEK  
LAMILGLVIG AYLIRS

> RXA00735 (1-669, translated) 223 residues  
GPTGAGKTTL VNLIMRFYDI NSGSITLGET AQDAVDIRTM AREDLRSRTG MVLQDTWLFA  
GTIRDNILYG RPEATEEEML AASKAAYVDR FVRSLEPGYD TVLDDEAMNL SVGERQLITI  
ARAFLANPRL LILDEATSSV DTRTELLIQR AMSKLRQDRT AFVIAHRLST IRDANLILMM  
KDGEIVEQGN HRELMALEGA YWELYSQFN APAKEELQAD GDH

> RXA00796 (1-198, translated) 66 residues  
MSKIAIITGS TRPGRVNIDV ANWVLERAQE RNDAQYELVD IADFNFPVLD EAMPAGYGQY  
ANEHTK

> RXA00801 (1-633, translated) 211 residues  
MAHDGLRVEN IVTSGIFALD GGEWEVDNNI WVGNDDEVF IIDAHAHTAAP IIEAVGGRAV  
KGILCTHAHN DHITVAPELS KEFDAPIFVH PGDQMLWEET HGNTLHEDLA DQOKFQIAGT  
ELIVLNTPGH SPGSSCFYLP EANELFSGDT LFQGGPGATG RKYSSFDITII ESLKTSILDL  
PAETTVRTGH GDHTSVGAEA PHLEEWIKRG H

> RXA00802 (1-714, translated) 238 residues  
MDLKLGGQVI LUVGGAGTIG SEVVKLLTEE GATAVAASRS TPLSIDASDE ASVRAGIDQV  
IAEHGRDLGL VVSSAPAAQT LSAETADDPD TVLAAIEGKA ITFMKAATVA LEKMREAGHG  
RIVALSGMNS YKTLSTTASA RNAALNVVVK NLADRHAGTG ITVNAISPGF VVAEPDAEVN  
RANGDTTWR RRRSRFCCR RAPHQFLERL FRWDIRRRAS SFLSSRELPK RKHPRVRA

> RXA00819 (1-990, translated) 330 residues  
MVGGSPEQAQ RLDAQIKSGE VKGVFALTEP DHGSDIAGGL ATTATKDA DT GEWIINGEKR  
WIGGASTADL IATFARDTAD NQVKCFLVAP QAEGVSMEII DRKASLRIMQ NAHITYNNVR  
VSGDARLHNI NSFKDVSECL RMRSDVAWM AVGAQAGAYE AAVKYVRSRE QFGRPIAGFQ  
LIQEKLALML GNLTA SLGMM VKLTDQQQAG IFKEENSALA KMFTSLKLRE TASWAREICG  
GNGIILDNDV ARFHADAEAV YSYEGTHEIN ALIVXXXILX XXFFLYYXXF EEDLHDYFHH  
PKPSFLSKTH QPSPARTWAF RSGALSPRRW

> RXA00821 (1-843, translated) 281 residues  
VTKLERMEHP AYSQLRPVTP SASVVLCPNP GYSSLEGTNS WVIRAPEDPR SIVIDPGPED  
EGHLNVLHSHK AEEVGLILLT HRHYDHADGA QRFRQLTNAP VRAMDPSYCA GAEEIHDGEI  
ITIDGVTPQI EVVATPGHTR DSVSYFIWSG VPHESTLEGI VSGDTIAGR H TTMISSETDGD  
LGEYLSLAI LEERGKDIPL LPGHGPDGQD VSSFARKYIE RRELRLNQIR EVWETRGRDV  
SMKDLIDAIY DDVDPVLRGA AEQSTHVAIR YLQAQEASAS N

> RXA00827 (1-753, translated) 251 residues  
VNLLIKINPV TRIIALMVL TPLLLSLDVM SAAIALVATI ILAPFAGVTW KMLLKRGWML  
FLMAPVAALS MALYGRPDGK EYFSFLIHV TDNSLALAAA IGLRVLAIGL PVVVL IARID  
PTDLGDGLAQ LLKLPERFVI GAVAGSRLMT LFREDWYSMS RARRARGIAD QGKIKHFFTM  
TFGLLVLSLR RGSKLATAME ARGFGRTTGR TWARESTVGA RDLVLILVCA AISAIALTVS  
IQTGFFKFLG T

> RXA00842 (1-1200, translated) 400 residues  
MIIQILRVAF AFVGIIVGAG FASGQEV MQY FVAFGIDGIW GVIVSAVIMS VMALIILQLG  
SYFNAGEHGE VFRRVSHPVF SKILDIGVVV TLFSTGFVMF AGAGSNLNQQ WGLPLWIGSV  
IMVLLVLAAG MLDVDKVTTV IGAITPFI III FITAASIYTL VGNFSSVEQL DSAALEVGT T  
LPHWAVAAVN YVGFNLMVAV SMAVVIGGSM FNPRVAGRGG LLGGLILGFL IISALT LFA  
TVEEVGQDDM PMLTIINN LN PLAGQVM AV IYGMIFNTAL GMFYALGRRL TAKNPQRFRP  
VYVVTVLIGF VLSFVGFKNL VGYVYPVLGY IGLLLIAVMM VAWVRGRVRI YKESERRMRI  
ADLLQIGHDG ALSGAELAVL NQEIQDSNLD EEQIKA AVRK

> RXA00847 (1-1449, translated) 483 residues

VACQANPGPA PVEEPTTATA TTTATETTTV ETEAPKQDRE TISIGIDPIR NGFNPHLLSD  
 DSPLVRDTAS LVLPSAFEGN QLNTDLLDNV EQVDETTVRY TIAQEAQWSD GTPITGSDFE  
 YLRRSIVAGT GTLNDSAYS AISEIRTSGGG KTVDVIFEHP VADWHLLFNN LLPSHLITGN  
 STFQTAFYDS IPASAGRYMV RSIDRQRGVI TLSRNDREWG ANPAHVEVLQ FNTVASASRA  
 GEYLRTGQSS FMNLSPQETL VDTLNLVPDT EVRVSDTTRT LELVFNAEAL APAQRAYLTS  
 LIDVPLTAKL AGGRSANLGV PQTVEASVDK QEIPALRLAA DPADDAGLAA ARGIVDMLAA  
 DGIKAQVVT DLNSAIAGNF DAIVAWTRTA TDSIALADRV GCGVNLAKWC AEGTTEYING  
 VLAGIEDFDP AWEQQFNTEN HLRVPILRET RVEAKNNGIL GAADGWPGGI SSAASWRKND  
 VEE

> RXA00851 (1-609, translated) 203 residues  
 MNSIPLGFYV DKQSVVHSFP ALWKFPLLLFI FIIGGSIAAS TPVHGLILVG IAVVFYVLAK  
 IPLKVAWEQL WPVLPILIML GAFQWWQRGF DFAATTVLTL FSAVMAAMLL TLTRLEALM  
 NAVERMLQPF ARFGLPVETI TLAISLTIRL IPLQLATVKE VLDARKARGA GFSIAAFGTP  
 VIIRSIKRAR NIGDALLARG AGD

> RXA00852 (1-690, translated) 230 residues  
 MPEIIFDNT VRYDDSLILE PLSLKLTEQR IGIIGANGGG KSTLIRMING LGPEPTTGRVL  
 VDGLDVSHSG REVRKKVGFV FSDAENQIVM PTVREDIAFS LRRHKMPRAE KAQRVDEMMA  
 RFNLSEHADQ SPHTLSGGQK QLLALAAVLI LEPEVIIADE PTTLLDLNRN LMIKDVFNKL  
 EQLIVVSHD LDFLSDFERV ICINDHKIAA DGPPQKSIDL YVSLMAEPAK

> RXA00856 (1-537, translated) 179 residues  
 VSDVSAGVNG AQDPSNQAVK PSNWNLPNFL TSLRIIVIP FAWLTLKGET ENNAFAWWAL  
 VVFILLMITD KLDGDIARAR GLVTDFGKIA DPIADKALMT TAFVCFNIIG ILPWWVTALI  
 VLREFGITIW RFFQLRAGNV VPASKGKGLK TALQTVAVAL YLCPFPSWMD IPSQIVMYA

> RXA00870 (1-1512, translated) 504 residues  
 MSEPTQISHW IDGAISPSTS GKTAPVYNPA TGQVTANVAL ASQEEIDATI ASATKAAKTW  
 GNLSIAKRQA VLFNFRELLN ARKGELAEII TAEHGKVLSD AMGEILRGQE VVELATGFPH  
 LLKGAFNENV STGIDVYSLK QPLGVVGIIS PFNFPAMVPM WFFPIAIAAG NAVILKPSEK  
 DPSAALWMAQ IWKEAGLPDG VFNVLQGD KL AVDGLLNSPD VSAISFVGST PIKYYIYETS  
 AKNGKRVQAL GGAKNHMLVL PDADLDLVAD QAINAGYGAA GERCMASVSV LAIESVADEL  
 IEKIKERIDT LRIGNGAGDE QGEPHLGPLI TDVHRDKVAS YVDIAEADGA KIIVDGRNCA  
 VDGHEEGFFF GPTLIDDIPL TFRAYTEEIF GPVLSVVRVA SFDEAIELIN SGFEFGNGTAI  
 FTNDGGAARR FQHEIEVGMI GINVPPIPVV AYHSFEGGWKN SLFGDAKAYG TQGFDFFTRE  
 KAITSRWLDP ATHGGINLGF PQND

> RXA00875 (1-567, translated) 189 residues  
 MTTEVELVL ADSEGNPIGT APKATVHTKD TPLHFAFSTY ILNPRGELLV TRRALSCKTW  
 PGVWTNSMCG HPGPDETAD AIRRRGVDEL GLEVDSFLDI QEILPDYQYR AVDASGIVEW  
 ELCPVHLVRL AVGEFVEPLD DEVEEFWEAE PQKLFDVADA TPFVVFSPWL DQLSAPELRQ  
 AILEAFDAE

> RXA00878 (1-1863, translated) 621 residues  
 MRLLGRILKT TSALWPYYLG IIVVSIVIAA LSLSPFILR EATDSIVSAV TGSNTVDAVT  
 RTIIFLALAL FVASFLNTVM TNIGGYIGDV MASRMQILA TRYAKLLAL PQKYFDNQVT  
 GTIARLDRS INGITQFMQS FSNNFFPMLI TMVAVLIISA IFYWPLAILL AMLFPIYMWL  
 TALTSKRWQK YEGEKNHEID VANGRFAEVV GQVKVKS FV AETRELADFG GRYGKTVAIT  
 RPQSGWWHRM DTLRGAALNI IFLAIHLLIF YRTLHGHFTI GDMVMLIQLV TMAQQPVYMM  
 SYIVDSAQRA IAGSRDYFEV MAQQVEPTAN KELVDATLAS DTPRISVGTP AALPAGEPAM  
 EFKNVTFAVE EGKPVISDV ITRHGERIA LVGESGGGKS TLVNLLGLY KPNSSGLAVC  
 GVDVKDLTSE ELRASVGVEF QDASLFSGSI AENIAYGRPG ATREEIIEVA KKANAHEFIS  
 AFPEGYETVV GERGLKLSGG QKQRVSVARA MLKDAPLLVL DEATSALDTK SEQAVQAGLE  
 QLMENRTTLM IAHLRSTIAG VDTIVTIQNG RVEEVGSPTE LAVSGGIYSE LLRLTNSTAE  
 ADRLRLRAFG FTGDAPAEED

> RXA00880 (1-1845, translated) 615 residues  
 MTSPNTLQEY TEPKYTIGE SETCLTALLD QIKTRPYGVL FSKPANYEWV NVTAKFQDE  
 VFAVAKGIIS VGVEQGDRVA LLSNTRYEWA VLDFAIWAAG AVSVPIYSSS SLSQIEWIIE  
 DSGAVLAITE TPDHTDLMKN LVIGEDGTPA IKGSPSKLRR ILEINSSALE TLKFEGRELS

DELVWERIHA TKAADLASLV YTSGETTGRPK GCELSHYHWL AEVRALITND IGAIAMPGSR  
 LLTFLPLAHV LARAVHLAFA VTGATQSHWS DFSTLTLELQ RSRPNLILGV PRVFEKVRNA  
 AAANAADGGA IKRIMFERAE KAAIEYSMAL DTAEGPSKSQ VMAHKAFDKL VYSKIRAAVG  
 GDVQYAITGG SAMGQELLHF FRGVGMTIYE GYGLTESAAA AAVDFTDQKI GTVGKPMGGM  
 TIKINEDGEI MLKGEMLFQG YWNNPEATAE ALHDGWFNTE DLGELLESGL LVITGRKKDL  
 IVTAGGKNVS PGMEDIIRA HPLVSQAMVV GDGKPFVGLL VTLDPMMLKR WKLNNHIAES  
 RTVSEIATDP ALRAEIQDAV NNANATVSHS EAIKRFYILD RDLTEEDEL TPTLVKVRNV  
 VVRRYADAID HIYNR

> RXA00899 (1-1266, translated) 422 residues  
 MEDVHDDVPD IPTGMDVSAE VESVIKLNRR LTRMPAVTGG NNGFYSDYRE SLKRMTAAID  
 EAEEYIYVEI YIMAWDSYTO PFFAALERAH NRGVKVRLLE DHVGSWKYPG YHRLKKELNR  
 MGFAWYMLLP LQPWRRRFRP PDLRNHRKML IIDGHTAFMG SQNLIAPSYL QKKNIKLGRE  
 WKDLMVELTG PIVSSMEMIF AGDWYVESNE ALDIRDHAEA HGYIGNTQKD SATNLVQLIP  
 SGPGYTTEPN LRMFNSIVHH AKERLILCSP YFIPDESLE AVTSACYRGV TVELFVSEQA  
 DQFAIDHAQS SYYQALLEAG VKIYQFPKPD VLHTKYMIAD PDDTTGNEAL GVLGSSNLDI  
 RSFGLNIEIS LMIKGNLIH ELNALTDRYR TVSFKLTLTK WNQRSWRRRY VDNVMRLTSA  
 LQ

> RXA00902 (1-1233, translated) 411 residues  
 MSSGFYVQH PRRALPPPPI ERKGPAALFL PGTFHPINPK NIAASHDQVL LSGWGKFVRW  
 LLVLLSILVI IIGINLILDG VYGFGTSTT QMYQVAKDPL IGVLLIGLAT ALVQSSTTTT  
 TLTVTAVGTG IVSVPVAIPI ILGANIGTTI TAMLVAFSYV GERREFKRAF TVAAMHVWFN  
 VLVILVLFV ELLFHPFTI SGAIATEITL TTGGSLEPTSG VMTKIFDPPT QLLGMNGLIG  
 SIGNPSISAI VCLVVGITLI LISVRAMSSQ IRTITAATVT SIMDKVINPE NSPKATILSN  
 FWSFILGVLF TLMVTASSVT VASMQPVAAS GVVVKQKPLL VILGANVGTT VTAMFATFAI  
 VSDQGEFAIQ AALIHLLVNF TGALLVLCIP QLANVIIHLA EKTANLTARS Y

> RXA00931 (1-846, translated) 282 residues  
 VKTIEDILTL EEIDRDIYRG PVIESYLART FGGQVAAQAL VAATHTVDKA FTVHSLHGYF  
 IAPGDPTAPA IYLVDRVRDG KSYVTRSVRG IQDGEVIFSM QASFHRGDEG IEHMDKMRKV  
 PAPDEIKGTV ERMPISRRV LDEWAEWDIR VIPQDQLELS DFTATEQAVW IRCTADLPDN  
 PTFHQCSLTY LSDMTLLHSA LVPHPGKMQ MASLDHAVWF LRPFRVDEWL LYDQRSPSAS  
 SGRALTHGRL FNQQGDLVAI VNQEGMTRTL HEGAQSIPMR KD

> RXA00941 (1-1317, translated) 439 residues  
 MNLTRNDRDL RLPVTSKHKK ILGGSGIGWA LDAMDVGLIS FVMAALATHW GLSPTETSLL  
 GSIGFVGMAL GASLGGLLAD KLGRRQVFAL SLLVYG VATG ASALSVSLAM LMALRFVVGL  
 GLGAELPVAS TLISEFSRPR VRGRMVVILE AFWALGWIMA AIVGTFVVG SDNGWRWALA  
 LGCVPPIAYV YVRLGLPESV RFLEKKGRHD EAEAIVSFE EAAAAEGKAA DATTAVVHDN  
 AAEGSVSIWS AALRKRTVAL WIVWFCINLS YYGAFIWIPL LLVADGFTLV KSFQFTLIIT  
 LAQLPGYAVA AWLIEKWGRR STLATFLVGS AISAALYGLA NVEWQILVAG CLLSFFNLGA  
 WGALYAIGPE LYPTNVRGTG TGAAAGFGRI ASIIAPLIVP PVIAFGGPIA LFALEFATAFA  
 IAAIAAFTLP EQKGKSLAD

> RXA00962 (1-666, translated) 222 residues  
 DKAIKADHDI REGHDEPAGF KDLLVDRIYRW ISIWALATF VTLLAWYGLG TWLPRLMETA  
 GYEFGHALMF TLALNLGAVI GSVVTAWAGD RFGPIRSGVI AAGIAGIAL LLLTYPPVTA  
 VYVILILAGV GTHGTQILII AAVANFYPSN LRGTALGWAL GVGRIGAVVA PQLAGLLLAW  
 NLGVNSNFIM FGTAALLSAL ALSVLLRLQK TYSVTHKVEI QG

> RXA01060 (1-924, translated) 308 residues  
 MNRTLRLTLGW LAAVIQEDPE PWFTTDPDTE YVPYVNSFSF ESLSLVPDAL MLLKRSLLHA  
 MEQQDLVPKD LQEALRHVLV FKHFREWE LELAWDSERT KSAVRIEST KESLADQYRD  
 YKYAFLPELI FQESRGIFDF ELEGYTLKVG QSTLSIPWDM IANGYVPASL RNFGELMDRD  
 TGDLDADPIL RPRELKFEIH NCPDLNPWIM RETFDFMMEI ATETGWFHAL NPAYNSVITY  
 DLISRPDFFL VEGSFRPHSV KRSWEKIQKI AKAVESYASH DYCMTSLTHD YRAIELSLTP  
 TKTEEPST

> RXA01067 (1-729, translated) 243 residues  
 VSEFQVPEIP AQFLPKHIAL VMDGNRWAT ERGMKRTEGH KRGEAVLLDV VDACIELGVP

YLSAYAFSTE NWRRTSTDEV FLMGFNRDVL RRQRDDLHEK GVRVRWVGRR PRLWRSVIRE  
 LETAEELTKD NTTMTLAMCV NYGGRAEIID AARDIARLAA EGKLRPEQIT EKTFFPNFLDE  
 PDMPDVLFL RPSGEKRTSN FLLWQSAYAE MVYQDKLFPD FTQQDLYDAV LEYAKRDRRF  
 GSA

> RXA01114 (1-792, translated) 264 residues  
 RLAEARETAG GRNHPIPGGM IETAENLRRE YGISREEQDK ISAASQQRWG KAADAGLFDD  
 EIVPVTVPAG KRGQEPTIVS RDEHGRPGTT VEKLAALRPI MGRQDAEATV TAGNASGQND  
 GAAAVIVTTR AKAEKGLRP VMRLAGWSVA AVPPETMGIG PVPATKKVLD RLGLTLEDIG  
 AIELNEAFAA QALSVLKEWN ISWEDERVNP LGSGISMGP VGATGARMV TLAHRMQREN  
 TQYGLATMCI GGGQGLAAVF EKEN

> RXA01136 (1-432, translated) 144 residues  
 MTLDFYKASG TDYALGLAAE SEGARRTGIT GMASAFKEFA GCGEIDLEAT RVEGGLKVSG  
 KLRWASNLCE DPVIVPAAKT AEGLQLLFAL GAETEGVTLG SSLALLGLNA TACAWVSFED  
 VFIPGAQILS HDFTLWHRC AQPS

> RXA01138 (1-417, translated) 139 residues  
 VVTTTDGEVD HGLTVSAFVS LSLEPAMVLV SIDKSSVVP FLEQGSPVAV SVLSEEQSDL  
 AITFGRHLEN KFDGVSIRK TNRAAVLEGA SAWLSGAVVD KYPGGDHFII TIAVEECAHD  
 EEQKPLLYHR GRLFQWQED

> RXA01172 (1-1455, translated) 485 residues  
 VLASFRFAFS SPRRFRTEVL AGLVVALALI PESIAFSVLA GVDPKMGLFA SCTMAMTIAL  
 TGGRPAMISA ATGAVALVIA PVVRDHGVEY FLATVILAGI IQIALSLLGV AKLMRFIPRS  
 VMLGFVNALA CLVFFAQLPH LIDVPWMVYP LFALGIGIML FWPKLTSVIP APLIVIVALT  
 AIVWVFGINI PNVSDQGELP SSLPEFLIPN VPLTLETCLI IGPYALGMSL VGLMESLLTA  
 KLVDDITEVH SNKSREAAGQ GIANIITAFI GGMGGCMIQ QTMINVKNIS ARTRLSTFLA  
 GGFLLLLVVL LGDVVGKIPM AALVAVMIIV SIDTADWHSI NPRTLKFMPL SETIVMFITI  
 IATLVTGNLA IGVILGVLTA MVMFARRVAH LVSVERTTDN NISTYTVKGQ LFWASSNDMV  
 YSFDYSDEAE QIIIDLTAEE IWDASTVATL DSIHKKYAR GKSVEIIGLD GPSRDLRLERL  
 SGKLG

> RXA01191 (1-1407, translated) 469 residues  
 VSLDANTIET AGRGDVISRI ADDSREVSTA ASTVVPLMVQ AGFTVVISAF GMAAVDWRLG  
 LVGLVAIPLY WTTLRVYLPR SGPLYTRERE AFGVRTQRLV GAVEGAETLR AFRAEDTELK  
 RIDAASGEAR DISISVFRFL TWAFSRNNRA ECITLVILG TGFYLVNIDL VTVGAVSTAA  
 LIFHRLFGPI GTLVGMFSDI QSASASLIRM VGVINAASNQ VSGTSPASAS TALTLFDVSH  
 HYHTAPVIKN ASVQLEPGEH IAIVGATGAG KSTLALIAAG LLSPTSGQVA LGGSSFSNVE  
 PEALRQKIAM VSQEIHCFRG SVLDNLRIAR PEATDADIHA VLADIGDSWL ERLPQIGIDI  
 VGDGAFRLTS VENQIMALAR VHLADLAIVI LDEATAESGS DHAKQLEDAE LKV TENRSAL  
 IVAHRLNQAK TADRIIVMDS GEIIESGTHE ELRAIGGRYE QLWTAWSAR

> RXA01205 (1-531, translated) 177 residues  
 VSAYPPAIIA AALVGICAGV LPHNFPSRI FMGDSGSMLI GLLLAASST ASGKINMSLY  
 GAADFIALIS PIIIVLAAVA IPLLDLVMV VRRVGRGASP FSPDKMHLH RLLSIGHTRH  
 RVVLVLYTWA SAVAFAVSF SVVPLFATG SSICGILIAV AVTAVPVMKS RRAAKLD

> RXA01212 (1-813, translated) 271 residues  
 GLNFHVQRGE VFGLLTNGA GKTSTLEVIE GLSAPSSGTV RISGLDPVAD RAILRPELGI  
 MLQSGGLPSQ LTVAETMDMW HGTCTYPRAI KDVLAADVLL HRENVKVGAL SGGEQRRDL  
 ACALLGDPSI LFLDEPTTGL DPESRRHTWQ LLLDLKQRGV TMMLTTHYLE EAEFLCDRIA  
 IMNAGEIAVE GTLDELVARE KSIISFVLRG GQVELPVLSG AEIIRDNNHV RIATTTLQOH  
 TLEILTAAE TGIALEGFAA KPATLESVFM D

> RXA01219 (1-882, translated) 294 residues  
 MDILLNQLVA GLSVGSVLLL VAVGLSLTFG QMGVINMAHG EFIMVGAYTA YVVQLVVGSA  
 GLSLLISIP LAFIIGGLFGV LLEQFLKYL YHRPLDTLLA TFGVGLILQQ LARNIFGAPA  
 VDVRAPEFLR GNEVVLGV LVPTARLFILAL AIASVTALAV FLNRTAWGRR IRAVVLNRDL  
 AETAGIDTRA TDRMTFFVGS GLAGIAGVAI TLIGATGPTI GQNYIVDAFL VVAAGGIGRV  
 KGAVIMAFVL GITQAFVEYT TGASIAKFIV LIAVVAFLQF RPQGLFQTQT RSLV

> RXA01220 (1-1077, translated) 359 residues  
MSTQLKLLKKP AKKKTTTPKLS VVNAPTLRTA ALGLAALAAV LLCAPLFLST FQLTLMSRLV  
CYAIVAVGIG LAWGRGGMLT LGQGVFFGIG AYIMAMHMLY SDSQIFGTTV PQWWSIFANP  
AVALIAVVAL PGIVAFVLGF SIFKRRIKGA YFAIVNQALA AAVVVLLVGQ QDSLGGSNGL  
SGFRSEFMGFA VYDPINRIMF YFTAVGVLLA LVAISYWLMR SRYGELLVAT RDAEERVVRL  
GYDPALIKTA AYVIAAMIAG IAGALFVPIV GIISPAEIGV VPSIVFVIAV AAGGRASLFG  
PVVGALVLGW VESTLAQTFP SMWSYFQGA I LVLVIVLLPG GIASIKLSAL KNKARKATS

> RXA01221 (1-726, translated) 242 residues  
MSLKITNLKV AFGSFIADVNE ISFQVLPGHV HFLIGANGAG KTTTCIDAISS LAPGQGSVQL  
DGTEILGTPV HRIARMGVGR TFQTASVFEE LSVLQNLDA CGIHRPLRAL LGVRHRIDPR  
IEHALEVTGL ADLVNAQAGT LSHGQKQWLE IAMLVQDAQ VLMLDEPVAG MSEEERVATG  
ELLQRVARGR VVLVVEHDME FMRRFATRVT VMNRGTILCE GSVDEIQANP DVQSIYLGTA  
GK

> RXA01222 (1-699, translated) 233 residues  
MLEITNLCAG YGRTQVLHSL SISTSSNGIL SILGHNGAGK STLLRTAVGL IKPTSGEVKL  
FGQDVTSLST HERVKRGMAY VPQGQQSFTQ LSCMENLQVV ADLQGRVGKA RIAEALDRFP  
ALTQVLDRQA GLLSGGQRQO LAIARALITA PKLLLLDEPT EGIQPSVVAE IQQTIIDLAK  
DGMSIVLVEQ NIGFALDAAT SYAIVARGQV VESGQGAETT AEKQTKVRES LAI

> RXA01235 (1-972, translated) 324 residues  
VVLFSGFSGV IDLSPTAVIR HLSGQDTLTP RDQAIFFDIR LPRIIAGVIV GATLAISGAA  
YQAVFRNPLA DPYLLGVSA SGLGVTAIV GGTVLGFSAP SIGVIGAAV GGVA AVLATL  
MVSRGVGGQS STTVVILAGV AVAAFASSIQ TYIQQRHIDT VARVYVWMLG NLNVTNWMSI  
FIVAVVAGLC AAVIMSCARL LDVMAVG DVE ARTLGVD PGL VRIGIVIVAT LGTAAVVSIS  
GLIGFVGIIV PHALRLIVGP GHRILLPLSF VWGAIFLVLA DTAGRTLMAQ QELPVGVVTA  
ALGAPFFLEI LRRTSRQRPV KRSA

> RXA01260 (1-1182, translated) 394 residues  
VTFNYEDAHK RSRGVSDKIV GGVHYLMKKK KIIEIHGLGN FKDAKTLEVT DGKDAGKTTT  
FDDCIIATGS VVNTLRGVDF SENVVSFEEQ ILNPVAPKKM VIVGAGAIGM EFAYVLGNYG  
VDVTVIEFMD RVLPNEDA EV SKVIAKAYKK MGVKLLPGHA TTAVRDNGDF VEVDYQKKGS  
DKTETLTVD R VMVSVGFRPR VEGFGLENTG VKLTERGAIE IDDMRTNVD GIYAIGDVT  
KLQLAHVAEA QGIVAAETIA GAETQTLGDY MMMPRATFCN PQVSSFGYTE EQAKEKWPDR  
EIKVASFPFS ANGKAVGLAE TDGFAKIVAD AEFGELLGAH LVGANASELI NELVLAQNWD  
LTTEEISRSV HIHPTLSEAV KEAAHGISHG MINF

> RXA01261 (1-171, translated) 57 residues  
VTEHYDVVVL GAGPGGYVSA IRAAQLGKKV AVIEKQYWGG VCLNVGCIPS KVSDQKR

> RXA01269 (1-441, translated) 147 residues  
VVFEMIKFRT MLEPDEKHVT DEQRLTKVGK LLRETSDEL PTLWNVFKGD MSLVGPRPLL  
VSYLEHYSSE QARRHEVRPG ITGLAQVNGR NQTTWDERLK LDVEYVDRCS LKLDKFILIA  
TVKTVLSKKG ISNEGHVTMP SFIEERK

> RXA01291 (1-933, translated) 311 residues  
VADQQDFLGR FDAMSSKATA TVIAHYSSSF TLASKLLSPK IRRDIEALYA MVRVADEVVD  
GAAAAAGCAP DAVAEILDNY ERQVLLSLV PFHTDPVIHA FGNTARKCGF EQAHIVAFED  
SMRRDLSQTS YDPTQLDEYI YGSAEVIGLM CLKIFLQDST ASPQDRATME HGARRLGAAF  
QKVNFLRDLA EDREGLGRSY LPVFTEEMRD EIVTDIREDL DAARLSIPLL PFGARTGVRA  
ATDLYGCLVD NLESASLEDL KNGRDFVPSL KKPAPQPKQC GKCKCFKNDKS SGHRRGTSRT  
SHHRTALTR I

> RXA01292 (1-1185, translated) 395 residues  
MTKAVVIGGG LAGLATTALL LREGYEVHLV EQNEHLGGRA GTFELDGFRW DTGPSWYLMF  
DAMSHFFKLC GTSIDDHLDL VPLEPAYRVI DDHGEFIDVT SDIDAMAELF ESREPGAGAK  
LRTYIDSATQ VYNLAIDGFL YTNFTNFIPY LSPGMLRLLP KLLASLSTSL KVKVNTQFRD  
TKLRQILSYF AVFLSSDPSH TPALYHLM SH TDLVQGVSYR RGGFTAFIKA LISLIDDAVL  
HLGTPVSAIT TQGRNATGVQ VGSEFIEADI VISCADQHHT ETQLLPASLC AKPETSWKNK



QPGLSTVLVL AGVKGEHTLL FPPTGTKISA KFSTAPPQNS RLQNPSRSPR PPQQIPMPHP  
KATRTESSWS QYPPMSPLVT GPLTEKNLTW WAGSQ

> RXA01293 (1-327, translated) 109 residues  
MVGRIAAIAV AQIGRWAGID GLESRIVVQR TIGPADFADR YNSWSGGSIG PSHTLAQSAF  
FRGSNKSARKV DGLYDAGDTT VPGVGVSMLC ISAENVLKRL RGDNSVDRT

> RXA01339 (1-1245, translated) 415 residues  
MTTESIVAHN AAGTAPQNVN SAKKKYLSVA QGVALIYGTN IGAGVLSLPY AARNGGFLAL  
VVALLIAGTL TTISMLYIAE VSLRTKKPLQ LSGLAKEYLG QWGRWLVFIA IVVNSVGALI  
AYASGSGILI GNLTGLPPIV GTLGFFVLGT LIMWKGLHTA SFVEALITTG MATIIIVLCG  
WTVLGPISIA DNLIVFHPFF IVPIMNLAVF TFLAQYVVPE IARGVNPATP KAVPRAIIG  
MVATGVTLAA VPFAALGLLG TGVSEVVTIS WGEALAPVAY YMANAFALLA MFTSFIAIGF  
TAMRNVLDIG HWPQHGQWRS VAVGLTVLPP LAISLAGLGG FVAALSYAGG FAGAIMSIIP  
VLLLRNSRKS GDQEPVWKAT WQAHPIFQIL LIVVYSLAFV YSVLAIVGLM PAGWA

> RXA01382 (1-1062, translated) 354 residues  
STSTAAGTGT ANEEGTITAA ISYELGTNGY DPMTTTSALT VAANWHTLEG LTEIDPATGE  
VYAALASALP SADATSLDIK LRDGATFHNG DAVTADDVVF SFERVLDPAN NSLYASFIPF  
IKSVTKKDDT TVTIDL DYAT GIISERLAVV KIVPKSVVEA DASGFDANPI GSGPYKMTDN  
GASKVVKFER NDDYNGPRPA RAAKMEWQII PDASTRTNSL QSGSTMAIDS VPYLSIPQLE  
ATSTVESVQG FGLLFAMFSC SEGNPFNDVR NRQAFLYALD MDKIVKTGMS DQATPATSEFV  
QKEHPNYNQA STVYSLDADK AKALFAETGL TSLNLLCTDH DWVKNCTPLI QESL

> RXA01399 (1-1119, translated) 373 residues  
ILSPATALVL AIGLIAAAII PLLAARGVK TAEARRAESS EAYLSSLDQV LSNQAALRVR  
GEMPAALSKA DVAARSYSSS LEAGAKDTAI GAASSLWIHG FTVIGVLMVS ASLYADGSHS  
PQWFGVLVLL SLAAFEAVSV LPDAAIARTR AADATRRALAE ISALPESVSL ELRTASDQPV  
LRAENLVYGW DSDLGTSNLD LTFGSRHEII APSGTGKTTL LLTLAGLLEP RGGQVLIDGT  
NPSELKNAVL FSPEDAHIFA TTVRDNLALG APEATDAEMT SILEHVGLSE WVQGLPDGLG  
TVLDSGADSL SGGQRRRLLL ARVLLSDAPI LLLDEPTEHL DTAGSSEILS MLASDELPGK  
RARRTVVIVR HVR

> RXA01419 (1-264, translated) 88 residues  
MLLSARTHTS FQELGLNASR RKAINWTLAL TVVLIASMFEV GVLIGASGTS VFSTWTVISH  
HLFGTELGGS DTADAIWYI RTPRVLLA

> RXA01420 (1-759, translated) 253 residues  
VTLGGLNVPS WSLGAEMLFY LTFPLFIPLV RKVKGVGNWW AFGITFAVSL ALITVIHFYA  
DGPKGIENFF VPRLWDTNVS PVAEVHADPV WFMQEEIPVL ESYWLSYYFP LTRLIEFYLG  
VFGAKLVAEG MFKNTNITIP LIALAVSFVA TWFEVPLAFKM SVIMSLPMAF VVATLAVRDI  
EGKSGEIASP RAVLLGNISF AFYMVQFPVM VFVQRYFIAG KEYGFLGWAF YAVVCFIVSV  
ILAWVLLPSL MIL

> RXA01467 (1-291, translated) 97 residues  
MDFNDKAASE NAVKTGAEGP NVFASVAKIL QDVGGISAED VTPESRFTED LAVSSLNIE  
LIVNAEDAFG VRIEDADAKD LTTVQDLIDF INTNKAD

> RXA01538 (1-390, translated) 130 residues  
MADNKNADDS QLVSASTGTP GPGDIAKANA PSLKQAAVTA SGRSALMGAI FLMATSAIGP  
GFLTQTAVFT NQLGAFAFA ILVSILIDIA VQLNVWRIIG VSEMRAQELG NTVIPGFGWV  
LAVLVCIGGV

> RXA01576 (1-759, translated) 253 residues  
VAPNRKISHH ALGSIPIMDA SKNSDFKDTW LVVPCYNEAT VIREVLENAL KTFPNIVAVN  
DGSPDNAAEE IHAAGAHLVN HPVNLGQGAA IQTGIEYARK QPGAKYFVTF DADGQHQVKD  
VIRMVERLRA EDVDIIVGTR FGRPRQADDQ VPLIKRLVLR TVVLLSPKTR RLGLTDAHNG  
LRVFNQKVAQ EMNIRMNGMS HASEIVDQID ERGWRISEEP VDILYTEYSM SKGQSLNNGV  
NILADGFLAR RLP

> RXA01580 (1-702, translated) 234 residues

MYKNMHIVAH RGAEDLHLEN TMTAFQAAAP ADAFELDIHA TADNQVVVIH DRTAARVAAP  
 DSLHRDTPVA RLSAAQIKEI TLIDGSPVPT LEEVLLQTSI PIQVEIKSAG AVPAAAALLQ  
 KYPEHLERLL FISFIDAALV EIVDRLPEAR VGILRDASMD DLRILDYIPL KNVGAILPSW  
 KALNVASIAD LHTKGIVKVC WTIRDENAFG IAQQAGVDYP TVSDPSRFSR PPLL

> RXA01584 (1-543, translated) 181 residues  
 VVFLGALLGA VIMGGFYPAF IQAGSTVFGG GHVVLPLEK LVVAPGFIKE TDFLSGYSAA  
 QAVPGPMFSF ASYLGAIIYG IGGAVLASLA IFFPAALLSI SGMFYWGRWR KAPRIQAAVT  
 GINAGVVGLL GAALYDPVFT HGITSVSALA IATVCWLGLA HWKIPPWAIA AGAALAGWVL  
 L

> RXA01591 (1-945, translated) 315 residues  
 ASLNWSVIVP ALVIVLATVV WGIGFKDSFT TFASSALSAV VDNLWAFIL FGTVFVFFIV  
 VIAASKFGTI RLGRIDEAPE FRTVSWISMM FAAGMGIGLM FYGTTEPLTF YRNGVPGHDE  
 HNVGVAMSTT MFHWTLHPWA IYAIIVGLAIA YSTFRVGRKQ LLSSAFVPLI GEKGAEGWLG  
 KLIDILAIIA TVFGTACSLG LGALQIGAGL SAANIIEDPS DWTIVGIVSV LTLAFIFSAI  
 SGVGKGIQYL SNANMVLAAL LAIFVFEVVG TVSILNLLPG SIVNYLSNFF QMVGRTAMSA  
 DGTPGEWLGG CTIFY

> RXA01604 (1-606, translated) 202 residues  
 DTPFADVEIA PDSGLTLLST GRESQSSSFS LVLSGRMRAS TGTIELNGEP IKATKLAKHV  
 ALAGIPEIDS LERLVTVRTV VREQLAWSSP WYLMVPRDIS DSGRWVDVEK HLGLNLNPKT  
 LIGDLSVLER FKLRIALALL ARPEAQLLVV DDPDQVRSME LRAEVLHALK GVAEDLPVVV  
 VSTNPFDDSL ADTALTITGA GN

> RXA01614 (1-1023, translated) 341 residues  
 MNQMQQWKPQ FLGEGYQNL IELGDDPDNE TDVVTTVVRY NPDNHADES F AARPALLWVH  
 GMTDYFFHTE FAEFFHNAGF AVYGIDLRKC GRSYRPGQW HYTSDLAHYF PDLTAAAEVI  
 SSTHPELVVP AHSTGGILVP LWMSQMRTSN PAAIEKIPAL VLNSPWLDMM YPPLFIKLIT  
 PMVRVLGKRS PTIIPGGGL GAYGKSIHN FYGEWDFDTT IKPVEGHKKS IGWLRAMVAG  
 QAEIHHDHVN VGVVLTLCN KSWLKESEY EDTNTSDAVL DVKHIQKWAP HLSSPSSRVD  
 VEIIDNARHD IFLSRKPARD HASEVLNNWL QSKLSSLKPS Q

> RXA01629 (1-1512, translated) 504 residues  
 VSPIRSKKKI KNEPRLTVDD VNVVPPKKIR PAIKGTVVGN FMEWYDFGIY GYLTVMTAV  
 FTQGLPQEWQ LLAVMFGFAV SYLVRPLGGL VLGPLGDKVG RQKVLYVTMA MNAVSTALIG  
 LLPTAASIGA WALVLLYLLK MVQGFSTGGE YAGATTYVAE FAPDRRRGFF GAFDLMGYSY  
 GFAAGASVVA ITTWVTTHFY GATAMEDFGW RIPFLTAIPL GIAVYLRTR IPETPAFENN  
 QDEPNVAVVEK DTEDPYARLG LAGVIRHHWR PLLIGIAIVA ATNTAGYALT SYMPVYLEEQ  
 IGLHSASAAA VTPVILVMS LLLPFVGMWS DRVGRKPVYA TAVATLILM VPAFLIMNTG  
 TIGAVLIALS MVAIPTGLYV ALSASALPAL FPTASRFSGM GISYNISVSL FGGTTPPLITQ  
 FLLQKTGLDI VPALYIMFFS AIAGVALLFM TESSQKPLL G SFPTVETKSE AVEIVKNQDE  
 DPNIDLSHMP FPDEENVGAE KQNA

> RXA01644 (1-1278, translated) 426 residues  
 MTIADIVEAT TTAIPFPHIT AFDGSFTGPE DAPYQLFVAN TDAVSYIATA PGDLGLARAY  
 LMGDLIVEGE HPGHPYGIFD ALKEFYRCFK RPDASTTLQI MWTLRKMNAL KFQEIIPMEQ  
 APAWRKALIN GLASRHRSR DKKAISYHYD VGNEFYSLFL DDSMTYTCAY YTPPESSLEE  
 AQENKYRLIF EKRLRLKEGDR LLDVGCWGG MVRVAAKHGV KAIGVTLSEQ QYEWGQAEIK  
 RQGLEDLAEI RFMDYRDVPE TGFDAISAIG IIEHIGVNNY PDYFELLSSK LKTGGLMLNH  
 SITYPDNRRP HAGAFIDRYI FPDGELTGSG TLIKHMQDNG FEVLHEENLR FDYQRTLHAW  
 CENLKENWEE AVELAGEPTA RLFGLYMAGS EWGFAHNIVQ LHQVLGVKLD EQGSRGEVPE  
 RMWWTI

> RXA01667 (1-1206, translated) 402 residues  
 MILGPKVLGL IGWSDHLSTY TTVLIAIVFA SMPYSMKFDR GVRTGMKTMW AYSTAMFVGQ  
 WGLFILLGLF LFQPVWGTDE WFGMMLPVGF VGGFGTAAAV GTALESSGAE AAMSLGFTSA  
 TVGTFAAIVG GIIFTTWGIK KGKTAAMPAQ LPWDLRSGYI DKLSDRPSIG KASTNPSAIE  
 PLALHTGIIL LTVAVAYSIN QWLGSMEPTV QIPLFAMSFV VGIVGMGIMR LLKKPEYLDL  
 DTVNSVSGAA TDYLIAFGIA SIAPAAIADY WVPLVVLVFL GTINCCFFFF WVAPRFFGEK  
 WLERAIFGWG WATAAVATGI ALLKIVDPKL KSGALNEYGV AYIGFAPFEI GMTIIAPIAV

LAGFTMGLGW ASLIVAIVIF GLAWGLKWLP ERGHVRGEGK PQ

> RXA01722 (1-1725, translated) 575 residues

MLSTMQDVPL SLTRILEYGS TVHGDTLITT WGGADGIEQA QQTFSAVGAR AAALAHALHD  
SLGITGDQRV ASMLYNCAEH METMFAVACM GAVFNPLNKQ LMNDQIVFIL NHSEAEVVIA  
DPRMAEQIGE ILKETPKVRA VVFIGPNDFS SAAAHMPEGM KLYSYEALLD GRSTVYNWPE  
QDERTAAAIIC YSTGTSGPPK GVVYSHRSly LQSLSLRTTD SLAVEHGETF LCCVPIYHVL  
SWGVPAAAFM SGTPLVLPGP DLSAPTLAKI ISTTLPRVAH GVP TLWIQLM VHLYKNPPER  
MSLRELYVGG SAVPPIVITM WEQRYGVDV HVWGMTETST VGT VSRPPSG VSGESRWNYR  
VSQGRFPASL QYRIVNDGQV MASTDRNEGE IQVRGPWVTA SYFHPDVEKE GGTASTFRDH  
DVEEENDEL F TADGWLRTGD VGSVTS DGFL TIQDRARDVI RSGGEWIYSA QLENLIVAXE  
EVVECAVIGF PDDKWVERPL AVTMLYPGIE RTRETAERLR DQLRDRLPNW MLPEYWTFVD  
EVDKTSVGKY DKKDLRNHLR NGDFEVIK LK GPGXK

> RXA01727 (1-1278, translated) 426 residues

MSKKSVLITS LMLFSMFFGA GNLIFPPMLG LSAGTNYLPA ILGFLATSVL LPVLAIIVAV  
LSGENVKDMA SRGGKIFGLV FPAAAYLSIG AFYALPRTGA VSYSTAVGVD NALYSGLFNF  
VFFAVALALS WNPNGIADKL GKWLTPALLT LIVVLVVLV SV AKLDGTPGEP SSAYAQQPAG  
AGLLEGYMTM DAIAALAFGI VVISAFKYQK VNKVRTATV SAFIAGILLA LVYLGLGSIG  
QVVNGEFADG TAILNYAALS TMQQAGRIMF VAILILACMT TAVGLISATS EFFNSLLPGV  
KYHVWATVFA LISFGVATMG LDTVLAVAAP VISFIYPSAI TLVFLSLIEP LLFRLKWTYL  
FGIWTAVVWA LFMSIPALNP FIEWAPLHSM SLGWVVPVLV ASAIGLAIDW NKKGAQSVAK  
KESISV

> RXA01737 (1-1059, translated) 353 residues

MGRMKNDGEL ADLPDHALLS IIRIPQAAKR SPWALILTRI GYAMVLLVIV TMVVYFDRNG  
YSEDLTFIDA LYYSTVSLTT VGYGDITPVT QSARLINIIV LTPARIGFLI LLVGTTLSVL  
TEESRRALQI QRWRKMRNH TVVVGYGTKG RSAVAALLGD GVPANQIVVI DTDQVSLDAA  
NNSGLVTVKG SATKADVLRL AGVSRARAVV VAPNLDDTAV LVTLSVREIA PQAMIVASVR  
ESENQHLLEQ SGADSVISS ETAGRMLGLA TVTPSVVEMM EDLLSPDEGF SVAERLVGED  
EIGSNPRHLA DIVLGVVRSG ELYRIDSPEA ETVEPGDRLL YVRRVFSEEV NDK

> RXA01755 (1-348, translated) 116 residues

MSTPDIKEGS AESPGVMV V GDRREWRRQA TGIAGLVLA ALVYLLFPSN SVETVMQSSG  
VDPETEYTN AMRLTAAVTI LMAVWWMTEA IPLAATALIP LVAFFPAFQV DFGKAA

> RXA01762 (1-1263, translated) 421 residues

MKVN LGIGSY PRRRATVRPE STAIEFEGTS ITYGEFSKRV NRLGHALLDL GVAHQDRVAY  
VGFNHPALLE VFFSTNLIGA TPVLVNPRLS ANEIDYIIQD SGASIVFYGI DLIEHATYLO  
ELHPEIIMVA VEGDEGPGLR RKALIEAASD ADIDLEVSD DLVLLMYTSG TTGRPKGAML  
SHRNLFNYF NALLSQEIEQ GAVLLSTAPL FHIAGLNMTT IPVMMKGGKV IIHREFRAEH  
VLDEIERSKV SESFMVPAMI DMLSNHPSFA ERDLSSLRAI MVGGSPLSER ALRIWQGRDV  
KIVQGFMT E TAPGACILEA TDTSTHLGTA GRAHFFTDIK LVDPKTGEEV PTGEAGEVLI  
RGPHVMTGYW NRPEDTASAL QNGWYHSGDI AIKDEDGYT IKDRIKMYI SGGENIYPAE  
V

> RXA01764 (1-933, translated) 311 residues

MSLNGKVAIV TGSGAGLGRS FAQELARQGA SVIVNDVNQA AADETVAAIT EAGGKAAAVI  
APVGPSESAA LLVREAVDKF GSLDILVTNA GILRDRSLLK MTDDDFDAVI NVHLKGTFTC  
VREAFGYFKE NGIAGRIVTI GSPTGQRGNE QGSNYAAAKA GIVGMVRTWA LEMKRAGVTI  
NAIIPAAATD MTKTVPYFQK AVEADERGEA MPAFFRET LG FGTPQDVAGL VAFLSSDEAA  
NISGQAIGAG GDRMQVWKHP EPAVTEFNPG GWTYEALQER GKNIEGNLQ SVGVVFPPEL  
AELQPQIPVK A

> RXA01766 (1-291, translated) 97 residues

MRDPIQGA VI PSDLFGFAEV LTEAERAVLL ETRRVLEEEV KPYINEAWDK AVFPDEIVQP  
LQDLQLDPP ALREAGESVR DIFTGFRNFE LARCDIN

> RXA01801 (1-1017, translated) 339 residues

MSNVNTFVQ NSTGMVELNR PKALNSLNQE MIDLVQEALT TWADDDQVQQ VLIYSSSERA  
FCAGGDVRAV RESVLEGDVA AGDKYFIDEF AMNNTLGTYP KPVISVINGV AMGGGMGISM

HGSHRIVTEK AFASMPMAI GYVPDVGFTY FGQRASSLAI ATFLAVTGWR MSPADMLWAG  
VATHFVEDAQ GFIDAVLNE LDGALEKFST QPTGSSELG VASQIEETFG HSSWALIDAS  
LRSHPDAEFV AKVDGLMASA APASVVATVK LMHQNSEATT LREGLDNELA MSLYMRQPD  
FAEGVRAVLV DKDRNAAFSP ANYEDVDESH FVTLFQRSS

> RXA01823 (1-777, translated) 259 residues  
MLQAHDLTSL YGGRNIVEGL SLDLPERGLS IIIGPNGCGK STVLKALGRL LKPQLGKITL  
GGRDISSMGT KHVAKHIGVL PQPPYAPDGV SVTELVSRGR YPHQHLLSQW SKDDEAIVAR  
SLAEVGMHHT AEHLVSELSG GQRQRAWIAM ALAQETDILL LDEPTTFLDV AHQISVLDLC  
SDLHQGRRTL AIVLHDLNMA ARYATHIAM RDGTIIDQGK PEEILTKALL KEVFDLDALI  
LKDPNNGRPL IVPTDRRNS

> RXA01833 (1-1407, translated) 469 residues  
MLFERIYEEG LAQASYFIGC QREGKAIIVD ARRDIIQTYLD LAAKNNMVIS AVTETHIHAD  
YLSGTRELAA ATGAEIFLSG EGGADWQYGF TGTTLMHNST IKLENITITA KHTPGHTPEH  
LSFLITDGAV SKDPGFMLSG DFVFGVDVGR PDLLEAAGG VDTRFAGAQQ LFHSLKEQFL  
ALPDHIQVYP GHGAGSPCGK ALGAIPSTTV GYEKANAWWA PYLRSDDEAG FVEELLGQGP  
DAHAYFARMK KQNKQGPVAV STLSPLVKLE AEEVVEKLGS EAVFVDTREQ NQVHLGTVVG  
ALNIPRGAKA SNFAAWVIDP QKDAQDLIVL APDANTAADF RDALLRVGID TVRYFTNSID  
GLPTFVPELI SPAELAETNY DALIDIRAKS EFAAGSIPGA QQLSGGSAMW RLNELPAGGT  
LVTFQCQSGAR NTVVANALRR AGFTVIELEG SYAAWEKSAA NPKNLQTAV

> RXA01853 (1-552, translated) 184 residues  
MEILGFAAGP YKTNCYVVRG ENEVAIIDPG MHAHDDLVEY ITTNNLSVDK IVLTHGHIDH  
TRDAGVVAKR FNAPVYIHPD DAFFLEVYKG SGTKTAMLF ADNMVSPDPE SLRDLVDGET  
ITLAGEEFTL KHAPGHSPGC TLIVGKEYCF SGDVLFKCSI GRTDFEWSA DAMNESLRTA  
VLPL

> RXA01881 (1-441, translated) 147 residues  
MANLINLENV SKTWGLKTLL DGVSLGVQTG DRIGVVGLNG GGKTTLLEVL TGIEKPDQGR  
VSHNSDLRMA VVTQRAELND DDTVADVVLG PLGLEVFWEA SNATVRDVLG GLGIVDLGLD  
TKVGQTFSGG RSADAPTWP RWFATLT

> RXA01894 (1-855, translated) 285 residues  
MPKPKNNAGR DLKAAIAVGI GLGVLVLLGI VLSWPWGYIL VAGFMAAATW EVGSRLKEGG  
YHLPLPIMII GGQAIWLSW PFGTMGILAS FVATVLVLMY FRIFYNGTEK EARNYLRTDS  
VGIFVLTWIP LFGSFAAMLS LMQNNISIPGT YFILTFLMLCV IASDVGGYIA GVFFGSHPM  
PLVSPKKSWE GFAGSIVLGS VTGALSVHFL LDHWWMMGVI LGCALVVCAT LGDLVESQFK  
RDLGIKDSMN LLPGHGGLMD RLDGMLPAAM VTWLILSVIS SSYPS

> RXA01897 (1-543, translated) 181 residues  
MKIGVILGSI REGRFGQVA DWVMEQIGAY DAPDVEFELI DLKAFNVPLL ESATVPGSAD  
KQYDDPRVTA WSQAIDACDA FLFITPEYNH GVPGAFKNAY DILGNEWLNK TVGFISYGAV  
EGIRVVEQWR QIVATFNMYD IRSQLSFSTF TENNNGTFAP NDRRPGELIR LLDSLLTAVR  
D

> RXA01946 (1-1275, translated) 425 residues  
IRKYSRLEEQ FQSLGGYEA AEAAQICDNL GLEARILDQQ LKTLSSGGQRR RVELAQILFA  
ATNGSGKSKT TLLLDEPTNH LDADSITWLR DFLAKHEGGL IMISHDVELL GAVCNKIWYL  
DAVRSEADVY NMFGSKYVDA RALDEARRRR ERANAEEKAG ALKDQAAARLG AKATKAAAK  
QMIARAERMI DNLDEIRVAD RAANIVFPEP APCGKTPLNA KGLTKMYGSL EVFAGVDLAI  
DKGSRVVVLG FNGAGKTLL KLLAGVERTD GEGGIVTGYG LKIGYFAQEH DTIDPDKSVW  
QNTIEACADA DQQLSRSLG SFMFSGEQLD QPAGTLSSGE KTRLALATLV SSRANVLLD  
EPTNNLDPI REQVLDALRT YTGAVVLVTH DPGAVKALEP ERVIVLPDGT EDLWNDQYME  
IVELA

> RXA01980 (1-633, translated) 211 residues  
MQIIDLSHAF APGQPHYPGD PDQEIKTVST IENDGFLMHQ YRLVGPWGTH VDAPAHFDPQ  
GRTLDQIPVE ETHLPLYCLR FSRPDLCTAA DIEAFEHTHG KIEPGSFVAL HTGWEWGKQG  
IAPGWSIEAL EILHARGVIA IGHDLPTDTP SLEAQRWWLC RDHWQIENLT NLDKVPATGA  
MIACPWPVPK DGASFPVRPI ALVPEHLSPT R

> RXA01983 (1-507, translated) 169 residues  
 MEGYGPTQIE KLLPAYTQVN TAGNNPATTP EQDLLGGAAT SPENYDHQLQ YAVDASPVHQ  
 NAAQAPPFLI MHGTGDRMVP PEQSAALHTH LVQAGRQSTL VLIEGFGHGF LNPGEVAELG  
 PNVRLDNRL EREPQTNFSA QQSPGNPFEL QGLAADHEMI KRFFTLHLR

> RXA02020 (1-1011, translated) 337 residues  
 MAKSNELGTL GLRTRHLMGL GLGSAIGAGL FLGTGVGIRA AGPAVLLAYI IAGAIVVLLVM  
 QMLGEMAAAR PASGSFSRYG EDAFGHWAGF SLGWLYWFML IMVMGAEMTG AAAIMGAWFG  
 VEPWIPSLVC VVFFAVVNLV AVRGFGFEFY WFAFIKVAVI IAFLLIIGIAL IFGWLPGSTF  
 VGTSNFIGDH GFMPNGISGV AAGLLAVAF AFGGIEIVTIA AAESDKPREA ISLAVRAVIW  
 RISVFYLGSV LVITFLMPYE SINGADTAAE SPFTQILAMA NIPGTVGFME AIIIVLALLSA  
 FNAQIYATSR LVFSMANRQD APRVFSKLST SHVPTNA

> RXA02029 (1-1314, translated) 438 residues  
 MAEARLRHLE PIDVEEWPGV ASVPNLAFAG ARARQAEYRF AKACSNAGLV LLGNPDPLII  
 DHEELFSRLA ASGWLGAEY YMAGEWRSER LADVLTALLG TGFKPRGKLS GSFTLPGQAV  
 DAGGALPNEL IRLSSGDGMS AFGGVFASGV PTTLRTAVKS HVPAGARNRE PASHFVDITK  
 ISEPVAVERE DLGEAQRRAA SFLLDGAKVK AGSHVLEFPS SGGALAILAA RRQGTVDALT  
 ADPAQVSSLE ETFVLAGEVE DIHIEVIPQA IPSPREWGA YDSIVAMEKL EVVGKHGSKR  
 FIKAIIDRLT TGGNVAMQSL VATDQWSPVC SEASISLLKAY IWPALHYPTV DEVHQLVDRD  
 SSLRVVKETH FAGHYLKSQV LQREVFEQOI REAAADGFDA VYRRMWVYHY ALIEALLRLG  
 CLNAVQFALT TRNRRGR

> RXA02030 (1-1386, translated) 462 residues  
 VTTTDHSTEL NPSDPGGQTA TLVIDKKTKR RVAAASTIGT TIEFYDFYAY AAAAVVVFP  
 LFFPANDNPT VNLLASFATF GLAFVARPLG SIIFGHFGDR VGRKATLIGS LLTMGIATIL  
 IGLLPTYGQV GIIAPALLAL MRFCQGLGLG GEWSGAALLA GENAENTHRA RAAMWPQLGA  
 PFGFFLANGF MLILVGVLAH QDGDHLGAFM TWGWRLPFLS SAIMIAVGLW VRFSLEETPV  
 FKQAVDQKK VKSPLKELFK TSPGPVVQAT LIMLSTYTLF YLVTTWILSY GIGNRSTGNG  
 LSIPIYFEFLQ LQLATIVFFA IMIPVSGWLA DVWGRKNTLT LASVLLLGFG LTFNLLLDPE  
 TATKTTVFIF LFGVMSIMGL IFGPMSAILP ELFPTNVRYT GSGIAYNVSS ILGAAIAPFI  
 ATWLVSSEFSV AYVGYLIIV TAITFVAVLT MKENKNHDLR EV

> RXA02073 (1-1530, translated) 510 residues  
 MISRLQLAK KVPPELGAST LLRLNQLLT AALIVFPWAV LSRKPDISLL AVAIIMALIA  
 LTAACRWGE QVCGHRAAFG LLAHMRVMLY DALVHKGSPS PIHGSGSIMS VATRDINSIE  
 VFFAHTIGPT VTAVLLSAGG VITLATLDPV AGLIGLLGLV IAWLIPLIGK QSSSSEATSR  
 GHIAQHLTED AAGRLEINSH GAQATRLNAL EVKEQQLEQV VTRQGLIVGI RQGAALLWPW  
 ISAVLLVALV PHVGIVAAAI ILGISPALDA VEGFARTMPT ALNSAQRYFQ IIDAPVAIAE  
 PDEPKPLPKG PLKLRIKSRV VSAKGTVSLE VAAGEHIGII GSSGSGKSTL AKLILKLAQL  
 RSGTITIGGV DIAEVSSAEL RKSVTLVEQK SVLFRASVLE NLRMGNPELS EDEAREALRL  
 ASISELPLDA DALRLSGGQQ QRLCLARALA RTPQVLIVDE ATSHQDALNQ ADLSQTLATL  
 KDTTVIIIAH RTAALTHVDR IIDLEEIKNP

> RXA02074 (1-1623, translated) 541 residues  
 MRSLLRDIPA VGWLITATIV VRTLVALVI VGIGLLIDVP SPAHSAMLWW VLAGATAAAA  
 LLCAEAVLPQ RIRARVERSW RRQLAAKNLE LNSSSSDDAQ LITLATEATS KASTYTMVFL  
 GPYFAVFLAP LTVIAVVGAA ISWPIAGILC LGLCVIPFVI SWAQRMLKGA GAGYGRASGQ  
 LAGVFLESVR TLGTTMMLNA AGQRRQIITQ RAENMRSQVM SLLYRNQLMI LVTGDFVFGVA  
 TTMVAAVFAI GGFSGSLTL GQAVALLVLA RLLIDPINRM GRTFYTGMAK KPSLIAIEKA  
 LATTFDQPT QQQQRHGDGL VVNNLKIARD HRDIVHGISE SIPRGSHIAV VGPSGAGKSS  
 VALALSGLE FDGAISLGGH NCEMLDLRAS VSFVPQSPTL FSGSIKSNID LARTGVDS DH  
 IHAALLGEEL PADLKVGETG KGVSGGQAR ISIARGLVKN AAVIVLDEAT AQLDYTNARQ  
 VRHLAKSLEC TLVEITHRPS EALDADFIIV LEDGQLTMD TPSNVSQHNA FFRTAVMEEE  
 Q

> RXA02095 (1-1404, translated) 468 residues  
 MKTEQSQAQ LAPKKAPEKP QRIRQLISVA WQRPWLTSFT VISALAAATLF ELTLPLLTGG  
 AIDIALGNTG DTLTTDLLDR FTPSGLSVLT SVIALIVLLA LLRYASQFGR RYTAGKLSMG  
 VQHDVRLKTM RSLQNLDPG QDSIRTGQVV SRSISDINMV QSLVAMLPLM IGVVVKLVLT

LVIMLAISPP LTIIAAVLVP LLLWAVAYSR KALFASTWSA QQKAADLTTH VEETVTGIRV  
 VKAFAQEDRE TDKLDTARE LFAQRMRTAR LTAKFIPMVE QLPQALVNV IVGGGYLAMT  
 GHITVGTFFVA FSSYLTSLSA VARSLSGMLM RVQLALSSVE RIFEVIDLQP ERTDPAHPLS  
 LPDTPGLLSF NNVDFRGILN GFELGVQAGE TVVLVGPPGS GKTMAVQLAG NFYQPDSGHI  
 AFDSNGHRTR FDDLTHSDIR RNLIADFDEP FLYSSSIPRE HLDGFGCQ

> RXA02099 (1-273, translated) 91 residues  
 MGADQIAAVS GNSAWMLMSA SLVLLMTPAL ALFYGGMSRQ KSVLNNMMMS FGALGVVTVI  
 YLLWGWSMSY GTQSIAGIFA NPFEFFGLKD S

> RXA02115 (1-1197, translated) 399 residues  
 TRATKSVGTV LALLWFAIVL DGFDLVVLGA TIPSMLEDPA WDLTAGQATQ ISTIGLVGMT  
 IGALTIGFLT DRLGRRRVML FSVAVFSVFT LLLAFTTNVQ LFSLWRFLAG VGLGGALPTA  
 IAMVTEFRPG TKAGSASTTL MTGYHVGAVA TAFLGLFLID GFGWHSMFIA GAVPGLILLP  
 LLYFFLPESP QYLKISGKLD EAQAVAASYG LSLDDDLRE HEEELGESSS LSSLFKPSFR  
 RNTLAIWGTG FMGLLLVYGL NTWLPQIMRQ ADYDMGNSLG FLMVLNIGAV IGLYIAGRIA  
 DKNSPRKTAL VWFVFSAFSL ALLAVRMPLI GLYGIVLLTG IFVFSSQVLI YAFVGENHPA  
 KMRATAMGFS AGIGRLGAIS GPLLGGLLVS ANLAYPWGF

> RXA02128 (1-1695, translated) 565 residues  
 MRGYQRSWLK GDVIAGITVA AYLVPQVMAY AVIAGLPAVV GLWGVLPAPMA LYFFLGTSRN  
 LSVGPESTTA LMTAAGVGAL VGAAGGPERY AEVAALLAIA VGIVCAVGFI GRGLFLTRLL  
 SRPVLVGyli GIAVLMIVSQ LSKVTQVNVE SGQTWQEIIS FIKVAGQAH I PTVILAVVVL  
 SLLYLANWLT PKFPSTLMVL LLSAAAVGFF HLDREFGLEVI GEVPRGLPQP SIPSIGDLEI  
 WSLLPYAVGI AIVGFSDNVL TARAFASGKD EVIDSNQELL ALGTANLANG FFQGFVPSSS  
 GSRTVLGDTA GARTQVHSLV VVALVIMVLL FAGPVLESFP DAALGALVIY AATQLIDIAE  
 IKRIARFRKS ELVITAATAA SVVASGVLAG IGVAVTSLIL DLIRRITRPY ADVLGYPGM  
 AGMHSLEDYP ESTAVEGLVV FRYDSPLFFA NADDFSKRAI EAVDEATQPV HWFLLNAEAN  
 TEVDLTAVDA MEALRKTEE RGIRFAMARV KQDLRRSLEP AGFIESVGEE YIFATLPTAV  
 KGYSVEFRDR FGNYPEGVPK EILEL

> RXA02133 (1-306, translated) 102 residues  
 ENPYIGGAGY NAAKFGVAAF NRVLRLETHQ QTLRVSEIDP GRVATEEFSL VRFGGDKERA  
 EAVYDDVLNL TAEDIAESVR WVASLPKHMN IDRMRITPRD QV

> RXA02150 (1-801, translated) 267 residues  
 VGNVFLEVPT AVKREEGVNP NIMKNNWYRL FKYVLIGPFL RVYNRPEIEG KENIPAEGAA  
 IMASNHEAVM DSFYFPLLCP RQLTFPAKAE YFTSPGIKKG MQKWFFTSVG QVPLDRTADN  
 AMDSLMTAK MVLDRGDLFG IYPEGSRSPD GRIYKKGKTGM AYVAMETGTT VIPVAMIGSR  
 DANPIGSWFP KPAKVRIKVG SPIDPLAFVK EHGLKPGTYE AARKLTDHVM FILADLTGQP  
 YVDAYS KDVK NALEEGKGY EGTAPSQ

> RXA02171 (1-1653, translated) 551 residues  
 MNSTILLAQD AVSEGVGNPI LNISVFVFI IVTMTVVLRV GKSTSESTDF YTGGASFSGT  
 QNGLAIAGDY LSAASFLGIV GAISLNGYDG FLYSIGFFVA WLVALLLVAE PLRNVGRFTM  
 ADVLSFRLRQ KPVRAAACG TLAVTLFYLI AQMAGAGSLV SVLLDIHEFK WQAVVVGIVG  
 IVMIAYVLLG GMKGTTYVQM IKAVLLVGGV AIMTVLTFVK VSGGLTLLN DAVEKHAASD  
 YAATKGYDPT QILEPGLQYG ATLTTQLDFI SLALALCLGT AGLPHVLMRF YTVPTAKEAR  
 KSVTWAIVLI GAFYLMTLVL GYGAAALVGP DRVIAAPGAA NAAAPLLAFE LGGSIFMALI  
 SAVAFATVLA VVAGLAITAS AAVGHDINYA VIRNGQSTEA EQVRVSRITV VVIGLISIVL  
 GILAMTQNVF FLVALAFAVA ASANLPTILY SLYWKKFNTT GAVAAIYTGL ISALLLIFLS  
 PAVSGNDSAM VPGADWAFIP LKNPGLVSIP LAFTAGWIGT LVGKPDNMDD LAEMEVRSL  
 TGVGVEKAVD H

> RXA02173 (1-1452, translated) 484 residues  
 MWVGMEHTSA LTLIDSVLDP DSFISWNETP QYDNLNQGYA ETLERARSKA KCDESUITGE  
 GTVEGIPVAV ILSDFSFLGG SLGTVASVRI MKAIHRATEL KLPLLVS PAS GGARMQEDNR  
 AFVMMVSITA AVQRHREHL PFLVYLRNPT MGGAMASWGS SGHLTFAEPG AQIGFLGPRV  
 VELTTGHALP DGVQQAENLV KTGVIDGIVS PLQLRAAVAK TLKVIQVEA TDRFSPTTPG  
 VALPVMEAlA RSRDPQRPGI GEIMETLGAD VVKLSGARAG ALSPAVRVAL ARIGGRPVVL  
 IGQDRRFTLG PQELRFARRG ISLARELNLP IVSIIDTSGA ELSQAAEELG IASSIARTLS

KLIDAPLPTV SVIIGQGVGG GALAMLPADL VYAAENAWLS ALPPEGASAI LFRDTHAAE  
IIERQGVQAH ALLSQGLIDG IVAETEHEFVE EILGTISNAL SELDNNPERA GRDSRFRFE  
RLAQ

> RXA02224 (1-1797, translated) 599 residues

MAQHERVADA LQPASLAESW RELKTMPSGP KAWWYVSFV ISVVTVVAMV GTSNLLGYSV  
DLINGQSLPL IGSGSTAMIW LLGLVGAGIL AETAGRALLQ LVINTLARRL SVDLRKAALS  
SALRAPVPDV MELGTGNVIS RLTQDIDNTV RIVGMVGVR L VITILILPSS LFALMTIHW  
FVILFIAVIV VLIPSGRKAV RAIPSATNIV SSTEARRNNL LLDITIRGIET LRVLKLGA  
VQMRQASWT AVQATADRAP IFTRLLALGS IAYGLLLIGV FGLSAFWVAQ DAMSIGAATA  
AVFVVVRMEI HVFNVLFFAS EIQSASTSLG RAVSLAQMAR RTEQLSESAD CTEPPSVTVQ  
DVTFKYPGGV AILEDENLVL EAGTTTALVG TSGAGKSTLA GVIAGLQRPD SGAVLVGGIN  
TATVTDWTWTT RQVALISQEV HLFAGTLAED LRMANAHATD AQLHAALESV GLGQMTTAFR  
RFFPSGLDTK IGAGAEELTP EIQQQISLAR IVLRNPPVLI MDEATSEAGS DDARMLEKAA  
TEIARNRTTL VVAHRLDQAV VADRIIVMEQ GTITEDGTHQ ELLAFEGRYA QLYQRWSAQ

> RXA02225 (1-882, translated) 294 residues

QTEERFGAAA DEALAIMLKE ARLQSLTTFV RQLVPAVFSV GLLAYASLLA FDGDITGGEM  
ISVTLLVPPS LTVLGVSLGM MTEIWARGQA STKRVQNLVT ELDKAAAEPR PQPATFEFEE  
GITVWDPSTP EARDVIDREL EALQVREDVI VAPHRVSVFE GVLKDNLNPM GTIAPEMLRA  
ALHAASCEDI LSRLGADLNM PGEFELPDTL IGEAGLNLSG GQRQRIALAR FLAVDPEVLI  
LDEPTTGLDA VTLDEVAHRV EKLRRGRKTV VITSNPTWHG VAKQMQSDFS EGVK

> RXA02233 (1-1212, translated) 404 residues

VLVTSTWGT VHGDGKKIEP GAVVAPKERL SWGRTIGIGM QHVIAMFGAT LLVPTLTGFP  
VNTTLLFSGL GTILFLLITR NRLPSYLGSS FAFIAPLTAT QVHGIGVQIG GILVAGLVLV  
AIGFVVKAAAG KRVIDAVMPP AVTGAIVALI GLNLAPTAAG NFSSQPLVAT ATLFAILIAT  
VAGRGMIA RL GILIGVVIGW VFAAITGNLS EGAADTIREA AWFGLPQFHK PEFQLSAILV  
TLPVIIIVLIA ENVGHVKA VS EMTGEDLDDL AGDALIADGF GTTLAGAFGG SGTTTYAENI  
GVMAATRVYS TAAYWVA ACT AIALAFIPKF GALIFTIPAG VLGGACLVLY GLIGMLGIRI  
WQDNKVNFFNN PVNLTMAAVA LVAGIGNLTL TVFGVTLEGI AWAL

> RXA02253 (1-927, translated) 309 residues

MIQSTGVTHT DKSAQENPVK YRDNFTPVII TGMMSGAGLST AARVLEDLW YVAHNIPPQI  
ILELIDMCAR EDSPVDKAV VCDVRSREFR GSILTQVVSEL RDKQLDPTVL FLEARDEVLI  
KRFDNVRTH PLQGSQTLQV GIERERTVLS PVKEDASVVI DTSLSVHDL RRAIESSFR  
IATRTHQVTI ESFGFKHGSP RDADFVVDVR FLPNPFVWPE LRPFRGVDPK VSDYVLSQKG  
AEFLNNFVD MLKDMPLPGYR HEGKNFITIG VGCTGGHRS VAVSEELAKR IADQTTLDVS  
VVHRDINRH

> RXA02261 (1-1356, translated) 452 residues

MDPSDLAWIL AAFALVSLMF PGLSLLYGGM LGGQHVLNTE MMVMSSLGII SLVYIIYGHG  
LVLGNSIGGW GIIGNPLEYF GFRNIMEDDG TGDLMWAGFY ILFAAISLAL VSSGAAGMR  
FGAWLVFGL WFTFVYAPLA HWVFAIDDE SGYVGGWMKN VLEFHDFAAG TAVHMNAGAS  
GLALAIVLGR RHSMVVRPHN LPLILIGAGL IVAGWFGFNG GTAGGANFLA SYVVVTSLIA  
AAGGMMGFML VERVFSKPT FFGSATGTIA GLVAITPAAD AVSPLGAFAG GALGAVVSFW  
AISWKKGHRV DDSFDVFAVH GMAGIAGALF VMLFGDPLAP AGVSGVFFGG ELSLLWREPL  
AIIVTLYAF GVTWLIATIL NKFMTRLITS EAEYEGIDRA EHAESAYHLN SNGIGMATRT  
NFGPEIPEET VPDVAVQVGD KQKIADTRKA SK

> RXA02268 (1-900, translated) 300 residues

MSQENSGLFK RAITRGVAKV RRNPREDFAE EFTQELYDHA TNITLPLTAR LKPNGFFQDD  
WRARPSGARP WPIVLIHSG ASKGSWEEMG AELRSKGWAV FAPDFGTRAT EPIAASAAQI  
GAYIDAVLLV TGAAQIVLVG HSQGGVVARY WMRTYGGYMK VRHMISISTP NHGTLMMGIL  
NPMTKVKSGE GTIEKLMHRL FGPTGFEQLR GHDIIEFLAD GGDLDPGVTY TCIGTHFDPF  
IQPPEVAFLE VNEDDDPNRV HNIWVEDEHP RAMIAHNDMV RDPRVIEIVR AELDRVARLG

> RXA02269 (1-972, translated) 324 residues

MVDALNDRR ELTNALRSV KNLPTDAPQ ADALPDDVVE EIAINFYRDP KNRGKLNEDK  
TDSLPLMARI RSRGLFEDDW RARPTEDRPV PVVLVHGTGS TKGDWQDLGA DLRRDGAWF  
APEFGQRATG SVAESSAQIG AYIDTVLLAT GASKVIVVGH SQGGVLLRYW MRVLGGASKV

KHMOVSLAVPN HGTMMGGIVS PLIRNNRGES VVNSVVQSWF GEAGFEMIRG HDTINAINEG  
 GDLDPDVTVL CIATHFDTVI QPPETCFLEA RNPEELKRVQ NIWVENLDPN SVVLHEAMPY  
 DPRVRALVRA DLSKLVEISE TAEN

> RXA02309 (1-975, translated) 325 residues  
 MSSGRTPVTR SHGLGKEGVS TTGASQVEFG DPELTARIND AMVQVEELLH TELSSGEDFL  
 VDIVMHLTRA GKKRFRPMFA LLASEFGEKP LSENVIKAAV VVEITHLATL YHDDVMDEAS  
 MRRGVPSANA RWDNSVAILA GDILLAHASG LMSQLGTDTV AHFAETFGEL VTGQMRETVG  
 PRDTPDIEHY TNVIREKTGV LIASAGYLGA MHAGAAPEHI DALKNFGAAV GMIFQIVDDI  
 IDIFSETHES GKTPGTDLRE GVFTLPVLYA LREDTPVGAE LRDILTGPPE DDETVDNHVLE  
 LLSQSGGRQA ALDEVYRYMD IANAE

> RXA02310 (1-1263, translated) 421 residues  
 VSTTFDVLII GAGPSGASAA VHAARTGLQT LLIDASSFPR DKTCGDGLTP RAIHQLELLG  
 VADQVTGDYF NKGLKLHGFG GSVEAPWPET YFTNKGSAVS RMEFDDLLFR LAKSHEEVTT  
 WENASAQDPI LRGNFLEGVV INHAGQEKTV KAKHVIIADG VRSPFGKKLG RQWQRDEVYV  
 IAARAYCETP LSDEPWIHSV VELRDEDEGVV QPGYGWIFPL NGTVDNLGCG ALSTDTRPAK  
 INTKKLLSFY AGQRRKAWQL GPEHDVASAL LPMGGAVSNV AGANWMLIGD SAACVNPLNG  
 EGIDYGLETA AMAVDTLVEN PKRDLTLVWP HRLRDAYGET FMLARTAARL LTYPQFLPMA  
 GPLAFRGPLQ KAIMPAAARL MGNLITEEDK DLLARGWQAA GSAISWARKG SPLWDSTSSL  
 V

> RXA02320 (1-588, translated) 196 residues  
 MTAAQTKPDL TTTAGKLSDL RSRLAEAAQAP MGEATVEKVH AAGRKTARER IEYLLDEGSF  
 VEIDALARHR SKNFGDLAKR PVTGVDVTGY GTIDGRKVCV FSQDGAVFGG ALGEVYGEKI  
 VKVMDLAIKT GVPLIGINEG AGARIQEGVV SLGLYSQIFY RNTQASGVIP QISLIMGACA  
 GGHVYSPALT DFIVMV

> RXA02321 (1-444, translated) 148 residues  
 EYGGILRRGA KLLYASXEAP VPKITVTMRK AYGGAYCVMG SKGLGSDINL AWPTAQIAVM  
 GAAGAVGFIY RKELMAADAK GLDTVALAKS FEREYEDHML NPYHAAERGL IDAVILPSET  
 RGQISRNLRL LKHKNVTRPA RKHGNMPL

> RXA02335 (1-1773, translated) 591 residues  
 VSVETRKITK VLVANRGEIA IRVFRAARDE GMGSVAVYAE PDADAPFVSF ADEAFALGGQ  
 TSAESYLVID KIIDAARKSG ADAIHGPGYF LAENADFAEA VINEGLIWIG PSPESIRSLG  
 DKVTARHIAD TAKAPMAPGT KEPVKDAAEV VAFAEFGLP IAIKAAFGGG GRGMKVAYKM  
 EEVADLFESA TREATAAFGR GECFVERYLD KARHVEAQVI ADKHGNVVVA GTRDCSLQRR  
 FQKLVEEAPA PFLTDDQRR LHSSAKAICK EAGYYGAGTV EYLVGSDGLI SFLEVNTRLQ  
 VEHPVTEETT GIDLVRMFR IAEGHELSEK EDPAPRGHAF EFRINGEDAG SNFMPAPGKI  
 TSYREPQGGP VRMDSGVVEG SEISGQFDSM LAKLIVWGDV REQALQRSRR ALAEYVVEGM  
 PTVIPFHQHI VENPAFVGND EGFEIYTKWI EEVWDNPIAP YVDASELDED EDKTPAQKV  
 VEINGRRREV ALPGDLALGG TAGPKKKAKK RRAGGAKAGV SGDAVAAPMQ GTVIKVNVEE  
 GAEVNEGDTV VVLEAMKMN PVKAHKSQT TGLTVAAGEG VNKGVVLEI K

> RXA02343 (1-414, translated) 138 residues  
 MTISSPLIDV ANLPDINTTA GKIADLKARR AEAHFPMGEK AVEKVHAAGR LTARERLDYL  
 LDEGSFIETD QLARHRTTAF CLGAKRPATD GIVTGWGTID GREVCIFSQD GTVFGGALGE  
 VYGEKMIKIM ELAIDTGR

> RXA02364 (1-627, translated) 209 residues  
 MEPLFQSLAE SDNISVIGGF TQGTNRNLYTT DAPVKRPADL AGKKIRVQES AMHIRMIELM  
 GGSATPLTYG EVYTAMQSGV LDGAENNEIS YVTQNHFEVA RYNSNTNHLV GLDYMVMRHD  
 LLDAMSEPDRL ELFLEWDAA MTEHTDLWNT ETDVIEKAK AGGAEFVEVD AQAFTDALAP  
 IKDEFILTSEF QRELYEAVRA ADTSGGAAS

> RXA02372 (1-555, translated) 185 residues  
 DAVNKMDRTD FVETFAPLFN SKTWPLETAW ESQPFANVTE LREAIQVAVL TAPLSDREEL  
 IHDYPDMAQL ILATEEEAAT ISQDRGSIGL DDLDDVDQEK LITVTEQYRE RFNMPYVAYF  
 DTMDSDVTIV AAGLRLDNS DEQEHRQALS EIIEIANDRF DILLADANPA RSAFDRKFTE  
 TDFLG



> RXA02377 (1-1191, translated) 397 residues  
VPPAPKLAAL GLQHVLAIFYA GAVIVPLLIA QSLNLDATT IHLINADLLT CGIATLIQSV  
GIGRHIGVRL PIVQGVTTTA VAPIIAIGLG VTDGQGGVAS LPAIYGAVIV SGIFTFFAAP  
VFARFLKFFP PVVTGTVLLV MGASLLSVSA NDFVNYADGV PAARDLAYGF GTLAVIILAQ  
RFRGFMGTL AVLIGLVGGT AVALILGDAN LDEVGNAAEF DITTPFYFGV PEFNAVAIFS  
MIIVMIITMV ETTGDVFATG EIVGKRTRRS DVTRALRADG LSTLMGGVMN SFPYTCFAQN  
VGLVRITGVK SRWVAAAAAG FMIILGVLPK AGAIVASIPS PVLGGASLAL FANVAWVGIO  
TIAKSDLADS RNSVIVTSAL GLAMLVSRFP DVAQGVF

> RXA02397 (1-996, translated) 332 residues  
MNDFETTIDR ISKEQDPAAR SRVEQFIVET VRALPNLTTK QGASLAIQLL DAVQLADAAG  
TKGGASTSNA SSLPDTFDAL TSLIGKLDVR SDSEWRSFGF QPSETAHPLM IAIPEIEIFY  
QHTDVEPGSD DAVAPDFQEN QDMWRRRLGS VTEPNLIYKE FSGPGKAQRA VEMLGNLWKI  
GVVVSNTES RLGLTRVEYT PTPGEVPVPL MSEKNCWYSI RVSETIGENQ VPEIVRCLGE  
IFCGYLPQMW LKEPVKAGKL RIQSEAAAY IAMARLDLSP RTGNTTWTNS YISTRPLSPA  
FRWDVVLEAS HQLENLLRGD TGPVTATQSA AG

> RXA02424 (1-381, translated) 127 residues  
TGATHYAPFL EVPALPSAVD VELHHGDSIE FEGHVFPI SI LRGHTPGGAV LTAEIDGKTH  
LFVGDLSLFP GLGKTSSEGD FVRLFNDVKE RIFDTYDDDS IVWPGHGKET TLGAERPQLE  
IWWERRW

> RXA02426 (1-1533, translated) 511 residues  
MLITLLLATV IVVAIGDKTG LPWPALMTIV AAGGALLPFL PEFTIPADLM LPIFIPPLLW  
ALARKSSWAV IRSQMSTIIT MSVLLVFVTI AALTGASMLL LPGIGLAGAI MLAAAIAPPD  
PVAVDVAEAP AGIPKRITTT LQTEGLFNDA ASIVAFHVAL AALVAGEDLS WSTGVLEFLW  
SCLAAVILGL VIGRAAAWFT DHVSSVEARN AFTWVLPFAI YVVAEEIGGS GVIAIVIAAV  
EMNSRASIGA EDRLTGSAFW GTIEVLFTGV AFGLIGLNV R AAIDEVGSSEL WHAVVVGIVL  
SVVAIVVRGV WMFAAYKRRR FKIDKKGATN SSLRAPLRLQ ESLLMTWAGM RGLVTLALVL  
SIPEDIFPYH HELQVIALVV LLITMVGPL TLPWLMRKLS LDKGPDAAGD ESIAALTERA  
HKAATTYLV TTELPMEQMV AIKNWFSQEI DADELQENV D KLHQRAHHAR VGAIKAAQEE  
LLKARRERGV NPAYVDEVLT NIDRMLVAEE R

> RXA02487 (1-288, translated) 96 residues  
VYPAEVEEVL AEHPDIEDSA VVGIPREDGS ENVVAAITLV EGAALDPDGL KEFARKNLTR  
YKVPRTFYHF EEMPRDQMGK IRRREVQAE L LKKLGK

> RXA02490 (1-813, translated) 271 residues  
MSAYETKEWL QHYPEWTPHS LEYGDTTLLD VYDNNLAINA DKPATYFFGR SQTYGELDKE  
VRKTAAGLRA LGVRPGDHVA IILPNCPOHI AAFYAVLKL AVVIEHNPLY TAHELLEPFK  
DHGARVAIVW DKASPTVEQL RGQTQLETIV SVNMINAMPP LQRLALRLPI PALRKSRESL  
SGAAPNTVPF ETLTSAAMGG DGDDVSEPT VTKEVALIL YTS GTTGRPK GAQLTHGNLF  
SNLLQGKHVV PGLGDKPERM LAALPMFHAY G

> RXA02511 (1-657, translated) 219 residues  
MLGLHGRKPA QVIVEPVAKL MIKLKVTNPQ LTLVSAGLTV GVALLLIPTG HLIWAAVLTG  
LFAAFDMIDG TVARMQGGGT KFGATLDATC DRITDGALFG AITWWLVYSY DAPQALVAAS  
LVCLVASQVI SYVKARGEAS GFTMDGGLVE RPERLIVSLV GLGLTGMGVP YAIIDVALWAL  
AAGSIYTVVQ RLVMAGKSPL AKEFTKAPAG AKADYSNTK

> RXA02512 (1-957, translated) 319 residues  
MKPKDFCTAE NWAENLSALG YLAGWRFRM LPLPIARRVF DLGADLASKS GKGMGQLRAN  
LARVGAENV TQALVKQATR SYARYWLEAF RLPAIARDPE LLARLRKGTV GLDLLDES LA  
AGKGVLTLP HSGNWDMA GA FLISHHGQFT TSAERVKPER LFEAFVEFRE SLGFEVLPLT  
GGERPPFEKL KERLTSGGIV CLLGERDLRH SGVETTFE KSMPAGPAQ LAIETGAALH  
VVHPWFDDDG WGLSVSDAVT VDNLSDTVQR IAHLFMANIT AHPADWHMLQ PLWFGDLDP  
RLKRSREQTN VHKPVALQE

> RXA02527 (1-1329, translated) 443 residues  
MFGLFIATIV AIILKPMMPG AVTIIGMIAA VLTGLVPLTA SSDDPGAVYG LIGFSNGTIW

LIVMAFLISR GFIKTGLGRR IALFFVSKVG GKMLGVTYGL ALADLVLAPA IPSATARGGG  
 IMAPIMKSPA LTYDSTPGPT RRRAGAFLAL NVGQVNAITC AMFLTAMAGN PLIASLASQM  
 DVNITWTNWA VGAIVPGLVA LIVVPWVYK IYPPELKDTP EVKKMASDEL KQLGGFTYGE  
 KVLAGTFVVL LLLWTGGDLV LGISATTTAF VGVIILLVAH VLTWEDIIQE KTAWDTMVWF  
 AVLYMMATAL SQYGFIAWIS EVIASSLGGM NWVVALVVLV LIYFFSHYFF ASATAHISAM  
 YLAFLGAAIA IGAPPLMAAL VLAYTSNLFS SLTQYSGGPS PTLFGLNYIT VGEWWRTSAI  
 AGAVSITIWL VIGGLWMNVI GLW

> RXA02547 (1-2124, translated) 708 residues

AARLTVDEYP AAREALESAG QRNVEDRTRA VDEFKAADQE LSSLSKGSSN IEYRLLQVRE  
 NLCQDLGVSP RDMPPFAGELI DPNNAEWEPV VQRILGGFAA EMLVPHGLLP RVRDWNNAKH  
 LAALLKFNGV VTTGEYKTSR FPADSLIRKV DVVESPFDRW VNQELGKRFN IRCVRTPEEL  
 SALGPRDQGV TILGVRKFAQ QTGDPTTRWE KDDRRKLGDR STYRLGSTND AKVETLRETV  
 KAGKAVVQAA DNRIANRAE LRELERQYQA SQEILKVSWA QIDVESADAA IAELDRLLLE  
 LNNTPEATEL SARHEAAKQT LARVSDLLVA AQSEETVASM NLKRAETELK RLESPLVAEV  
 SEEIAREVEK LFLANTRRVH AANVDEQTIA LREDLDKQID ANEAE LRCE NQIVGILRSY  
 IETWPANRAD LQAEPEFVGE AINRLGELRS DRLAEFTAKF LGLMNEMSTR NLGQISRRLR  
 DARREIEERI EPINASLAQS EFNEGRFLHI DIRDQSGPIV REFQOKLDAA TSGDLGTSTE  
 KQAFARYALI AEIISKLAH DSADARWRNT VLDTRRHVRF IGLERDSDGA TVNTYVDSAS  
 LSGGQAQKLV FFCLAAALRY QLAEPGAHYP TYATVILDEA FDRADPAFTR QTMNVFHSFG  
 FHMVLATPLK LIQTLGDYVG STIVVSYTEK PNAQGAIQGN SSFSRIEK

> RXA02561 (1-660, translated) 220 residues

MVGASNGVTL SMGSLAAHL AGASWGGSSA TLTIGAAIF SIPLARMVST YDRRTSLSTG  
 MLLGCVGALL AILGAQFGLF PVVLLAFLFL GSMSAVNLQA RFAATDVASE ETRGRDLSIV  
 VWSTTIGAIA GPNLFEPSAR FSETLGLEQH AGAYLLCLFG QLIAIAVWRF TLPKGLKPEA  
 TPNAPTEKKR LTPKALQAIT SVATAHFSMV GLMSMAAIHM

> RXA02566 (1-438, translated) 146 residues

ISLHVAGMYA LSPVFGLLTD KLGRNVITIYS GFAMLATSAA FLIIWPEPQW AMITSMILLG  
 LGWNSALVGS STLLVDATPI HHRTYAQGRS DLTMNLAGAS GGLIAGPLIA MGGMPLLAGV  
 VLAVVALQTV LSFRTSIEK TPASCF

> RXA02571 (1-1029, translated) 343 residues

VVALTQIVGP SGSGLTRELE KRYRETPGAV MLTADPRAHI TYLRATVAEE LAFGLEQIRGI  
 VPAQMWERVR NIGLLENLL DRAPAQLSGG QTRRLAIGTV AILEAPTMLL DDPLSGLDTS  
 SRAQLITMLE SYEGDVIVAA HKRWLDAPTV YLGDLEELSL PARVEFSGPS RTFSAITGTR  
 GQQRRRWQF NESQPQFQIG PLDITVSAGQ VLWLQGPNGS GKSTLLRGLA NEPGTEMLQ  
 NPSDQVIDST VANWVPGSNS EEHPLDLSQR ELRLAQCDAA LGNNPEVLLA DEPDVGLDVG  
 GRNAIHQRFA DFLGNGGALI LTCHDETFA EVAEYAIIVKE MGL

> RXA02578 (1-1104, translated) 368 residues

MSTQSYAPIR HRGFISSLEG LRAIASLGVL ATHVAFQTSV DPASNIGAVL ARFDFFVAVF  
 FALSAFVLWR RRAGQPVGLY YLKRLARIMP AYWATVIAVL LFIPTGPWLA NLTMTQIYWP  
 DGLMTGLTHL WSLCVEVAFY LVMPLLAWVL DRFGRPVRL LIVGGAVLSL AWPWIPLVEH  
 ALDEGWANMQ IWPPAYACWF AVGMIAAEIE GVRFRVPVSF VWVGLALVVA WIAGQEWFGP  
 LGLVHPSPWE FNLRVLAGTL FAVFLVVPYA LGTPSRLLDS SWMKT LGTWS YSIFLWHLPV  
 LTIVFPLLGL PLFSGNLLV FIVTVLLTIP VAAISYTFIE EPISGGPGAP FRLGVVRIHH  
 FSGGRSGK

> RXA02581 (1-1527, translated) 509 residues

VPVPLYDPNE PGHADHLNAV FADSEPVVVL TNSKSAGAVR KHFSPLPAE RPRILSVDSL  
 PDSLADSYEN PMLTEAGRRL AALRQSAPID LTAFLQYTSR STRTPAGVVL TNRSILTNVL  
 QIFSAQLKT PLRLVSWLPL HHDMGIILAA FVTMLGLDNE FMNPRDFVQQ PSRWIKQLNR  
 RESDVDVNVY TVVPNFALEL AARYAKPAEG ETLDLSALDA IIGSEPVTE NALTTFREAF  
 EPYGLPVQTL RPSYGLAEAS LLVTPQTEN RPLISYFDRE ALAENRVELV EKGNNKAVAF  
 VSNGQVAAPQ QLVIDDSETG TELADGQIGE IWTGENTAA GYLDREEDTA ETRNRLTTR  
 LEENSRAEGA ADDNYWMATG DLGVIVDNEL YITGRLKDLI VVAGRNHYPQ DIEYTVQAAS  
 AHIRADSVAA FAVPGDDIEK LIILAERDTT ANEADDAEAE EAIRSAVGTA HGVVPEEIRI  
 LAPDEIARSS SGKIARRVNQ RNYIQEQAN



> RXA02638 (1-504, translated) 168 residues  
 MARKRLNAGS LVGIFPEATV SRSFEIKELK TGAVRIADSA NVPLLPLIIW GGQRIITKDI  
 ERDFGRSHIP VFISVGEPVD ASGDPDEATE RLYEAMKKLL DETRTAYEQK YGPFEGGELW  
 RPKSLGGGAP TLEQAKMLEI AERERRQAKR AAKVAKKRTT FIRKIFKK

> RXA02659 (1-312, translated) 104 residues  
 FGNDPDLMLR WWYAGDVWTD SRMHWKGSSES YDQVQNLLEE GIRATDKAEQ QDIWNRTFDV  
 ISDNVPLYPL FHRKVPTAWN SNALVDFKPI SLTGLNFSGV ATTE

> RXA02676 (1-1389, translated) 463 residues  
 MDTWEQTLGT GPLLGIAAGA IALILVLVIV FKLHAFLLTI LVSIVTALAA GIPVTAVVDT  
 LLDGFGKTLA SVALLVGLGA MLGRLVETSG GAKSLADTMV RIFGEKRAAF ALGVASLIMG  
 FPIFFDAGLV VMLPVIFAVA RRLNGSVLTF GIPAAGAFSV MHVVFPPHPG PIAASEFFGA  
 QVGIVLIAGI IVALPTWYLT GYLLGKFLGR KFPLPVPDLL SGGAQEDDQP QNPANAVSII  
 VILLIPMLLI FGNTGTSMVA SAGLLDAEST MVKILGFLGE TPVALLITLI IALFFLGNNR  
 GINGSALEKT IEGALGPICS VVLITGAGGM FGGVLRSTGI GGALADSMAD LGLPVIAGCF  
 IVAAVLRVAQ GSATVALTTA AALMAPAVAA ADFNEFQLAA IVISTAAGSV IASHVNDSGF  
 WLVGRLMNAD VPTTLKTTWTV NQTCIAIVGF VMAYAMFGLA SLA

> RXA02677 (1-759, translated) 253 residues  
 MKVIAHRGLS SRPELTESA FRAALELPIH GIETDVRLTK CGEVVNVHDP IVDRVSNGRG  
 RVSRLDLESL LSLNFGTKET PEKVLTLNNL LDIFEDYDPK HLYIETKHPM RYAVMLEEEI  
 TKILKYRGLT EDPRIHIISF ALPAMYRMAR LAPQLDRIHL RRSWERWGNP RDVRCGVPTG  
 LGLSLERAKM DPRMIGAKGL PTYLFRTVDKQ KDMLWAREQG VDMLATNYPD RAAELLNAHP  
 KPAMYANAHG KED

> RXA02691 (1-807, translated) 269 residues  
 MNTMPDQPLN QDGFPTASKG VEPDNLPRV LVDGLKPKHQ QLREILEEIC TTQLQPGDML  
 PGERILEEKY GVSRTVRRR IGDIVASGRL KRARGKGTFFV AHSPLISRLH LASFSAEMAA  
 QKLSATSRIIL SSSRGPPAPDD IADFFGTDRR AQHITLRLR FGNGRPYAI NGWYNSEFAP  
 DLLENDVYNS VYSILDRVYG VPVTQAEQTV TAVAAEDETA RLLDVTPGAP LLRILRQSLS  
 GDKPVWEVCV LYRTDRYSLK TLVTRSED

> RXA02718 (1-1047, translated) 349 residues  
 VRDRLTQFLD AQELTIADIG APVTDVAHL RSFVLNGGKR IRPLYAWAGF LAAQGHKNSS  
 EKLESVLDAASLEFIQACA LIHDDIIDSS DTRRGAPT VH RAVEADHRAN NFEGDPEHFG  
 VSVSILAGDM ALVWAEDMLQ DSGLSAEALA RTRDAWRGMR TEVIGGQLLD IYLESHANES  
 VELADSVNRF KTAAYTIARP LHLGASIAGG SPQLIDALLH YGHDIGIAFQ LRDDLLGVFG  
 DPAITGKPG DDIREGKRTV LLALALQRAD KQSPEATAI RAGVGKVTSP EDIAVITEHI  
 RATGAEEVE QRISQLTESG LAHLDDVDIP DEVRAQLRAL AIRSTERM

> RXA02749 (1-876, translated) 292 residues  
 MSPILKVRDL VKRYGDTVAV DGLNFDVSQG EIFAFLGENG AGKTTTISCL IGIDQATSGE  
 IELQGGQVDS EKLGVVFQQS VLDPLLSAKE NLETRGQLYP GVGKQ RVAQL IEQIGMEGFA  
 DRRYGVLSGG EKRRTDIARA LLHSPDILFL DEPTAGLDPR SRRQVWDTIN SLRNDVGLTV  
 FLTTHYMEET ELADSVLIID RGKEVASGTP MELRARTTT ELTLRTNDPT HSGKELAHLS  
 PEIDGDLRI KLENGLEAAR LATELDGVLD VEIRHGSMDD VFLAVTAERK RS

> RXA02762 (1-285, translated) 95 residues  
 MLSELFPLAM RGFAIGISVF FLWIANAF LG LFFPTIMEAV GLTGTFMFA GIGVVALIFI  
 YTQVPETRGR TLEEIDEDVT SGVIFNKDIR KGKVH

> RXA02767 (1-783, translated) 261 residues  
 MRELALNMAG VTVRERGEKLL LDDISLSIPQ GSHWAVLGPN GAGKTTMLKI AATLLYPSEG  
 TVDILGHRFG RVDTRRELKKT IGLVDPKQRF TNLPAHEIVL SGLTASNGLL PRWSASASEL  
 ERCALMLELV GMTARADRYW ADMSQGEKAR TLIARALIIS PTLLELDEPT TGLDLPGRET  
 LLSVIDGLRA ALPGLTTVMI THHVEEIAAS TTDILMIKDA RILASGTVSE VMTPENLGAL  
 YDMSVSLET V RSRWFADFAL H

> RXA02792 (1-753, translated) 251 residues  
 MIEATHLRHS FGDNIVIDDV TLHLPAHGT V SLVGPN GSGK TTLRLALYGA LQPNEGHIHV

DGVPLISLHR KDIAKTMAVV IQEHSDSLPM TVADLVLLGR LPHQKMFAGN SQADQLLVKE  
ALTRVGAIHL ADRQFGALSG GERQRVLIAR ALVQNATHIL LDEPTNHLDI RYQHEVLHLV  
RELSSSSIIV LHDNLNLAGAY SDHIILLDQG RVVTQGTPE VLTPEHLEPV YGVRVERFDL  
GDEVHLRFKR H

> RXA02794 (1-621, translated) 207 residues  
MAASGLIFFV ARAAGRISST RLLMSGVAIG YMLSAATSFL IFSSDSAEGS RSVLFWLLGS  
LGLAAWNPGM AIIFLIVGIA LALLMVLGPQ LDALNSGDET ALTGLGVSPDR LRILLLVITC  
LLVGSMVAMA GSIGFIGLVI PHLARREVSF KHRLMLPVSA LMGAILLIWA DIAARTLLAP  
QEIPIGIITA LIGAPFLIL VRRMHTY

> RXA02809 (1-273, translated) 91 residues  
AALTNALSYL SAEWNNKAAG IVSYGSAMGV RAAEHLRGIL SELQIAHVQK TGLLSIFTDF  
EYPNFKPSEQ GISSVDAMLE QLVVWTKAMS T

> RXA02811 (1-384, translated) 128 residues  
VTESTLGASN SSQTIENTKGL TILGISGRRL AAVLIGWFFV IFDGYDLIVY GTVQSALAKE  
WNLSSATLGT IGSTAFFGMA IGAVFIGRLS DRVGRKAAVI GSVLILSVFT MLCAFAPNPV  
VFGAFRFI

> RXA02836 (1-306, translated) 102 residues  
MTIDEGRQF EVNVFGAMAL TRLVLPBMQK QKWGTIVNIT SMGGKIYTPL GGWYHGTKFA  
LEALSDALRL EVAPFGIDVV VIEPGGIATE WGGIAADNLD AV

> RXA02850 (1-492, translated) 164 residues  
EELGGATTHM VTAGNSHYTA ATDEEALDWV QDLVSFLPSN NRSYAPMEDF DEEEGGVEEN  
ITADDLKLDE IIPDSATVPY DVRDVXECLT DDGEYLEIQA XRAENVVIAF GRIEGQSVGF  
VANQPTQFAG CLDIDSSEKA ARFVRTCDAF NIPIVMLVDV PGFL

> RXA02851 (1-519, translated) 173 residues  
PRQKADIMIG SIQENINDVD LELDTIIPDS PNQPYDMKEV ISRIXDDAEF FEIQEDYAEN  
ILCGFARVEX RXVGIVANQP TQFAGXLDIK ASEKAARFIR TCDAFNIPIL EFVDVPGFLP  
GTNQEFDGII RRGAKLLYAY AEATVGKITV ITRKSYGGAY CVMGSKDMGA GLV

> RXA02865 (1-1017, translated) 339 residues  
LSRTGVSKKP KLTAPVVIIG TLVLLIIAFT ASLMLGPVTV PLNELATNPV VTDIRAPRII  
IAALVGAALA VSGAIMQTVF HNPLADPGIV GVSSGAAVAA VLAIVTGASF FGQWTVPFAA  
FVGALVTVAV VYLIASSRAM DGRGADPATL VLVGMAITAF LGAVISSATA NAPQDSELRS  
VTFWLNGDLV SRTWEHVGVA IPIIIVGLIL AIGGSRDNLN LLLGDSTAQT SGLNVNRARI  
ILLALAALLT ATAVAVSGTI TFGVLVPHL VRIVLGADHR ALLPAAAILG ATFVIVSDTV  
ARMIFSPIVL QTGVVVAFIG SPIFLYLLLS MRKRRGLGL

> RXA02900 (1-852, translated) 284 residues  
MSNPAASTPA NNSDDVAKEN WDSSFTPKTD IDSSQPVNNS TGEAAARAVN LYKAYQGQDT  
TVTALDHVNV EFEKNKFTAI MGPSGSGKST LMHCMAGLDA ATGGSFIGD TDLRLKDKKE  
MTSLRRDRLG FIFQSFNLVP TLTASENITL PTDIAGRKID QSWFDEITSR LGLTERLKHR  
PAELSGGQQQ RVACARALVS RPEIIFGDEP TGNLDSNSSR EVLDILRTAV DQDDQTVVIV  
THDAKAASYA DRVIFLADGR IVNQLFDPTI EEILATMNGI EDIA

>RXN00024 TRANSLATE of: rxn00024.seq check: 2799 from: 1 to: 945  
MEHGVTVIKGTEFDVFPLNLGGNTFGWTSNREQTFVLDFAVAAAGGNFVDTADSYSAWVE  
GNEGSESERELGAWIKERGADKLIIATKSGALEPVAGRSREATFKAVEGSLERLGVESID  
IFYHYDDEAVSIDEQVAIANDLIAQGGIKHLALSNYSAERLAEFFEKSVGTPAQPVALQ  
PHYNLVSRLDYENVQPLAEKHGVAVFPYFALAAGLLTGKYTSKEDISGKARAGQLDRYA  
SDEAFVVTTELRAVADELGVAPTTVALAWLVAHGVTAPIASVSKVEQLKDLMAVKDVELS  
AEQLARLDKVSEPPA

>RXN00092 TRANSLATE of: rxn00092.seq check: 5543 from: 1 to: 666  
MTNTPFPLELQNISCAFGEPRHVSALNNVSLAVNPGLVAIMGPSGSGKSTLLNVAGLL  
QRATSGHVLIDGASASDLNAKRAAETRRRHIGVIFQYNLVPTLTVGENVGLPLELDGKT  
DRQAVAIALAIEVGLGEGFDDRFPEEISGGQAQRVAIARALIGPRKILLADEPTGALDTSTG

DAVLRVLRQRIDSGAAGLLVTHEPRFAAWADRTIMLRDGEIQ

>RXN00099 TRANSLATE of: rxn00099.seq check: 3872 from: 1 to: 1173  
 VKNPRLIALAAIILTSFNLRTAITALAPLVSEIRDDLGVSAASLIGVLGMIPTAMFADAAF  
 ALPSLKRKFETTSQLLMFAMLLTAAGQIIRVAGPASLLMVGTVFAMFAIGVTNVLLPIAVR  
 EYFPRHVGGMSTTYLVSFQIVQALAPTAVPISQWATHVGLTGWRVSLGWSALLGLVAAI  
 SWIPLLSLQGARVVAAPSKVSLPVWKSSVGVGLGLMGFTSFATYILMGFMPQMVGDPQL  
 GAVLLGWWSILGLPLNILGPWLVTFRFTNCFPMVVIASVMFLIGNGGFCLAPDVAPWLWAT  
 LSGGLPLAFPMALT LINIRAETSAGASALSSFGQGLGYTIACFGPLLTFIVDATGSFRT  
 IFVLFAVATL FVIRGGYFATRQVYVEKLLNR

>RXN00113 TRANSLATE of: rxn00113.seq check: 9363 from: 1 to: 5622  
 VRIVLTTEGEVAAKLVTFRFAIRGRITTNEMAAPADSYGARDEVVEATPRSFIRQATVSAP  
 ADMTPFAMVSGDYNPIHTSDNAAKLVGLDAALVHGMWLSATAQHLAGLGSEVIGWTYSMY  
 GMVQLNDVVDITVERVGRAGLKPAYEVTCRIGNVVSRRGQALLKAPSTAYVYPSQGIQAK  
 GMGQGDRTASAEARAVWERADAHTRANLGFSIQQVIDENPTLKVGDITFVHPAGVLNLT  
 QFTQVALAVVAYAQTERLKAANAIVDGSLYAGHSLGEYALASLGNIFELEGVIDDVFSR  
 GSAMHSLVPRDEKGRSNYGLAAFRPNMINVAATEVENWVDRVAEESGEFLQIVNYNVDGQ  
 QYAVAGTLAGLKALKASASANPRAYVNI PGIDVPFHSSVLRPGVPAPFAEKLELLPETID  
 IDALRGYIPNLVARPFELTQSFVDAILAVVPSERLKGIKVEDTDENTLARLLLI ELLSW  
 QFASPVRWIETQALI IDTVDQII EVGLAASPTLTNLALRTMDVIGKSRPVFNVERDQDTV  
 MLNDVRQAPVAEVEEEAVEEAPAAAAAPAAEAPVAAAPVAAAAAPVGNAPELKFNAANA  
 IMVLFAVQNKINIDQITAADTSETLTNGVSSRRNQMLMDMSTELSVPTIDGAADADVATL  
 QGRVPNTAAPGYKPFPGPVLSETVRRRLRALTGAAGLKTSYIGDRVTGTWGLPESWTAHVEV  
 ELLLTREGESVRGGNLGSLPANASSKGDVDALIDAAVQNVAANGTSVSMSSGGAASGG  
 GVVDSAALDAYASTVTGEEGVLANVARGILSQLGLDTKDEVEGAIEIDTELYDAVEAELGT  
 GWLKLVTVPFVSADRAILFDDRWASAREDLARLANGEDIAVERFAGTGETTVKQAAWAAEH  
 VEDTALAATLKQVSEVAAPANEPIHDDVALVTGAAPESIA GAVAAARLLSQGATVILTAS  
 NVSQARKEYARKLYAANATPNAKLWIVPANMSSYRDVDAVIDWIGNEQRTVTGSTVTVTK  
 PALTPTLAYPFAAPSVSGTLADAGPQAENQARLLLWSVERTIAGLADLASRGVDGRVHV  
 LPSGPNRGMFGGDGAYGEVKAADFADILAKWGSETGWPFVSLAQARIGWVAGTGLMGRND  
 VLI PAAEKLGHVYTPPEEISSSELLGLASAESREKALEAPIDYDLTGGLSGGVSIAALAAS  
 LESDAVETTSAAEDTIKALPSPKHPEQPVGTPVGEVKTDLEDMMVMVGVEVSSWGSGR  
 RFEAEYGIQRDGSVDLTAAGVLELAWMMGLISWSEDPKPAWYDADGTEVPEEEIYERFRD  
 EVIARCGVRELVDDAFLVDGGSGLDAAEVFLDRDISFSVTSAAEAQAYVDADASVTVEEAD  
 GEWIVTKKKGSTSFVPRKATLTRSVAGQLPTDFDPAKWGIPASMDALDNIAAWNLTAV  
 DAFLSSGSFPAELLQSIHPADVSTTQGTGIGGMQSLRKL FVNRF LGQDRPSDILQETLPN  
 VVAHTMQSYVGGYGQMIHPVAACATAAVSVEEGVDKIRLNKADFVAGGIDDIQVESLT  
 GFGDMNATADTQAMLDKGI DPRFISRANRRRAGFLEAAGGGTVLLARASVAAELGLPVL  
 AVVAHAQSYADGAHTSI PAPGLGALGAARGGKKSVLARELNKLGLTPDDVRVSKHDTST  
 NANDPNESELHNLWKTIGREADNPMFVVSQKSLTGHSKGGAAALFQIGGLVSIETGKLP  
 QNASLDCVDPMEAKGENFVWLRLKPLDLGAGSIKAGVLTSLGFGHVAAVVVLATSGIFEQ  
 AMRNAGLDVEAWRARATQRLRTGANRLEAGMVGRAPLFEQVDGRRLPEHGAHQAEINLLI  
 DADARLGADGIYQG

>RXN00164 TRANSLATE of: rxn00164.seq check: 2228 from: 1 to: 1689  
 VGRI PRAKWWFLGALVLLSAGAYASVLVPQVLGRIVDLVSDGAQMRDFVELSVILIAVAI  
 AGAVLSACGFYVVSRISEKIIANLREDMVGTALGLPTHQVEDAGSGDLVSRSTDDVSELS  
 AAVTETVPILSSSLFTIAATIIALFSLDWQFVLIPVVVAPVYFASKHYLSKAPDRYAAE  
 RAAMAERARKVLEAIRGRATVRAYS MEDAMHNQIDQASWSVVVKIRARTTMLILNMWML  
 FAEFLMLAVALVIGYKLVIDNALTIGAVTGAVLMIIRLRGPMNMFMRVLDTIQSGYASLA  
 RIVGVVADPPIPVDPDSGVKAPQGKVELRNVFSFSYGDSWAVKDIDITINSGETVALVGASG  
 AGKTTVAALLAGLRVPDQGVLDVDFPVSHLSDRERIRLAMVSQEVHVFSGTLRQDLTL  
 AKPDASDEELAHALGQVNALDWLESLEPEGLD TVVGARGIQLEPVVAQQALARVLLNPA  
 IVIMDEATAEAGSAGASALEEAADAVSKNRSALVVAHRLDQASRADQILVMDKGEVVESG  
 THQELLDHGGIYQRLWTAWSVGR

>RXN00193 TRANSLATE of: rxn00193.seq check: 1918 from: 1 to: 594  
 KAFXQREGFISAFGFTVLVIVSVITVNI FAFLLAWLLTRKLRGTNFFRTVFFMPNLIGG  
 IVLGYTWQTMINAVLSHYATTISADWKFGYAGLIMLLNWQLIGYMMIIYIAGLQNVPEL  
 IEAAELDGVNKWEMLRHVTIPMVMSITICLFLTLSNSFKLFDQNLALTNGAPGGQTEMV

ALNIINTLFNRMNVEGVG

>RXN00201 TRANSLATE of: rxn00201.seq check: 716 from: 1 to: 192  
VADCGLPIPEHVEIIDLALVFGIPTFEQVLNALKPEVVVEGAVIAEGAPQRIREMVDTDV  
EVCA

>RXN00243 TRANSLATE of: rxn00243.seq check: 3186 from: 1 to: 1017  
VTSEQALDPIHPGQFRLSRIQLINWGTFHGTVDIPVTREGILVTGGSGSGKSTLIDAITA  
VLLPQGKLRFNSAAQANTPRNKGRSLVTYIRGAWRAQEDPLQDQIVSTYLRPRATYSLVG  
LTYSNGEGVEHTLVAIFYLKSGHNLTSDISSYYGVFPVDQDINALDLFLKEGIDKRQIRA  
AFKEAIFSEQHSVFSGRFRSRLGISSEEAALLLHRAQSAKDLQSLDDLFRDYMLVEPDTF  
SIAKTAVEQFQDLEGAYEQVEDIKRQIHTLDPLVQLKNRREKAQQSKDHANALKKALPTV  
GNRIKKEEQEPLVRQFTVEQTQSRRWSPPKLRQIVPAK

>RXN00297 TRANSLATE of: rxn00297.seq check: 2827 from: 1 to: 912  
MGFTVVFIVIGIGWILGRRDTLGTHAQKPLSLFVYYVATPALLFDRVTKSDTSTIFSLNF  
VVIALSALIVGFLFFLLMRVFIKRTAAVSVIGMLAASYANAGNLGIPLAAYILDDFTVVI  
PVILFQVAFYAPITMTIMEMLTNKKSTNLVRNLLVTPLTNTMVLAAIAGIAVSLTSMSPV  
VVIAQPVEMLANASVPLALVVFGLSLSKSKILEKGQVSRDVFATAALFKNVLHPHIVAGLL  
ALAFGMEGTALLSAVILGALPTAQNVYTYALRFRTAESMARDTGVVTTLISFPVLVAVSI  
IFGS

>RXN00298 TRANSLATE of: rxn00298.seq check: 2826 from: 1 to: 1845  
MSSNIAITTEPEGKKNKKGLKSDPFIFSISVGFIVVFVIATIALGEKARTTFSATAGWLL  
NLGWMYIGGVSLVFIFLMGIFASRYGRVKLGDDDDPEHTLIVWFCMLFAGGVGAVLMFW  
GVAEPINHAFFNPMANEESMSEAAIVQAFAYTFYHFGIHMVIMALPGLSLGYFIYKRKL  
PPRLSSVFSPILGKHIYSTPGKLIDVLAIVGTTFGIAVSVGLGVLQINAGMNKLWSTPQV  
SWVQLLIILIIITAVACISVASGLDKGIKLLSNINIAMAVALMFFILFTGPTLTLLRFLVE  
SFGIYASWMPNLMFWTDSFQDNPGWQGWTFVYAWTICWSPYVGMFVARISRGRTVREF  
IGGVVALPAIFGVVWFSIFGRAGIEVELSNPGFLTQPTVVEGDVPAALFNVLQEYPLTGI  
VSFAFALVIVIFFITSIDSAALVNDMFATGAENQTPTSYRVMWACTIGAVAGSLLIISPS  
SGIATLQEVVIVVAFPPFLVQFVMMFSLKGMSEDAAVRRVQTRQWEKTDTPKLEEHS  
SQPAPGYDDEGNPLPMPALEHDEGDNIVIPGNVIEGDLGVVGDVDDPEEAQEMGSRFK  
IVEQTRPQSRDEYDI

>RXN00349 TRANSLATE of: rxn00349.seq check: 102 from: 1 to: 1467  
MLSFATLRGRISTVDAKAAPPPSPLAPIDLTDHSQVAGVMNLAARIGDILLSSGTSNSD  
TKVQVRAVTSAYGLYYTHVDITLNTITIFTNIGVERKMPVNVFHVVGKLDTNFSKLSEVD  
RLIRSIQAGATPPEVAEKILDELEQSPASYGFPVALLGWMMGGAVAVLLGGGWQVSLIA  
FITAFTHIATTSFLGKKGLPTFFQNVVGGFIATLPASIAYSALALQFGLKPSQIIASGI  
VLLAGLTLVQSLQDGITGAPVTASARFFETLLFTGGIVAGVGLGIQLSEILHVMPLPAME  
SAAAPNYSSTFARIAGGVTAFAVGCYAEWSSVIIAGLTALMGSAFYFLFVVYLGPPVS  
AAAIATAVGFTGGLLARFLIPPLIVAIAGITPMLPGLAIYRGMYATLNDQTLMGFTNI  
AVALATASSLAAGVVLGEWIARRLRPPRFNPYRAFTKANEFSEFQEEAEQNQRQRKRPK  
TNQRFNGKR

>RXN00368 TRANSLATE of: rxn00368.seq check: 9416 from: 1 to: 1575  
MRGLVWLIVAGLFITPLALVVGLALGQNQFPALWDSGLGKALWNSAYTTVLSAVGATIIG  
TIMALTLDRTDVFGRTALRLFLLSPLLIPIFFIGAIWLQFLGKNQGINRFFGTEVWDIYG  
ADGVTFLLIVHSYPTVYIIVSAALRQLPSDLQAARIAGADTFTVLRITLPLLPKALLS  
AFTLTAVANLADFGIPALLGSPARFETLATMIYRFMESGTVSNPLQVSTIGIVLLFLGI  
AAVTADYLVSLYAASKLQDAGTPHRFTLNKSRIPVSVITWIIALIITAAPLLGLAYRALL  
PAPGVFPNLDNITLNNFEAALSNNPRVIEGFSNSLMLSGLAALICGVLGWLIGVLITRTQH  
FANVPLTLTVLLPTALPGMIIGVGWLILGRYTGINTPWVILGAYVCAFTALVVQAVRGP  
LSQAPEAIEEAARISGAGRLRSIMDTTGAMAIAPAFAGAVLVAVTAVRELTVSILLIAPG  
TTTLGVQVFNLQQAGNYNQASALSLMFAIIGIVALALTVRSQKEF

>RXN00378 TRANSLATE of: rxn00378.seq check: 9591 from: 1 to: 2610  
VDKAVNTAISDAKTAALKAGVGLNRATASEEEEEELSSSIKVSALAFELEGLSNAPSLMVVE  
KALEKIPGVSADLIYPSQTAWITATDRVHPETLIEVFEQFGIKAHLNSSSLLRRHQQLSA  
EVNREARLDYRYSRMDAKRISPRVRRHNRQEMVHAVRARESGWIKRRNHTTSQHEDPMSG

DVLFARALITPKRLWVSLPFALIVLALSLSNPWSQFDYWQWLSAVLAI PVVVWGAWPFHR  
AAAGGIRRGISALDATSSIAIAAAYAWSIAMLLFETPGGKSWRSYPSWFAFDHGTLTQNE  
IYFDVACGITVLLLGRLLTRRRSQSSLLAELGRLQIDPQRIVTVVRKHRLKRVRVQELNI  
PVQEVVRVNDVVKVPNTTIPVDGTVIGGGSRIAASIIMGQDQDVKVNDKVFAGSLNLES  
EIKVRVIRTGHRTRIAAVHRWVKEATLKENRHNRAAIRSAGNLVPITFTLAVVDFCLWAL  
ISGNINAAFTTTLAVLACVAPVALALSAPLATRNSIEAAARHGILVRSGEIFRVLDDVD  
AVFNRVGTLTLDGEMTVETVTADKGEDPELVLRVAGALAMESHHAISKALVKASREARDTG  
AGGEDVPHWIEVGNVEITEAGSFQATIELPLIKPSGEKIMRTTEALLWRPRSMTEVREHL  
SPRLVAAATSGGAPLIVRWKKGKDRGVITLSDHVRSDSSDAIIAIEEQGIETMMLSRDTYP  
VARRYADSLGITHVLGAIAPGKKAQVVRVAVHTRGSTVAMIGDESVMDCCLKVADVGVLMGV  
DRPSDLRDDSDDDPAADVVMREEVMSVPTLFKLARRYAKLVNGNIALAWIYNGVAMVLAV  
SGLLHPMAATVAMLASSLLIEWRSGRARKY

>RXN00410 TRANSLATE of: rxn00410.seq check: 1977 from: 1 to: 666  
MMIYGKGSTEVRLDGISVQIQSDKWTSSIMGQSGSKTTLQCLSGLAQPTSGRVTLNKN  
NITLSSLSSENKRAKLRRTHISMVQDFNLVPILSVKDNILLPLRLAHRVDKQWFEHITS  
VLKIDNRMRHLPGELSGGQQRAAIARALMSRPDIVIADEPTGSLDSVTSDAVLNLFRSI  
VDDFGQSLVFVTHDKDAAHRGDVLITMRDGKIIDTADLRVGR

>RXN00411 TRANSLATE of: rxn00411.seq check: 5242 from: 1 to: 675  
MNEMILAADWNRLGPTFQTAIIDTLLMVIITMVVAGLLGLVGLLLYTTRAGGILKNKVI  
YTILNVLVNEFVRPIPFIIILIAAIKPLTVAVMGTSIGRDAGIFVMVAAIFSVARIVEQNL  
VSDIDPGVIEAARSMGASPMRIATVVIPEALGPLVLGYTFLFIAIVDMSAMVGYIGGGGL  
GDFAIVYGYRAFDNEVMYVAVLVIVIIVQAAQLLGNWLSKKIMRR

>RXN00412 TRANSLATE of: rxn00412.seq check: 7568 from: 1 to: 1080  
VSHTASTPTPEEYSAQQPSTQGTRVEFRGITKVFSSNNKSAKTTALDNVTLTVEPGEVIGI  
IGYSGAGKSTLVRLINGLDSPTSGSLLNGTDIVGMPESKLRKLRNIGMIFQQFNLFQS  
RTAAGNVEYPLEVAKMDKAARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQVRGIARALA  
TNPTLLLADDEATSALDPETTHEVLELLRKVNRELGITIVITHEMEVVRSIADKQVAVMES  
GKVVEYGSVYEVFSNPQTQVAQKFVATALRNTPDQVESEDLLSHEGRFLTIDLTETSGFF  
AATARAEEQGAFFVNIHGGVTTLQRQSFQKMTVRLTGNTAAIEEFYQTLTKTTTIKEITR

>RXN00419 TRANSLATE of: rxn00419.seq check: 8218 from: 1 to: 759  
MLNAVKGAKNILLGGTSEIGISIVSRFLKQGPSHVTLAARKDSPRVDAVAEIKAAAGAA  
SVAVVDFDALDTESHPAIDAFAFENGDDVDAIVAFGILGDNEAQWRDQALAVEATTVNYT  
AGVSVGLGQKFEQGHGTIVALSSVAGQVRVRSNFVYGSAGAGFDGFTYQLGEALRGS  
GANVLVVRPGQVRTEKMSADGGEAPLTVNREDVADAVYDAVNKKDII FVHPLFQYVSFAF  
QFIPRAIFRKLPF

>RXN00432 TRANSLATE of: rxn00432.seq check: 8334 from: 1 to: 1485  
MELLETFITDVINDNLWMILPFLLVAAAGLYFGGRTLLVQIRMIPFMFKAVVEKPAKDGFE  
ADKQDISAFKAFTISAASRVGTANVAGVALAITLGGPGAVFWMWIIALVGGATSFIESTL  
GQLWKVKDGDYSYRGPPAYMTLGLNARWLAVVFGVAITLTTFGFVYNALQSNVAVEAITVS  
LGTPSTTAKAFVGLGMAGLSALVIFGGVQRIANVTQWMPFMAGAYIIVGVVVIVINIQQ  
VPTMINDI IAGAFGFRPVATASVWGAFLAFMNGMRRGLFSNEAGEGSVPNAAATATVSH  
PVKQGLVQTLGVYFDTLVCSITAFVILLSGVEYATGDIQSSSLTQSALASVVGWGTHTF  
ITVVMFFLAFSSVLGNYYLAQANIQYFTDSKTVMTVFRLLVLLSVFSGAVASVPLI WALG  
DTFAGIMVLINLAAI IPLGGVAVKLLKNYTIQKKAGLDPVFHRDMMPEVRNIACWNGKDA  
ATSNYHEAMEVIKKS

>RXN00443 TRANSLATE of: rxn00443.seq check: 5344 from: 1 to: 804  
VNKSIRRALYSFITISAGISLVACSSSDTASTTTQNASATEAAGVSGTASVFAAASLTNV  
AEDLAAAFNEDNPDAKLEFNAGSSALVRQISEGAPSDLFISADIANMDDALALPEFAGA  
TSKVIATNKLVLVTADGNPGEISELADVKDSLVAICAPEVPCGTITHEALDYADIELNTS  
SEEANVADVATKISTGAVDAGFVYQTDQSLAKTQDNTVIELEGIDANEYPMALTTTGED  
NEVAKAFAEFLSSDRAKEILASYGFGTN

>RXN00444 TRANSLATE of: rxn00444.seq check: 7535 from: 1 to: 837  
MVLAQTKKARRSENHILPGWLLIPATLAMLLIIGPIFALLQIPWDRSWELLTAPESLGT  
ARLSIGTALFSTALCAIVGFPLALALHLYERSHPRVTSVLTVLVYAPLVLSPVVSGLALT



FLWGRRGFLGSWLDQVGLPIAFTTTAVVFAQVFVALPFFISTVTTALRGIPKQFEEIAAT  
EGATRWEIMHKMI IPLAMPGIFTGMILGFARALGEYGATLTFAGNIAGVTRTIPLHIELG  
LSSNDMDKALGAVIMLLAVYVLIIGAIGALRLFSKVRKV

>RXN00449 TRANSLATE of: rxn00449.seq check: 92 from: 1 to: 1581  
MSTPDIKEGSAESPGEVMVVGDRREWRQATGIIAGLVLAALVYLLFPSNSVETVMQSSG  
VDPETEYTNAMRLTAAVTILMAVWWMTEAIPLAATALIPLVAFPAFQVDFGKATAPYA  
NPTSFLFLGGFLMALGLQKWNLHRRMALAVVLAVGTPKPKQLVLGFMVATGFLSMWVSNTA  
TAVVMLPIGMSVLALTAETVGGMKNQKKFATGLMLSIAYSASIGSLGTILGTPPNALLAA  
YMSESHDIHIGFGQWMLGVPIAVVFTIIAWLVLTTFVKPEMKEIPGGRELKREIAEMG  
PWTAPQVTVGVIFAAAAALAWFIPLTLDWTGSQSLINDSLIGIAAGLLMFIVPANFKTGE  
RILDWRTAGELPWDVLLLFGGGLSLSAMFTSTGLSLWIGELAKGLDALPFIILIFAIAVL  
VLFLTEFTSNTATAATFLPIMGGVAVGIGLTAGGEQNVLLLTIPVALSATCAFMPLPVATP  
PNAIAFGSGYIKIGEMVKGGLWLNIIAVILITIFTYFVAIPLFGIML

>RXN00456 TRANSLATE of: rxn00456.seq check: 2097 from: 1 to: 1377  
VLQALLAIMVSLSVAAILEGNRALVGLLLATTGLGVAQWIKVVAEDLGQHYVHEVRRE  
LVGAALVPGNTASLGVTVTRASNDLTAVRNWVALGIVPMVTGLPLIAIVLVALFIQDLRT  
GVAVTVPLLMCAVAVLPVVARWTLKRARELRKKRGRMAARIADSVMAGELLHATGAIDREL  
NAVTRDSRVDVIAAVRRSWATGFSRALMAMAASLGTVSIVISGHLEVSEVAGIMMLLGVL  
ATPVAELGRVVEYRQNYKAATRILIPLLQRGSEFKHSQQKLPLQLQATEGIPGVYVKGISA  
LPGERIYLGHSADATRKWVTSLSAMEEGTDVIVNGQRLSQLPLKQRRALIGIASAHHHLS  
RGSVSRVLVGLRVPDATVEEIEQALEQVGLNNTGKQRLKNGGHPWSTSQINKLKIASATLR  
TPPLLVLGITPENLLNYPGVIISTVQENPSETWRQVNI

>RXN00466 TRANSLATE of: rxn00466.seq check: 8825 from: 1 to: 996  
VQSRLSKILRSSVVGAVLALLAGCSNNADDTADSTSTGNSAFPVSIEHEFGTTTIDDV  
PERVVTGLGVTADIVLALGTVPGNTGYKFFENGLGPWTDELVEGKELTLLDSDSTPDLE  
QVAALEPDLIIGVSAGFDDVVEYQLSDIAPVVARPAGTAAYAVAREEATNLVARAMQSE  
KGQELNEETDALIQAARDENPSFDGKTGTVILPYQKGAYLPGDARGQFLDSLGLISLPE  
AVLSRDTGDSFFVDVPAESVKDVGDLVLSNDENLDITAENPLFETLNVVQKDAVIVA  
TTEERGAITYNSVLSVPFALEHLAPRIAEALK

>RXN00477 TRANSLATE of: rxn00477.seq check: 7063 from: 1 to: 1644  
MKVSTKTPRSSGTAVVIGAGVAGLATSALLARDGWQVTVLEKNTDVGGGRAGSLEISGFPG  
FRWDTGPSWYLMPEAFDHFALFGACTSDYLDLVELTPGYRVFSGTHDAVDVPTGREEAI  
ALFESIEPGAGAKLGNLYLDSAADAYDIAIDRFLYNNFSTLGPLLHRDVLTRAGRFLSLLT  
RSLQKYVNSQFSSPVLRLQILTYPAVFLSSRPTTTPSMYHLSMHTDLVQGVKYPPIGGFTAV  
VNALHQLALENGVEFQLDSEVISINTASSRGNTSATGVSLLHNRKVQNLDAVLVVSAGDL  
HHTENNLPRELRTYPERYWSNRNPGIGAVLILLGVKGELPQLDHHNLFFSEDWTDFFAV  
VFDGQPLTRPHNASNSIYVSKPSTSEDGVAPAGYENLFVLIPTKASSIGHGDAYMQSAS  
ASVETIASHAINQIATQAGIPDLTDRIVVKRTIGPADFEHRYHSWVGSALGPAHTLRQSA  
FLRGRNSSRKVNNLFYSGATTVPVGVI PMCLISAENIIKRLHADTSAGPLPEPLPKTTP  
SQKTSYDH

>RXN00523 TRANSLATE of: rxn00523.seq check: 9218 from: 1 to: 1026  
MSLSHQLKRQRASRNSRRWLIVAALGVVTLGIFAFSLMWGEVFGPAQVLKVLSGQQVPG  
ASYSVGVLRLPRAVMGLTAGLAFGAAGVIFQTVLRNQLASPDIIIGISSGASAAGVICIF  
FGMSQSAVSAISLCAVALLIYLVAIRGGFSATRLILTIGIGIAAMLNSLVSYSLSKAD  
SWDLPTATRWLTGSLNGATWDRAMPLIVTTVVLIPLLVANARNVDLMRLGNDASVGLGVA  
TNRTRVIAIIAAVALIAVATAACGPFAFVAFVSGPIAARILGSGGSLIIPSALIGGLIVL  
IADLIGQYFLGTRYPVGVVTGAFGAPFLIYLLIRSNRAGVTL

>RXN00525 TRANSLATE of: rxn00525.seq check: 5915 from: 1 to: 1263  
MSLAESILLALTSLSRNSKMRALLTLLGVIIGIASVIGILTIGKALQDQTLNSLES LGAND  
LSAQVEERPDEDSPEPDMFAFSGAANSSGNLIPEETVDTLRDRFAGSITGISVGGMGTOG  
TLIGDTADLKSDDLGVNEDYMMNGVEMNYGRAITQDDVAAQRPVAVIAPDFTNTLFDAN  
PNLALGSEVAFELNGQETFLRVIGVYKEAAAGGLVGSNPTVHTYTPYTVANDITHTEDGL  
NTLSIRAAQGVDDQSLKGSLOTYFDALYANNDSHHVAMLDLFRKQIEEFNTILGAMSLGIS  
AIGGISLLVGGIGVMNIMLVSVTERTREIGVRKALGARRRDIRLQFVVEAMIICFIGGIL  
GVLLGGILGLIMSSAIGYISLPPLSGIVIALVFSMAIGLFFGYYPANKAAKLDPIDALRY

E

>RXN00559 TRANSLATE of: rxn00559.seq check: 9522 from: 1 to: 1017  
 MSDNPHENPRENPHRSPEVVLRFMAAPTDVLMAGSHGVGGGRVLEWIDKAAYACATQWSG  
 TYCVTAYVGHIFHTRPIPSGHMVEVRSRIAMTGRSSMHIVNEVLSADPRDGNVTRACDCL  
 VIFVAKDTATGRATPVPSFTPKNEEEEQVRLEAANSRIGLRKAIEAEMEKQTYNGPSEAPR  
 LITRFLAKPTDINWGGKVHGGTAMEWIDEAGAACTMEWSGNHTVAVYAGGIRFYQPIQIG  
 DLIEVDARMMRTDKRSMQMSIHVRAGDAHRGRAELETAIHATVTVTLGIDVDGEPLPAPQF  
 VPRTPEDIQLAEHANILRDLRADYTPMPLFQRRVPLQID

>RXN00563 TRANSLATE of: rxn00563.seq check: 2005 from: 1 to: 2739  
 FYKDLIARSARGTAALWIVAANLSSYSIDIDAIINWVGSEQTTTVNGASKLVKPALVPTLL  
 FPFAPRVSGSMADAGPQAESQMRLLLWSVERLIAGLAPLGSSINVGHRLHVVIPGSPNR  
 GRFGGDGAYGESKAALDAVVTRWNAEQAAWGAHTSLVHAHIGWVRGTGLMGGNDPLVKAA  
 EEAGVETYSTQEIIEKLLSQATSTVREQAASAPITVDFTGGLGESDLNLAEMARAEAAKA  
 ANAPVVEAPRTVAALPTPYRPVVQTTDFAGQVTQNLDEMVIIVGAGELGPLGSARTFRD  
 AELNGSLSAAGVIELAWTMGLIHWEDEPKPGWYDDSDDAVAEEDIFDRYHDEVMARVGR  
 KYNDMPYEGMIDNFAPELTTVYLDQDLTFNVGSREEALTYVDSEPELTFASFDEAAGEWK  
 VTRKAGSAIRVPRRMAMTRFVGGQVPKDFDPAVWGIADMDVNDLDTVALWNIVCTVDAFL  
 SAGFTPAELLASVHPARVSSTQGTGMGMESLRGIYVDRILAEPRANDVLQEALPNVVAA  
 HVMQSYVGGYGQMIHPVAACATAAVSVEEALDKIRIGKSDFVAGGFDALSVEGITGFGD  
 MAATADSAEMEGKGIEHRFFSRANDRRRGGFIESEGGGTVLLARGSLAADLGLPVLGVIG  
 FAESFADGAHTSIPAPGLGALGAARDGVESRLAVALRSVGSADAESIISKHDTSTNAND  
 PNESDLHERIASAIGRADGNPMYVISQKSLTGHAAGGAAAFQMIGLTQVLRSGLPANRA  
 LDCVDPVLSKSHSLVLRKPLDLRAKAPKAGLVTSLGFGHVSALVAIVHPDAFYEA VRVA  
 RGAEAADVWRASAIAREEAGLRTIVAGMHGGVLYERPVERNLGVHGDAAKEVEAAVLLDS  
 RARLVGVLRAEG

>RXN00570 TRANSLATE of: rxn00570.seq check: 2677 from: 1 to: 852  
 TRPRPQEIGNGLVALIFSASGPIAVILAAAAAGNLSPDQTSSWIFGAFLGNGLLTLWLTY  
 MYRSPQAYFWTIPGTIVIGDSLTHLSFAEVIGAYLVTGVVVFALGWTGLIGRIMAVLPPT  
 IVMAMVAGIFLRFGLDLIDASVTDPLIALPMVIVFVALSMSRPLASIAPPVAVAAVGTI  
 VAIASGKLASGILDNGIISRPVFTAPEFSFAAIMELVVPLAITVVIQNGQGVAVLKAAG  
 HRPGVNLAAAASGLWSLPMALIGNITTCLTGPTNALIVAGAKSH

>RXN00571 TRANSLATE of: rxn00571.seq check: 33 from: 1 to: 1257  
 TLVPQVYEIVYIYGAVLSAVHEDPTQIGALSPAVAGTLGSYAMIGVMIGALSAGAVGDRLG  
 RRRKVMLTAIVWFSVGMALTAFASSIALFGFLRFLTGLGVGMIVATGGAIIEAFAPANRRN  
 LFNAIVYSGVPAGGVLASILALLFEDVIGWRGLFLIGGSPLFLFLPLAYFFLPESPRWLT  
 SRGRAADAKALCARYGLPTEEFVVEKQOQETKGTGFAGIFSSKYLMTILIGAMSFIGLLS  
 TYGLNTWLPKIMESNGATSHDSLYSLLFLNGGAVFGGLIASWFADRIGAKTVITSTFALA  
 AICGLVLPNISSWPMMYTAIAFAGVGVLGTQVLTLYGLTSNFFGTECRAAGVAWCAGFGR  
 LGIVGPAIGGLIIGAGFGPSSAFLIFAAAAAIGAVCTLLIPRSPAEEVEVKVAQEPLARV

>RXN00590 TRANSLATE of: rxn00590.seq check: 3570 from: 1 to: 1188  
 MADNKNADDSQLVSASTGTPGPGDIAKANAPSLKQAAVTASGRSALMGAIIFLMATSAIGP  
 GFLTQTAVFTNQLGAFAFAILVSILIDIAVQLNVWRIIGVSEMRAQELGNTVIPGFGWV  
 LAVLVCIGGVVFNIGNIAGGGLGNALLGWDVVKVGGVITAAIAIAIFLFRKRLGAALDKFL  
 VVLGVVMILLTVYVAFVSQPPVGSALKNAVLPTIDWLVIITLVGGTVGGYITYAGAHRM  
 LDSGRTGPNNVKAVSNSSITGILITGLMRVVLFLAVLGVVAGGVTLSTTGNPAEEAFQHA  
 AGDIGLRIFGAVLWAASISSVIGASYTSATFLVENKPEKKRLQNWVTIIFILISCSVFIM  
 LGTAPAILLVFAGAFNGLVLPVGFTLMIYVAIFRQK

>RXN00661 TRANSLATE of: rxn00661.seq check: 3591 from: 1 to: 690  
 MNPITELLDATLWIGGVPIWREIIGNVFGFLSAWAGMRRIWAWPIGIGNALLFTVFM  
 GGLFHTPQNLDLYGQAGRQIMFIIVSGYGWYQWSAAKRRALTPENAVAVVPRWASTKERA  
 GIVIAAVVGTLSFAWIFQALGSGWPADAWIFVGSILATYGMARGWTEFWLIWIAVDIVG  
 VPLLLTAGYYPYSAVLYLVYGAFVSWGFVVWLRVQKADKARALEAQESVTV

>RXN00733 TRANSLATE of: rxn00733.seq check: 1945 from: 1 to: 885  
 MSNTAGPRGRSHQADAAPNQKAQNFGPSAKRLEFGILGHDRNTLIFVIFLAVLSVGLTVLG

PWLLGKATNVVFEGFLSKRMPAGASKEDI I AQLQAAGKHNQASMMEDMNLVPGSGIDFEK  
 LAMILGLVIGAYLIGSLLSLFQARMLNRIVQSAMHRLRMEVEEKIHRPLSYFDSIKRGD  
 LLSRVTDNDVNIGQSLQQTLSQAITSLLTVIGVLVMMFIISPLLALVALVSIPVTIVTV  
 VVASRSQKLFAEQWKQTGILNARLEETYSGHAVVKVFGHQKDVQEAFFEEENQACV

>RXN00784 TRANSLATE of: rxn00784.seq check: 3499 from: 1 to: 735  
 MSIEFSAPAKMKIEVWSDIMCPFCYIGKKRLDDALSTFDQAGRIEVEYKSFELMPGLETH  
 PLRSDVEYLADAKMSLEQARQMNGQVQAMAQATGLEMNPDETIAANTINAHRLTHFAKA  
 HGKQQEVAQELFKAHFVDGKNVDDLVLVSIAAEVGLDASAAREALESVDYTNVQQQDVH  
 EARQLGVQGVFFVFDKRYAINGAQQEEVFTGTVEKAFFEEWAAENPVSPFEVIDGQSCSV  
 DGTCN

>RXN00792 TRANSLATE of: rxn00792.seq check: 6734 from: 1 to: 1197  
 MSQEILSHFAPALERIRSGAVEREQQRALPVEEIKELVELGFTGLRVPEELGGAGASLES  
 VVELLIEIAGADSNIAQALRGHFAFVELLLEAPESEFRTHWLREVATGRLVGNAESEKRG  
 VYGDPTFTIDEVETENGPIFVLNGTKFYTTGTTFADYTWTALLRNLNGQETLVSLPVDL  
 HAPGVDVADDWSGFGQKLTAAGTTTTFKDLEVDPRWIIPTDAPTLVWTYLQSLTLTVLVG  
 SAAADEVVARAQSSSTRNAWNPGVERRSDPAATIAIGDARSRTVIRGALLDATRHVSN  
 AATIVTPEAFNEADAIVAALWPIVSGQALVVTSNVFDVAVGASAVLGEHSIDRHWRNVRTV  
 SSNNPVFLAKNAVGEYALNGTPVGTNIGKALSPPVSLSS

>RXN00819 TRANSLATE of: rxn00819.seq check: 3788 from: 1 to: 1329  
 MRDPIQGAVIPSDLFGFAEVLTEAERAVLLETRRVLEEEVKPYINEAWDKAVFPDEIVQP  
 LQDLQLLDPPALREAGESVRDIFTGFRNFELARCDINVGTYYNASAGLFRACMVGGSP  
 QAQRLDAQIKSGEVKGVFALTEPDHGSIDAGGLATTATKDADTGEWIINGEKRWIGGAST  
 ADLIATFARDTADNQKCFVLVAPQAEGVSMEIIDRKASLRIMQNAHITYNNVRVSGDARL  
 HNINSFKDVSECLRRMRSDVAWMAVGAQAGAYEAAVKYVRSREQFGRPIAGFQLIQEKLA  
 LMLGNLTASLGMVVKLTDDQQAGIFKEENSALAKMFTSLKLRETASWAREICGGNGIILD  
 NDVARFHADAFAVSYEGTHEINALIVGRXILGXLFFLYXXFEEDLHDYFHHPKPSFLS  
 KTHQPSPARTWAFRSGALSPRRW

>RXN00832 TRANSLATE of: rxn00832.seq check: 2297 from: 1 to: 1050  
 MPFSWLKPIDYARIFVGWASIFIPLITLPSIIELALIVAVILFCAFGVVKMAERLAHIL  
 GDPFGSLILTLISIVIIIEVILICAVMLGPADSTTAGRDSVMAVSMIIMGLVVGLCLLIGGL  
 RHGSMPHNGVGTPTYLVLVLIATFSVIAFAVPAFRGEYSTGQALVISTLTAVVYGFFLFRQM  
 GAQAGEFQEEVEAEKADDAKWEVPFRGLILITVLPVLLSHDMATVMDEVLASLGAPV  
 AMAGLIATIVFLPETITSLKAAWTGEIQRVSNLAHGAQVSTVGLTIPAVLVIGVITGQD  
 VVLGETPINLLLTGTIAVTAIAFSSKKVSAVHGSVLLMLFGVYMMMSMFA

>RXN00842 TRANSLATE of: rxn00842.seq check: 5448 from: 1 to: 1200  
 MIIQILRVAFVFGIIVGAGFASQEVQMVFVAFGIDGIWGVIVSAVIMSVMALIILQLG  
 SYFNAGEHGEVFRVSHPVFSKILDIGVVVTLFSTGFVFMFAGAGSNLNQWGLPLWIGSV  
 IMVLLVLAAGMLDVKVTTVIGAITPFIIIFITAASIYTLVGNFSSVEQLDAALEVGT  
 LPHWAAVAVNYVGFNLMAVSMVAVVIGGSMFNPRVAGRGLLGGLIILGLIIISALTFLFA  
 TVEEVGQDDMPMLTIINNPLNPLAGQVMAVVIYGMIFNTALGMFYALGRRLTAKNPQFRFP  
 VYVTVLIGFVLSFVGFKNLVGYVYPVLGYIGLLLIAMMVAVVRGRVRIYKESERRMRI  
 ADLLQIGHDGAELAVLNQEIQDSNLDEEIQIKAAVRK

>RXN00931 TRANSLATE of: rxn00931.seq check: 6454 from: 1 to: 846  
 VKTIEDILTLEEIDRDIYRGPVIESYLARTFGGQVAAQALVAATHTVDKAFTVHSLHGYF  
 IAPGDPTAPAIYLVDRVRDGKSYVTRSVRGIQDGEVIFSMQASFHGDEGIEHMDKMRKV  
 PAPDEIKGTVERMPISSRRVLDEWAEWDIRVIPQDQLELSDFTEQAVWIRCTADLPDN  
 PTFHQCSLTYSMDMTLLHSALVPHPGKMQMASLDHAVWFLRPFRVDEWLLYDQSRSPSAS  
 SGRALTHGRFLNQQGDVLAIVNQEGMTRTLHEGAQSIIPMRKD

>RXN00934 TRANSLATE of: rxn00934.seq check: 9723 from: 1 to: 1083  
 VRIGMVCPYSFDEPGGVQAHILDLARTFIAQGHEVQVLGPCSADTQVPDFVVRGGGSIPI  
 PYNGSVARLSFGPKMFKAVRTFLREGNFDVLHIHEPNSPSFSMAALRFAEGPIVATYHAS  
 SSGSKLLKAFLPVLSPMLEKVRAVSEMAARRWQVEQVGGDPVLIPNGVETSMFKAARQ  
 IEPNDPVEIVFLGRLEDSRKGLDILLRALTRLDPRFTCTVIGGGTPREVAGINFEVGRVSD  
 EEKAAILGRADIYVAPNTGGESFGIVLVEAMAAGCAVVASDLEAFSLVTDSEAAQPAVGL

FKTGSDADLAKKLQALIDDPSSRSTLIAAGLKRANAYDWSTVSTQVMAVYETIAIDKVRL  
G

>RXN00960 TRANSLATE of: rxn00960.seq check: 4118 from: 1 to: 1035  
MARHCCSNRYASTVFSGLIAYGASQALYPWLLKDHQSVTEIDLDAAGALQPYFNIEMPPPF  
EVMTALLLAFLCLGLGMAVIKSDTLFKVTRERLVRVMTITAFVIPLPLFIFGIFLGMGM  
NGGLEIMSAFGKVLILAVVGTLLFLAIQFIIAGAVSKKNPWKLFKNMPLPAYFTALTGTSS  
SAATIPVTYQQTLKNDVDVNVAGFVVPCLATIHLAGSMMKIGLFTFAVVFMYDMEVGVGL  
SIGFLLMLGITMIAAPGVPGGAIMAATGMLASMLGFNTEQVALMIAAYIAIDSFGTAANV  
TGDGAIAVIVNKFAGKQLHTTSPDEIEEDDRVAFDITPSDVEHHK

>RXN00980 TRANSLATE of: rxn00980.seq check: 2367 from: 1 to: 1794  
MLADAFMIAAAIVAGWPQIAQSAYQALRIRMVSIIDLVVVAAGVAMFINNYWESAAVTFLF  
ALGKALERATMNRTRKALSDDLVAAPETATRLNADDSTEVELWELEPGDIVLVRNGEQI  
PVDGNVIAGVGGIDESNITGESMPAEKQGSVDVYAGTWLRSGLRVEATGIGSDSTLAKI  
IHRVEDAQDDKARTQTFLEKFSKWTTPGVMAAAVVGLITWDVELALTLLVIGCPGALVI  
SIPVSIVAGIGRAARDGVLIKGEYLETAAKVDVVVDKGTTLTGRPELTDVEIEPAY  
SQGEVLELAARAETAHEPLADAIIRGAQDRGLSTTLVEAAENITGRGIANVDGQAVAV  
GSAELLDHEPDSTRILELNAEGKTAMFVGNGHAIGIVAVADAVRSDSASAIESLHKAGI  
QVVMATGDAHRVAQNASKLVDEVYSELLPEQKLELVRDLQAAGKTVAMVGDGVNDTPA  
LAAADIGVAMGVAGSPAAIETADIALMADRLPRLAHAVTLAKRTVRTMRINILIALATVM  
VLLAGVLFGGVTMSVGMVLVHEASVLLVISIAMLLLRPTLKEDAAQASDIKRSEIQQIA

>RXN01000 TRANSLATE of: rxn01000.seq check: 4854 from: 1 to: 846  
MSTLTSHRTVPAPSSPPARPKNKLARNIVAIVAALIVLIATGTLKIEWNELPQMPAQVWHY  
LELMFSDPDWSKFGRAVQEMWRSIAMAWLGAILCVVSVPLGMLAARGVGPYWLRTVLR  
VFAVIRAFPEVVIAIILLTVTGLTPFTGALAGISGIGQQAQWTYEAIESTPTGPSEAVR  
AAGGTTPEVLRWALWPQVAPSIASFALYRFEINIRTSAVLGIVGAGGIGSMLANYTNYRQ  
WDTVGMILLIVVVVATMIVDLISGTIRRRIMKGASDRVVAPSN

>RXN01002 TRANSLATE of: rxn01002.seq check: 1757 from: 1 to: 804  
MNSDASATTNSWAINFDHVSVTYPNGTKALDDVSLTINPGEMVAIVGLSGSGKSTLIRTI  
NGLVRATEGTVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSESSVFQNVLVGRFAHT  
AWWRNLLGFPTEHDKQIAFHALESVGLHKVWTRAGALSGGQKQRVAIARALSQDPSVML  
ADEPVASLDPPPTAHSVMRDLENINNVEGLTVLVNLHLIDLARQYTRLVGLRAGKLVYDG  
PISEATDKDFEAIYGRPIQAKDLLGDRA

>RXN01007 TRANSLATE of: rxn01007.seq check: 4278 from: 1 to: 1707  
VFKKRRHGLGSPETKPRSITRRFFATAAATLAGLAVLSGCTAQPSQAEDNTLTYLEPQFF  
RTLYPPSAGFYPNGSVVNNIADRLLYQDPETLELKPWIATELPEVNEDATEFTFNIRTDV  
TYSOGTPLTAENVVKNFDLYGLGDQDRRLTISEQITNYDHGEVVDVETVRFHFSEAPGPF  
AQATSSFNAGLYADSTLEFANEDFAPGNAQNVIGSGPFVITDETGLTNLTLTAREDDWA  
PPSREHQGRKLDVANYVLAGEESVRIGAVAGQGDIAEQIEAPVEAHLKDAGIPIISAA  
TNGVNNNSFNFRKNEILLSDIRVRQALIHAIIDREKIMRVLFSDSYPLATSVLAQNALGYKE  
QVDAYVYDLKATALLDEAGWTLDSGMRKDGELLELTTFNEALPQPRSREVVTMVQEQL  
GDLGIKVNLPNGDQAQDADSKDLNKIQVRHTMVGRADYDVLKSQLYSTNRNELLNMTVE  
GETADIGDPHLEELLMAIASSPREEDRAAASAAAQDYITEQAYVLPLFEPPVYGVQPYV  
KGFSPFVIGRPSFYETYIDHSSDHSSEED

>RXN01090 TRANSLATE of: rxn01090.seq check: 2624 from: 1 to: 798  
MALPLPSKSARALVTGASQIGLAIKDLARYGHNILVARREDVLKEIAADLEKKHGV  
VEVRPVDLSDEPARKVLIDEIKTREINIIINSAGIASFGPKDQDWSYETAQFSLNATAV  
FELTHAVLGGMIDRGTAICNVGSAAGNVPIPNNATYVLTAKGVNAFTEAMHYELRGTV  
ACTLLAPGPVREAEIPESEKSIVDKVVPDFLWTTYESCSAETLRALSQNRVVPGLPSK  
AMNFVSSVAPTAVLSPVMGWVYKMG

>RXN01114 TRANSLATE of: rxn01114.seq check: 9460 from: 1 to: 1224  
MNPQDIVICSPLRTPVGAYGGSFTGVPVEELATTVINAIVEATGITGDDVDDLILGQASP  
NGAAPALGRVVALDSKLGQNVPGMQLDRRCGSLQAIIVTAAAHVASGAADLIAGGAESM  
SRVEYTVSGDIRWGVKGGDMQLRDLAEARETAGGRNHPIPGMIETAENLRREYGISRE  
EQDKISAASQQRWGAADAGLFDDEIVPVTVPKRRGQEPTIVSRDEHGRPGTTVEKLAA

LRPIMGRQDAEATVTAGNASGQNDGAAVIVTTRAKAEKGLRPVMRLAGWSVAAVPPET  
MGIGPVPATKKVLDRLGLTLEDIGAIELNEAFAAQALSVLKAWNISWEDERNPLGSGIS  
MGHPVGATGARMAVTLAHRMQRENTQYGLATMCIGGGQGLAAVFEKEN

>RXN01139 TRANSLATE of: rxn01139.seq check: 1443 from: 1 to: 954  
MESHDLQQRSYAHNPDGHDHSHDGLGHSHAPSSLKALFAVIFTSIIFLAELIAGLISGS  
LALLADAMHMLS DSTGLIIAAVAMLIGRRARTSRATYGYKRAEVLAAAMVNATVVTALSVW  
IVVEAIRMLGKDLEIQTNLMMLIVAVIGFVTNGISALVLMRHQDGNINMRGAFLHVLSDML  
GSVAVIIAGLVIRYTGWMPADTIIASIAIAAIIIPRAFSLLKEALNILLERVPTGAEPAEV  
DAALRKVPGVSDVHDLHIWSIDGKEILATVHLVVDSSSTNQLHSCGVLDRAEAELSKLGIL  
HSTIQLESADHSDHESVC

>RXN01141 TRANSLATE of: rxn01141.seq check: 9956 from: 1 to: 825  
LSTALAGAARYVTSTSNNEPADNTPLTIGYVPIAGSAPIAIADALGLFKKHGVNVTLLKKY  
SGWSDLWTAYATEQLDVAHMLSPMTVAINAGVTNARSPTLSFTQNTNGQAITLASKHYG  
SVNSAADLKGFMVLGIPFEYSVHALLLRDYLVSNAVDPIADLELRLLRPADMVAQLTVEGI  
DGFIGPGPFNERAISNGSGRIWLLTKQLWDKHPCCAVAMAKEWKAHPTAAQGVNLAALEE  
ASAILSNPQFDDSSARTLSQEKYLNQPATLLDGPS

>RXN01142 TRANSLATE of: rxn01142.seq check: 3960 from: 1 to: 498  
LTARGNIDFGLRSARPSLSKTERADITRTHLEQVGLTDAAERRPARLSGGMQQRVGIARA  
FAIDPPIMLLDEPFGLDALTRRELQQLLNIWEASRRTVVMVTHDVEAILLSDRVLVM  
SKSPEATIITDIPVNLPRPRHELSEDASVEAETTALRKRMLHLLH

>RXN01164 TRANSLATE of: rxn01164.seq check: 868 from: 1 to: 1635  
VTLFVRLAALAVGGFLVFASNEPIGWVAVAGIVGTALFFISLAPWDLGVPQRRKKNEPVP  
FLQOMSTGPTVVQGMLLGFVHGLVITYLQLLPWIGEFVGS LPYVALSVVEALYSIALGAFG  
VLIARWRDWKVLFPAMYVAVEYLRSSWPFDDGFAWVRLAWGQINGPLANLAALGGVAFVT  
FSTVLAAGVAMVIISKRLAGAIITASVIAIGAVSSLYVDRNGTSDESIEVAIIQGNVP  
RMGLDFNAQRRAVLANHARETLKLDEQVDLVIWPNSSDVNPFSDAQARAIIDGAVEHVQ  
APILVGTITVDEVGPRNTMQVFDPEGAEEYHNKKFLQPFGEYMPFREFLRIFSPYVDSA  
GNFQPGDGTGVVEMNAANLGRAVTVGVMTCYEVI FDRAGRDAIANGAEFLTPTPTNNATFG  
FTDMTYQQLAMSRMRAIEFDRAVVVAATSGVSAIVNPDGSISQNTRIFEAATLTESIPLK  
DTVTIAARVGFYVELLLVIIGVLAGLFAIRMNSRSKSAKGSARPAQVRVKKVPAKKAATN  
RRKVK

>RXN01168 TRANSLATE of: rxn01168.seq check: 6703 from: 1 to: 810  
MSSEAVDATTLVIIPTYNELENLPLIVDRVRTATPDVHVLIVDDNSPDGTGERADKLAAD  
DDHIFVLHREGKGGCAEYMAGFQWGLERDYQVLCMDADGSHAPEQLHLLLAIEITNGAD  
LVIGSRYPGGRVNWPKNRWLLSKGGNVYISVALGAGLTDMTAGYRAFRREVLEALPLD  
ELSNAGYIFQVEIAYRAVEAGFDVREVPITFTEREIGESKLDGSFVKDSLLEVTKWGLKH  
RGGQAKELSKEMVGLLNYEWKHFKKRNTWL

>RXN01191 TRANSLATE of: rxn01191.seq check: 2562 from: 1 to: 1590  
VGGLVDKLLATPSMRDVVVFALLIVAGGVVSSLGTWWGSALMARALEPAIAGLREDVLRA  
AVSLDANTIETAGRGDVISRIADDSREVSTAASTVVPLMVQAGFTTVVISAFGMAAVDWR  
GLVGLVAIPLYWTTLRVYLPRSGPLYTREREAFGVRTQRLVGAVEGAETLRAFAEDTEL  
KRIDAASGEARDISISVFRFLTWAFSRNNRAECITLVILGTGFYLVNIDLVTVGAVSTA  
ALIFHRLFGPIGTLVGMFSDIQSASASLIRMVGVINAASNQVSGTSPASASTALTDFDVS  
HHYHTAPVIKNASVQLEPGEHIAIVGATGAGKSTLALIAAGLLSPTSGQVALGGSSFSNV  
EPEALRQKIAMVSQEIHCFRGSVLDNLRIARPEATDADIHAVLADIGDSWLERLPQIGIDT  
IVGDGAFLRLTSVENQIMALARVHLADLAIVILDEATAESGSDHAKQLEDAALKVTENRSA  
IIVAHRLNQAKTADRIIVMDSGEIIESGTHEELRAIGGRYEQWLTAWSAR

>RXN01212 TRANSLATE of: rxn01212.seq check: 3583 from: 1 to: 924  
MPMTTTPAIDVTDLVRTYGDYTAVKGLNFHVQRGEVFGLLGTNGAGKTSTLEVEIGLSAP  
SSGTVRISGLDPVADRAILRPELGIMLQSGGLPSQLTVAETMDMWHGTCTYPRAIKDVLA  
DVDLLHRENVKVGALSGGEQRRDLACALLGDPSILFLDEPTTGLDPESRRHTWQLLLDL  
KQRGVTMMLTTHYLEEAFLCDRIAIMNAGEIAVEGTLDELVAREKSIISFVLRRGGQVEL  
PVLSGAEIIRDNNHVRIATTTLQQHTLEILTWAETGIALEGFAAKPATLESVFMIDIASL  
ENTSLQTA

>RXN01285 TRANSLATE of: rxn01285.seq check: 1049 from: 1 to: 726  
 LNVITPDNTFTAIIGPNGCGKSTLLRGFSRVLPQHKGKVLDDGRQLDSFKPKKEIARELGL  
 LPQTSIAPEGIRVYDLIARGRAPHYQSLIQQWRTSDEDAVAQALASTNLTELAARLVDELS  
 GGQRQRVWVAMLLAQQTPIMLLDEPTTFLDIAHQYELLELLRAFNEAGKTVVTVLHDLNQ  
 AARYADHLIVMKDGHVHATGTPEEVLTAEVQGVFGLPCIISPDPVTGTPTVPLSRSGA  
 GA

>RXN01298 TRANSLATE of: rxn01298.seq check: 8940 from: 1 to: 930  
 VSTLISEPEVDKLRKRAKRSRTEWWLAAALLAPNLLLLAIFTYRPLLDNFRLSFFNWN  
 SSPTSTFIGFDNYVEFFTRSDTLQVVLNTVIFTACAVIGSMVLGLLLAMLLDQKLFGRNF  
 VRSMVFAPFVISGAAIGVAFQFVFDPNFGLVQDLLGRIGVDSPOFYQNPWALFMTFTF  
 VWKNLGYSFVIYLAALQGLNKDLSEAPVDGASAWTRFWKVTLPQLRPTTFFLSITVTLN  
 SVQVFDIHTMTRGGPLGNGTTTLVYQVYTETFTNYRAGYGATITILFLLLLIITVIQV  
 RYMDKENKQK

>RXN01338 TRANSLATE of: rxn01338.seq check: 9102 from: 1 to: 1902  
 KTYTPNPWMLFIRSFDTGIIITVAALVAIAIHLILWLALDLDGLAKNWPLIAIVIVGGIPLM  
 WDVLSAIAKTRGGADTLAAVSIITSVLLGEWLVAIIIVLMLSGGEALEEASRRASGTL  
 ALARRAPSTAHRLLGATILDGTEEIAVEEITVGDVAVLPHELCPVDGEIVAGHGTMD  
 YLTGEPYVVSQSKSGQAMSGAVNGDTPLTIVATKLAHDSRYAQIVGVLHEAENNRPEMRR  
 MADRLGAWYTVIALALGGLGWIVSGDPVRFLAVVVVATPCPLLIAPVVAIIIGAI  
 GIIIVKNPGMLENASGVKTVMFDTGTLTGRPVITDIHTAPGVEEDTVLALAASVERYSR  
 HPLADAIREGAKARELHLPDVVEVSERPGQGLTGTVEHLVRITNRRSTLEIDPDSKNYI  
 PVTSSGMESVVLVDDKYAALIRLRDEPRASASEFIAHLPPKKHKVDKLMIIISGDRASEV  
 RYADKVGIDEVHAEASPEDKLNIVNRHNEHGATMFLGDGINDAPAMAVATVGVAMGADSDV  
 TSEAADAVILDSSLERLDDLLHISARMRRIALQSAGGGMALSVIGMILAVFGFLTPLMGA  
 IFQEVIDVLAILNSARVALPRGAISDFDTQEKVS

>RXN01382 TRANSLATE of: rxn01382.seq check: 7830 from: 1 to: 1092  
 MCTNNTGTSGSTSTAAGTGTANEEGTITAAISYELGTNGYDPMTTTTALTVAANWHTLEG  
 LTEIDPATGEVYAALASALPSADATSLDIKLRDGATFHNGDAVTADDVVFSFERVLDPAN  
 NSLYASFIPFIKSVTKKDDTTVTIDLDYATGIIISERLAVVKIVPKSVVEADASGFDANPI  
 GSGPYKMTDNGASKVVKFERNDYNGPRPARAAKMEWQIIPDASTRTNSLQSGSTMAIDS  
 VPYLSIPQLEATSTVESVQGFGLLFAMFSCSEGNPFNDVRNRQAFLYALDMDKIVKTGMS  
 DQATPATSFVQKEHPNYNQASTVYSLDADKAKALFAETGLTSLNLLCTDHDWVKNCTPLI  
 QESL

>RXN01411 TRANSLATE of: rxn01411.seq check: 3735 from: 1 to: 765  
 MLGVGWRIPLFLMAVPLGLIGWWIRTGAQENVRPASERPEAPIKQALRTEWKMMRLVGGFI  
 SCTGLSFYIFTTYMTTFLRSTVGLEGTLVLAGNIIALSMAAIVAPFVGRAIDKFPRRNIM  
 AFATLSTVIMAIIPAYIIAGQGTLTASLIAQVMLGIGAVTANCVTSVMMAEVFQEVTRGTS  
 AGITYNVTYAIFGGSAPFISTALVSWTGSPLAPAVYMIIIALFAFTASRFIPETSPVFVT  
 ATPAIKAPKVLVNP

>RXN01421 TRANSLATE of: rxn01421.seq check: 1863 from: 1 to: 387  
 MTSKSIKGRPNLPSLTGARWLAALAVYFLHALVFLSVYPFQQSELFATIHKFVPMQLGS  
 AGVTFFFILSGFLIYWSNSQLKGMKNVLYYCKRRITKIYPMHLIALPMFIEASAKFTTTG  
 ITWVLILRE

>RXN01602 TRANSLATE of: rxn01602.seq check: 2220 from: 1 to: 1530  
 MAKTHIRLQDLSLSYSTPLITKLNITVSSGQCAVIVGENGRGKTTLLRALAREFPSPAG  
 EILTHGTVAIAHQHPAGDLSVGEICDEAIRDSKNALEELERAGALLETNTAHALDGYQQ  
 ALDAAEVLDAWNAEHRLEKALRSFGAITDRSRALSELISIGQRYRVRRLACLIGGDADILL  
 DEPTNHLDRGALNYLTEAITSHKGVVLVSHDQALIKDVADFIIDIDSTPDGLPRIYHEG  
 FDSYRRQRSALLETWRQDYAAAQTVQQQLQEDLEHARQVRNSSWKPPKGTGKHTRASRAP  
 GVVQALKRAQDALDSKALDVPPAPAPLLLPTLKVRPDKPMVDFSDLFVPHRLRLPGSHSV  
 VSGDKIVITGDNGAGKSTLIEVLSGVLTASGVSANHARTGVLGQESLVGEVPSIARDHA  
 VKWGLLSVEESRFALQEFISIGQRRRLDLAMSLAGNPELLLLDEPSNHLMSHLVSALTEWL  
 DTTAAAVIMVTHDRQLLRDTAHRHIELKS

>RXN01604 TRANSLATE of: rxn01604.seq check: 7962 from: 1 to: 648  
MNTPLLRSSGLSIRDTPFADVEIAPDSGLTLLSTGRESQSSSFSLVLSGRMRASGTIEL  
NGEPIKATKLAKHVALAGIPEIDSLERLVTVRTVREQLAWSSPWYLMVPRDISDSGRWV  
DVEKHLGLNLPKTLIGDLSVLERFKLRIALALLARPEAQLLVDDPDQVRSMELEAEVL  
HALKGVAEDLPVVVVSTNPDFDSLADTALTITGAGN

>RXN01722 TRANSLATE of: rxn01722.seq check: 9580 from: 1 to: 1725  
MLSTMQDVPLSLTRILEYGSTVHGDTLITWGGADGIEQAQQTFSAVGARAAALAHALHD  
SLGITGDQQRVASMLYNCAEHMETMFAVACMGAVFNPLNKQLMNDQIVFILNHSEAEVIA  
DPRMAEQLGELKETPKVRAVVFIGNDFSSAAAHMPEGMKLYSEALLDGRSTVYNWPE  
QDERTAAAICYSTGTSGPPKGVVYSHRSLYLQSLSLRTTDSLAVEHGETFLCCVPIYHVL  
SWGVPAAAFMSGTPLVLPGLDLSAPTLAKIISTTLPRVAHGVPWLWIQLMVHYLKNPPER  
MSLRELYVGGSAVPPIVITMWEQRYGVDVHVWGMTETSTVGTVSRPPSGVSGESRWNYR  
VSQGRFPASLQYRIVNDGQVMASTDRNEGEIQVRGPWVTASYFHPDVEKEGGTASTFRDH  
DVEEENDELFTADGWLRTGDVGSVTSDDGLTIQDRARDVIRSGGEWIYSAQLENLIVATE  
EVVECAVIGFPDDKWVERPLAVTMLYPGIERTRETAERLRDQLRDRLPNWMPLPEYWTFVD  
EVDKTSVGKYDKDLRNHLRNGDFEVIKLGPGKEK

>RXN01732 TRANSLATE of: rxn01732.seq check: 6268 from: 1 to: 1050  
MFKLSKPSKSMRVAVSTLAISTLALVGCSSSSDESSSSSSASSSSDAASQWPESITLSLVP  
STEGEDLAEALAPLTDYLSENLGIEVNGVVASDYAATVEALGADQAQVIITDAGSLYNAI  
EQYDAQLILRDVRFGATSYSAVAYTNNPDKYCDDAPVAASYAASDVMMLYCNGIETEGQA  
ATGEGPAALDALEKIESGDKVALQAATSPAGYQYPIVAMQDLGMDTDSAFVQVPVEGNNN  
AVLSVLNGDAEVSFGFWDARSTVLSEAPNAAEDVAFAYTEMIPNGGVAASKSLPSDLVE  
KLTELMDDYADSSEEAKDVMFDMVGLSDWTADTAQDEITRYGEILKKFSN

>RXN01762 TRANSLATE of: rxn01762.seq check: 8097 from: 1 to: 1536  
MKVNLGIGSYPRRRATVRPESTAIEFEGTSITYGEFSKRVRNLGHALLDLGVAHQDRVAY  
VGFNHPALLEVFFSTNLIGATPVLVNPRLSANEIDYIIQDSGASIVFYGIDLIEHATYLO  
ELHPEIIMVAVEGDEGPGLRRKALIEAASDADIDLEVSDDDLVLMLYTSMTTGRPKGAML  
SHRNLFFNYFNALLSQEIEQGAVLLSTAPLFHIAGLNMTTIPVMMKGGKVIIHREFRAEH  
VLDEIERSKVSSEFMVPAMIDMLSNNHPSFAERDLSSLRAIMVGGSPLSERALRIWQGRDV  
KIVQGFMTETAPGACILEATDTSTHLGTAGRAHFFTDIKLVDPKTGEEVPTGEAGEVLI  
RGPHVMTGYWNRPEDTASALQNGWYHSGDIAIKDEDGYTIKDRIDKMYISGGENIYPAE  
VEQALQELEAVLDAAVIGVDPDERWGETGIAFVSISRESYLTNPPTGPPELRELLGSLVARYK  
LPREIHIIIEELPRNATGKIQKNILRDFTIPVS

>RXN01881 TRANSLATE of: rxn01881.seq check: 7932 from: 1 to: 435  
MANLINLENVSKTWGLKTLDDGVSLGVQTDGRIGVVGLNGGKTTLLEVLTGIEKPDQGR  
VSHNSDLRMAVVTQRAELNDDDTVADVVLGPLEVFEWASNATVRDVLGGLGIVDLGLD  
TKVGKPPFPVGEAPTHQPGRRAGSRP

>RXN01936 TRANSLATE of: rxn01936.seq check: 5923 from: 1 to: 1272  
VSFRDIFADTRPLKEPAFKRLWLGNAVTVIGAQLTVVAVPVQIYQMTGSSGYVGLTGLFG  
LIPLVIFGLYGGSIADAFDKRIVLICTTIGMCVTTAGFWVLTLGNENIWLILLINFSLQQ  
AFFAVNQPTRTAILRSILPIDQLASATSLNMLLMQTGAIVGPLIAGALIPLIGFWLYFL  
DVVSIPTLWAVWSLPSIKPSGKVMKAGFASVVDGLKYLQGPVLLMMVMDLIAMIFGM  
PRALYPEIAAEVNFGGGDAGATMLAFMYSSMAVGAVLGGVLSGVVARISRQGVAVYWCIIA  
WGAVALGGVAIVVSPGAVTAWAWMFIIMMVIGGMADMFSSAVRNAILQQSAAEHVQGR  
QGVWIIIVVGGPRLADVHLGWAAEPLGAGWTVLWGGVAVVVLTAICMVAVPKFWKYEKPK  
ITGI

>RXN01946 TRANSLATE of: rxn01946.seq check: 7246 from: 1 to: 1275  
IRKYSRLEEQFQSLGGYEADAEAAQICDNLGLEARILDQQLKTLSGGQRRRVELAQILFA  
ATNGSGKSKTLLLDPTNHLDDADSIWLRDFLAKHEGGLIMISHDVELLGAVCNKIWYL  
DAVRSEADVYNMGFSKYVDARALDEARRRRERANAEEKKAGALKDQAARLGAKATKAAAK  
QMIARAERMIDNLDEIRVADRAANIVFPEPAPCGKTPNNAKGLTKMYGSLEVFAVGLAI  
DKGSRVVVLGFNGAGKTTLLKLLAGVERTDGEIGIVTGYGLKIGYFAQEHDTIDPKSVW  
QNTIECADADQQLSLRSLGSMFSGEQLDQAGTSLSGGEKTRLALATLVSSRANVLLD  
EPTNNLDPIISREQVLDALRTYTGAIVVLVTHDPGAVKALEPERVIVLPDGTEDLWNDQYME  
IVELA

>RXN01995 TRANSLATE of: rxn01995.seq check: 3763 from: 1 to: 1338  
 MDIRQTINDTAMSRQWFIVFIAVLLNALDGFVDLAMSFTANAVTEEFGLSGSQLGVLLS  
 SALFGMTAGSLLFGPIGDRFGRKNALMIALLFNVVGLVLSATAQSAGQLGVWRLITGIGI  
 GGILACITVVISSEFSNNKNRGMAMSIYAAGYGIGASLGFGAAQLIPTFGWRSVFAAGAI  
 ATGIATIAATFFFLPESVDWLSTRRPAGARDKINYIARRLGKVGTFELPGEQSLSTKKAGL  
 QSYAVLVNKENRGTSIKLWVAFGIVMFGFYFANTWTPKLLVETGMSEQQGIIGGLMLSMG  
 GAFGSLLYGFLTTKFSSRNTLMTFMVLSGLTLILFISSTSVPSIAFASGVVVGMLINGCV  
 AGLYTLSPQLYSAEVRTTGVGAAIGMRVGAISAPLLVGGLLDGWSPTQLYVGVAIVIVI  
 AGATALIGMRTQAVAVEKQPEALATK

>RXN02062 TRANSLATE of: rxn02062.seq check: 5414 from: 1 to: 1170  
 MRVGMMTREYPPEVYGGAGVHVTELTRFMREIAEVDVHCMGAPRDMEGVFVHGVDPALES  
 ANPAIKTLSTGLRMAEAANNVDVHSHSTWYAGLGGHLLAARLHGIPHVATAHSLEPDRPWK  
 REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAAYPRIEPDNVRVVLNGIDTELW  
 QPRPTFDDAEDSVLRSLGVDPQRPIVAFVGRITRQKGVHEHLIKAAALFDESQVLVLCAGA  
 PDTPEIAARTTALVEELQAKREGIFWVQDMLGKDKIQEILTAADTFVCPSIYEPLGIVNL  
 EAMACNTAVVASDVGGIPEVVVDGTTGALVHYDENDVETFERDIAEAVNKMVADRETAAK  
 FGLAGRERAINDFSWATIAQQTIDVYKSLM

>RXN02074 TRANSLATE of: rxn02074.seq check: 7807 from: 1 to: 1623  
 MRSLLRDIPAVGWLITATIVVRTLVVALVIVGIGLLIDVPSPAHSAMLWWVLGATAAAA  
 LLCAEAVLPQRIRARVERSWRRQLAAKNLELNSSSSDDAQLITLATEATSKASTYTMFEL  
 GPYFAVFLAPLTVIAVVGAAISWPIAGILCLGLCVIPFVISWAQRMKGAGAGYGRASGQ  
 LAGVFLESVRTLTGTTMMLNAGQRRQIITQRAENMRSQVMSLLYRNQMLILVTDGVFGVA  
 TTMVAAVFAIGGFFSGSLTLGQAVALLARLLIDPINRMGRFTYTMAGKPSLIAIEKA  
 LATTFDQPTQQGQRHGDGLVNNLKIARDHRDIVHGISFSIPRGSHIADVGPAGKSS  
 VALALSGLLEFDGAIISLGGHNCMLDLRASVSFVPQSPTLFSGSIKSNIDLARTGVDSH  
 IHAALLGEELPADLVGETGKGVSGGQAARISIARGLVKNAIVLDEATAQLDYTNARQ  
 VRHLAKSLECTLVEITHRPSEALDADFIIVLEDGQLTMMDTPSNVSQHNAFFRTAVMEEE  
 Q

>RXN02096 TRANSLATE of: rxn02096.seq check: 3261 from: 1 to: 1692  
 MGLDVSDEQIEHAARLAQAHDIDRLPNKYEEVIGERGLTLGGQRQRIALARAFLAHPK  
 VLVLDATSAIDASTEDRIFQALREELHDVTILIIAHRHSTLELGDVGLVEDGRVTALG  
 PLSEMRDHARFSLMALDFQDSHDPEFTLDNGSLPSQEQLWPEVSTEKQYKILAPAPGRG  
 RGMSMPATPELLAQIEALPAATEETRVDAGRLTSTSGFKLLSLFKQVRWLVAIALLL  
 VGVAADLAFPTLMRAAIDNGVQAQSTSTLWWIAIAGSVVVLWSWAAAINTIITARTGER  
 LLYGLRLRSFVHLLRLSMSYFERTMSGRIMTRMTDIDNLSSFLQSGLAQTVVSVGLIG  
 VVTMLAITDAQLALVALSVVPIIIVLTLIFRRISSRLYTASREQASQVNAVHESIAGLR  
 TAQMHRMEDQVFDNYAGEAEFRRLRVKSQTATIAIYFPGLGALSEIAQALVLGFGALQVT  
 RGDISTGVLVAFVLYMGLMFGPIQQLSQIFDSYQQAAGVFRRITELLATQPSVQIWAPTG  
 TLGRLPRSLYCLTTSPSAIQTIRS

>RXN02148 TRANSLATE of: rxn02148.seq check: 4200 from: 1 to: 1143  
 VSASRKTLLVTNDFFPRIGGIQSYLRDFIATQDPESIVVFASTQNAEEAHAYDKTLDYEV  
 IRWPRSVMLPTPTTAHAMAIEIREREIDNVWFGAAAPLALMAGTAKQAGASKVIASTHGH  
 EVGWSMLPGSRQSLRKIGTEVDVLTYYISQYTLRREKSAFGSHPTFEHLPSGVDVKRFTPA  
 TPEDKSATRKKLGFDTTPVIACNSRLVPRKGQDSLKAMPQVIAARPDAQLLIVSGGRY  
 ESTLRRLATDVSQNVKFLGRLEYQDMINTLAAADIFAMPARTRGGLDVEGLGIVYLEAQ  
 ACGVPVIAGTSGGAPETVTPATGLVVEGSDVDKLSSELLIELDDPIRRAAMGAAGRAHVE  
 AEWSWEIMGERLTNILQSEPR

>RXN02168 TRANSLATE of: rxn02168.seq check: 2810 from: 1 to: 2814  
 VSISSLTPLHSFKEPAILYAGQASAWQQVIADSSSEDHITATHLRELLSRRAKTAPFARQ  
 ITAIVPGSLARLEELTREDAQIGADIDAQPAVSIPIGILLQIAATROLRLDGLDVAAASR  
 LGHSQGI LGVEAVDNEEDVLAFAILLGAAASQFAGKGAHMLSVRGLSREIIQDTIAGVDG  
 VEVSLRNARAHFVVS GKPEALKKAAAALQRAADVYNEDINEKRKGGSLAEPKFDYLDVAI  
 PFHHSSMQDAADLAVEWATTCGLNVNARALAEAILVNPADWVEQIANLKADYVLSLDAGV  
 SRFTAPLLDGRGISLVPAFSAERDNLARPGFHVPTAEDWSEFAPKLVKLPNGEHKVLGTG  
 FSRLTGYSPIVLAMTPTTVDP EIVAAAANAGHWAEMAGGGQYSEEVFTKNKEKLVSLLK



VGRSAQFNSMFFDRYMWNLQFGAQRIVSKARATGTSINGVVVSAGIPEVEEATELINDLN  
ADGFPYVAFKPGTVDQIRATLKIADANPETKIIIIQIEDGHAGGHHSWVNLDDLLLTYYAE  
LRSRKNVVVMIGGGIGTPAKAAYYLTGEWSTD LGFPAMPVDGILVGTAAMATKEATTSPQ  
VKQALVDTPGVDPHDAGGWVGRGDARGGVTSGLSHLHADMYELDNDSSAAASRLISSIDSD  
DYADHREELIEAINKTAKPFFGEVEEMTYAEWIQRWVELAYPTQDPTWDDRFLDLVHRIE  
ARLNEAEHGAITTLFPDHASVENEEEAVEKLLAAYPQAREIQVSARDAAWFGLCRKHHK  
PMPWVPADADLARWWGLDTLWQSQNERYGANSVRVPGPVSVAGIDRVDEPVAELLGRF  
EAACVDALDGEPEEIFARLNEKNEREFLLATPHIVWHGNLIDNPAHVLNEGAFELIEED  
GYWVIRILADS YFDDL PVEQRPYL VQHVDI PVELGDAG

>RXN02233 TRANSLATE of: rxn02233.seq check: 3705 from: 1 to: 1287  
VLVTSTWGWTVHGDGKKIEPGAVVAPKERLSWGRITIGIMQHVIAMFGATLLVPTLTGFP  
VNTTLLFSGLTILFLLITRNLPSYLGSSFAFIAPLTATQVHGIGVQIGGILVAGLVLV  
AIGFVVKAAGKRVIDAVMPPAVTGAIVALIGLNLAPTAAGNFSSQPLVATATLFAILIAT  
VAGRGMIAIRLGILIGVVIGWVFAAITGNLSEGAADTIREAAWFGLPQFHKPEFQLSAILV  
TLPVIIIVLIAENVGHVKAVSEMTGEDLDDLADALIADGFGTTLAGAFGGSGTTTYAENI  
GVMAATR VYSTAA YWVA ACTAIALAFIPKFGALIFTIPAGVLGGACLVLYGLIGMLGIRI  
WQDNKVNFNPNVNL TMAAVALVAGIGNLTTLTVFGVTLEGIAWGSVGIIVLYPIMKRLYLS  
IGEGKNAKF

>RXN02309 TRANSLATE of: rxn02309.seq check: 2713 from: 1 to: 1050  
MSSGRTVPTRSHGLGKEGVSTTGASQVEFGDPELTARINDAMVQVEELLHTELSSGEDFL  
VDIVMHLTRAGGKRFRPMFALLASEFGEKPLSENVIAKAAVVVEITHLATLYHDDVMDEAS  
MRRGVPSANARWDNSVAILAGDILLAHASGLMSQLGTDTVAHFAETFGELVTGQMRETVG  
PRDTPDPIEHYTNVIREKTGVLIASAGYLGAMHAGAAPEHIDALKNFGAAVGMIFQIVDDI  
IDIFSETHESGKTPGTDLREGVFTLPVLYALREDTPVGAELRDILTGPLEDDET VNHVLE  
LLSQSGGRQAALDEVYRYMDIANAELDRLPDSTVKEALRNLATFTVKRVG

>RXN02321 TRANSLATE of: rxn02321.seq check: 7699 from: 1 to: 1629  
MTISSPLIDVANLPDINTTAGKIADLKARRAEAHFPMGEKAVEKVHAAGRLTARERLDYL  
LDEGSFIETDQLARHRTTAFCLGAKRPATDGIVTGWGTIDGREVCIFSQDGTVFGGALGE  
VYGEKMIKIMELAI DTGRPLIGLYEGAGARIQDGAVSLDFISQTFYQNIQASGVIPQISV  
IMGACAGGNAYGPALTD FVVMVDKTSKMFVTGPDVIKTVTGEEITQEELGGATTHMVTAG  
NSHYTAATDEEALDWVQDLVSFLPSNNRSYAPMEDFDEEEGGVEENITADDLKLDEIIPD  
SATVPYDVRDVIECLTDDGEYLEIQADRAENVVIAFGRIEQSVGFVANQPTQFAGCLDI  
DSSEKAARFVRTCDAFNIPIVMLVDVPGFLPGAGQEYGGILRRGAKLLYAYGEATVPKIT  
VTMRKAYGGAYCVMGSKGLGSDINLAWPTAQI AVMGAAGAVGFIYRKELMAADAKGLDTV  
ALAKSFEREYEDHMLNPYHAAERGLIDAVILPSETRGQISRNLRLLLKHKNVTRPARKHGN  
MPL

>RXN02342 TRANSLATE of: rxn02342.seq check: 2806 from: 1 to: 807  
MNVDISRSREPLNVELLKEKLLQNGDFGQVIYEKVTGSTNADLLALAGSGAPNWTVKTVE  
FQDHARGRLGRPWSAPEGSQTIVSVLVQLSIDQVD RIGTIPLAAGLAVMDALNDLGVEGA  
GLKWPNDVQIHGKKLCGILVEATGFDSTPTVVIGWGTNISLTKEELPVPHATSLALEGVE  
VDRTTFLINMLTHLHTRLDQWQGPSVDWLDDYRAVCSSIGQDVRVLLPGDKELLGEAIGV  
ATGGEIRVRDASGTVHTLNAGEITHLRLQ

>RXN02348 TRANSLATE of: rxn02348.seq check: 8038 from: 1 to: 1884  
MLNRMKSARPKSVAPKSGQALLTLGALGVVFGDIGTSPLYSLHTAFSMQHKNKEVTQENV  
YGIISMVLWTITLIVTVKYVMLVTRADNQGQGGILALVALLKNRGHWGKFVAVAGMLGAA  
LFYGDVVITPAISVLSATEGLTVISPSFERFILPVSLAVLIAIFAIQPLGTEKVGKAFGP  
IMLLWFVTLAGLGIPQIIGHPEILQSLSPHWALRLIVAEPFQAFVLLGAVVLTVTGAEL  
YADMGHFGARPIRVAWFVMPALILTYLGQGALVINQPEAVRNPMFYLAPEGLRIPLVI  
LATIATVIASQAVISGAYSLTKQAVNLKLLPRMVIRHTSRKEEGQIYMPLVNGLLFVSVM  
VVVLVFRSSSESLASAYGLAVTGTLVLVSVLYLIYVHTTWKTA LFIVLIGIPEVLLFASN  
TKIHDGGWLP LLIAAVLIVMRTWEWGS DRVNQERAELELPMDKFLEKLDQPHNIGLRK  
VAEVAVFPHGTSDTVPLSLVRCVKDLKLLYREIVIVRIVQEHVPHVPPEERAEMEVLHHA  
PIRVVRVDLHLGYFDEQNLPEHLHAIDPTWDNATYFLSALTLSRLPGKIAGWRDRLYLS  
MERNQASRTESFKLQPSKITITVGTLEHL

>RXN02372 TRANSLATE of: rxn02372.seq check: 3258 from: 1 to: 1887

VPPAPKLAALGLQHVLAIFYAGAVIVPLLIAQSLNLDATTIHLINADLLTCGIATLIQSV  
GIGRHIGVRLPIVQGVTTTAVAPIIAIGLVTDGQGGVASLPAIYGAVIVSGIFTFFAAP  
VFARFLKFFPPVVTGTVLLVMGASLLSVSANDFVNYADGVPAARDLAYGFGTLAVIILAQ  
RFFRGFMGTAVLIGLVGGTAVALILGDANLDEVGNAEAFDITTPFYFGVPEFNAVAIFS  
MIIVMIITMVETTGDVFATGEIVGKRTRRSVDTRALRADGLSTLMGGVMNSFPYTCFAQN  
VGLVRITGVKSRWVAAAAGFMIIILGVLPKAGAVASIPSPVLGGASLALFANVAWVGIO  
TIAKSDLADSRNSVIVTSALGLAMLVSFRPDVAQAFPEWARI FVSSGMSVGAITAILLNL  
LFFHVGRQSGGQVATSKGERINLDAVNKMDRTDFVETFAPLFNSKTWPLETAWESQPPA  
NVTELREAIQVAVLTAPLSDREELIHDYPDMAQLILATEEEAATISQDRGSIGLDDDDV  
DQEKLIITVTEQYRERFNMPYVAYFDTMDSVDTVVAAGLRRLDNSDEQHRQALSEIIEIA  
NDRFDILLADANPARSAFDRKFTETDFLG

>RXN02395 TRANSLATE of: rxn02395.seq check: 9305 from: 1 to: 1890  
MSTNSGNNLPESQESPEEPHYPHDTHPGLVPGISVDAQRNKFGLDKTVFGVTAALILAFI  
AWGISSPDSVSSVSSTMFWSAMTNTGWLLNFVMLIGITMLYIAFSRYGRIKLGTEDEP  
EFSRFSWIAMMFGAGIGVGIFFFGPGSEPLWHYLSPPPHTVEGSTPESLHQALAQSHFHG  
LSAWGLYALVGGALAYSSYRRGRVTLISSTFRSLFGEKTEGIAGRLIDMMAIATLFGTA  
ATLGLSAIQVGQGVQIISGASEITNNILIAIAILTIGFISSVSGVSKGIRYLSNLNIS  
LTLGLVLFVFITGPTLFLNLIPSSVLEYGSEFLSMAGKSLWGEETIEFQAGWTAIFYWA  
WWIAWTPFVGMFIARISGRRTLREFALITMAIPSFILILAFITFGGTAIMNRENVDFD  
GSSSKEQVLFDMFNSLPLYSITPFILIFVLAVFFVTSADSASVVMGMTMSSQGNPAPNKLI  
VVFGLCMMGIAVVMLLTGGESALTGLQNLILIAIPFALVLIVMAIAFIKDLSTDPAAI  
RQRYAKAAISNAVVRGLEEHGDDFELSIEPAEEGRGAGATFDSTADHITDWYQRTDEEGN  
DVDYDFTTGKWADGWTPESTEEGEVDAKKD

>RXN02424 TRANSLATE of: rxn02424.seq check: 9493 from: 1 to: 600  
MTNELTLHHISVSQMDNNCYLLAANGNGLLIDAADDAAALLKLAEDAGVTITKVLTTTHR  
ADHVRALPEVLQKTGATHYAPFLEVPAIPSAVDVELHHGDSIEFEGHVFPISILRGHTPG  
GAVLTAEDIGKTHLFGVDSLFPGGGLKTSSEGFVRLFNDVKERIFDTYDDDSIVWPGHG  
KETTLGAERPQLEIWWERRW

>RXN02442 TRANSLATE of: rxn02442.seq check: 5164 from: 1 to: 849  
MKFFTDALIVPFDVSFISRALVAGCLAAILCSLIGTWVILRRLTFFGDAMSHGLLPGVAT  
ASLLGGNLMFGAAISALIMSAGVWVTSRKSSLSQDVSIGLQFITMLSLGVVIVSHSDSHA  
VDLTSFLFGDILGVRPSDIFIIAIAITVLGGLTIFLFHRQFTALAFDERKAHTLGLNPRFA  
HLLMLALIALATVVSFQVVGTLVLFGLLIGPPATAALLVQDKASISLIMIVASLLGCAEI  
YLGLLISWHASTAAGATITLLSAAIFFATLLTKSAISRLNFTA

>RXN02443 TRANSLATE of: rxn02443.seq check: 7945 from: 1 to: 954  
VILKIDIFNNGELFGASSAKNFRKLLAVPAVAASLAFGITACSAVDDTPDIVVTNIGDV  
VSHIVGDSADVQVLMKPNADPHSFGVSAQDAAAMEHADLIVANGLGLEEGLQSNVDNAKS  
QGVFVLEVGEHIDVIDYSPGVDPDPHFWTDPARMIAATEVIEAELIKELDPSLTESITQSA  
QHYREELVALDEEVTELLSGVAPENRKLVTNHNVFGYLASRFNYTVIDTIIIPGGSTLAAP  
SASDLNDISTAIEDNNVPAIFTDTSSPQRLAEVLASNAGIDVQVVSIFTESLTADGEAP  
TYISMQKINAERIASTLS

>RXN02447 TRANSLATE of: rxn02447.seq check: 8454 from: 1 to: 1095  
TVVPVYLAELAPLEIRGSLTGRNELAIVTGQLLAFVINALIAVTLHGVIDGIWRIMFAVC  
ALPAVALFLGMLRMPESPRWLVNQGRYDDARRVMETVRTPERAKAEMDEIIAVHSENNAA  
LPGVKQSSSQASQGVSSKHTHMSIGEVLNKNWLVRLLIAGIGVAVAQQLTGINAIMYYGT  
RVLEESGMSAEMAVVANIAFGAVAVIGGLIALRNMDRLDRRTTFIIGLSLTTFHLLIAA  
AGTLLPEGNSIRPFAIMILVVGFLVLSMQTFLNVAVVWVLAEIFPVRMKGIGTGISVFCGW  
GINGVLALFFPALVSGVGITFSFLIFAVVGVIALLAFVTKFVPETRGRSLEELDHAFTGQ  
IFKKA

>RXN02487 TRANSLATE of: rxn02487.seq check: 2200 from: 1 to: 1704  
MSAYETKEWLQHYPEWTPHSLEYGDTLLLDVYDNNLAINADKPATYFFGRSQTYGELDKE  
VRKTAAGLRALGVRPGDHVAIILPNCPQHIAAFYAVLKLGAUVIEHNPLYTAHELLEPFK  
DHGARVAIVWDKASPTVEQLRGQTQLETIVSVNMINAMPPLQRLALRLPIPALRKSRESL  
SGAAPNTVPFETLTSAAMGGDGDVSEPTVTKESVALILYTS GTTGRPKGAQLTHGNLF

FNLQKGHWVPGLDKPERMLAALPMFHAYGLTMVGTLVSFIGGEMVLLPTPRIDLIMNV  
MKKHTPTWLPVPTLYEKIVDASEKEGIPIKGVNRAFSGASTLSQRTVERWEKHTGGRLV  
EGYGLTETSPIIVGNPMSDHRQGYVGI PFPDTIVRIANPENLDETM PDGSEGEVLVKGP  
QVFKGYLNQEEATKNSFHGEWYRTGDVGVMEE DGFIRLVARIKEV IITGGFNVP AEVEE  
VLAHPDIEDSAVVGIPREDGSENVAAITLVEGAALDPDGLKEFARKNLTRYKVPRTFY  
HFEEMPRDQMGKIRREVVQAELLKKLGK

>RXN02512 TRANSLATE of: rxn02512.seq check: 4913 from: 1 to: 963  
MKPKDFCTAENWAENLSALGYLAGWRFVRMLPLPIARRVFDLGADLASKSGKGMQLRAN  
LARVVGAENVTOALVKQATRSYARYWLEAFRLPAIARDPELLARLRKGTVGLDLLDES LA  
AGKGVVLTLP HSGNWD MAGAF LISHHGQFTTVAERVKPERLFEAFVEFRESLGFEVLPLT  
GGERPPFEKLKERLTSGGIVCLLGERDLRHSGVETTTFFGEKTSMPAGPAQLAIETGAALH  
VVHPWFDDDGWGLSVSDAVTVDNLSDTVQRIAHLFMANITAH PADWHMLQPLWFGDLDP E  
RLKRSREQTNVHKPVALQEDN

>RXN02515 TRANSLATE of: rxn02515.seq check: 4857 from: 1 to: 756  
MSTLEIRNLHAQVLPSESAEPKEILKGVNLTINSGEIHAIMGPNNGSGKSTLAYTLGGHP  
RYEVTAGEVLLDGENILEMEVDERARAGLFLAMQYPT EIPGVSVANFLRSAATAIRGEAP  
KLREWVKEVRTAQEALAI DPEFSNRSVNEGFSGGEKKRHEVLQDLLKPKFAIMDETDSG  
LDVDALRIVSEGINSYKQETEGGILMITHYKRILNYVKPDFIHFV FANGQIVTTGGAELAD  
KLEADGYDQFIK

>RXN02547 TRANSLATE of: rxn02547.seq check: 8918 from: 1 to: 2139  
LELNNAARLTVDEYPAAREALESAGQRNVEDRTRAVDEFKAADQELSSLSKGSSNIEYRL  
LQVRENLCQDLGVSPRDMPPFAGELIDPNNAEWEPVVQRILGGFAAEMLVPHGLLPRVRDW  
VNAKHLAALLKFNGVVTTG EYKTSRFPADSLIRKVDVVE SPFRDWNQELGKR FNIRCV R  
TPEELSALGPRDQGV TILGVRKFAQQTGDP TTRWEKDDRRKLGDRSTYRLGSTND AKVET  
LRET VKAGKAVVQAADNR IAA NRAELRELERQYQASQEILKVSWAQIDVESADAAIAELD  
RLLEELNNTPEATELSARHEAAKQTLARVSDLLVAAQSEETVASMNLKRAETELKRLES L  
PVAEVSEIEIAREVEKLF LANTRRVHAANVDEQTIALREDLDKQIDANEAE LRRCENQIVG  
ILRSYIETWPANRADLQAEPEFVGEAINRLGELRSDRLAEFTAKFLGLMNEMSTRNLGQI  
SRRLRDARREIEERIEPI NASLAQSEFNEGRFLHIDIRDQSGPIVREFQQLDAATSGDL  
GTSTEKQAFARYALIAEII SKLASHDSADARWRNTVLDTRRHVRFIGLERDS DGATVNTY  
VDSASLSGGQAQKLVFFCLAAALRYQLAEPGAHYPTYATVILDEAFDRADPAFTRQTMNV  
FHSFGFHMVLATPLKLIQTLGDYVGSTIVVSYTEKPNAQGAIQGNSSFSRIEK

>RXN02566 TRANSLATE of: rxn02566.seq check: 3653 from: 1 to: 1209  
MHASSPQPHQRTRVLSGLIFAQIMVGASNGVTLSMGSLAAHLAGASWGGSAATLT TIG  
AAIFS I PLARMVSTYDRRTSLSTGMLLGCVGALLAILGAQFGLFPVLLAFLFLGMSAV  
NLQARFAATDVASEETRGRDLSIVVWSTTIGAIAGPNLFEPSARFSETLGLEQHAGAYLL  
CLFGQLIAIAVWRFTLPKGLKPEATPNAPTEKKRLTPKALQAITSVATAHFSMVGLMSMA  
AIHMQGHGASLTIIGFTISLHVAGMYALSPVFGLLTDKLG RNV TIYSGFAMLATSAAFLI  
IWPEPQWAMITSMILLGLGWSALVGSSTLLVDATPIHHR TYAQGRSDLT MNLAGASGGL  
IAGPLIAMGGMPLLAGVVLAVVALQTVLSFRTRSIEKTPASCF

>RXN02571 TRANSLATE of: rxn02571.seq check: 6786 from: 1 to: 1029  
VVALTQIVGPSGSLTRELEKRYRETPGAVMLTADPRAHITYLRATVAEELAFGLEQRGI  
VPAQMWERVRNIGLGLENLLDRAPAQLSGGQTRRLAIGTVAIL EAPTMLLDDPLSGLDTS  
SRAQLITMLESYEGDVIVA AAKRWLDAPT VYLG DLEELSLPARVEFSGPSRTFSAITGTR  
GQQR RRWWQFNESQPQFQIGPLDITVSAGQVLWLQGPNGSGKSTLLRGLANEPGTEMLQ  
NPSDQVIDSTVANWVPGSNSEEHPLDLSQRELRLAQCDAA LGNNPEVLLADEPDVGLDVG  
GRNAIHQRFADFLNGGALILTCHDET FVAEVAEYAI VKEMGL

>RXN02581 TRANSLATE of: rxn02581.seq check: 7801 from: 1 to: 1860  
MDLDKAIGSFFDENGEINLPPFLT LAAMGEFMYQADIAEGGGDKPRMHFWDFSED RDGKL  
IQYTRNEIDTRIKAVAGRLQQVATLGDRAAILANNSPEYIFSFLGAIYAGMVPVPLYDPN  
EPGHADHLNAV FADSEPVVLTNSKSAGAVRKHFSSLPAAERPRILSVDSLPSLADSYE  
NPMLTEAGRRRLAALRQSAPIDLTAF LQYTS GSTRTPAGVVLTNRSILTNVLQIFSAAQLK  
TPLRLVSWLPLHHD MGII LA AFV TMLGLDNEFMNPRDFVQQPSRWIKQLNRRES DVDVNV  
YTVVPNFAL ELAARYAKPAEGETLDLSALDAIIIGSEPV TENALTTFREAFEPYGLPVQT

LRPSYGLAEASLLVTTTPQ TENRPLISYFDREALAENRVELVEKGNKAVAFVSNGQVAAP  
 QQLVIVDSETGT ELADGQIGEIWTHGENTAAGYLDREEDTAETFRNRLTTRLEENSRAEG  
 AADDNYWMATGDLGVIVDNELYITGR LKDLIVVAGR NHYPQDIEYTVQAASAHIRADSV  
 AFAVPGGDIEKLIILAERDTTANEADDAEEAIRSAVGTAGHVVP EIRILAPDEIARS  
 SSGKIARRVNQRNYIQEQAN

>RXN02595 TRANSLATE of: rxn02595.seq check: 5016 from: 1 to: 1164  
 VIVVAMASIMACLKAARLNNPMKILLLCWRDTTHPQGGGSERYLERVGEFLADQGHEVVF  
 RTAGHTDAPRRSFRDGVRYRSRSGGKFSVYPKAWVAMMLGRVIGTFSKVDVVDTQNGIP  
 FFGKFFSGKPTVLLTHHCHKEQWPVVGRLAKVGLW LIESQIAPRAYKTAPYVTVSEPSAE  
 ELIALGV DQQR IHI VRNGVDPVPLHTPKLDRDGGH AVTLSRLVPHKQIEHAMDVVAALDG  
 VVLDV VESGWWQKELVDYARTLGVS DRVVFHGGQVAEDHKHALLERATIHLMP SRKEGWGL  
 AVTEAAQHGVPTIGYRSSGGLRDSVVDGETGLLVDSKAELISATKTL LIDASLRSKLGAS  
 AKQRAENYKWDTAGAQFEELLGLASKK

>RXN02613 TRANSLATE of: rxn02613.seq check: 5283 from: 1 to: 957  
 MKFKKIALVLAFLGLASCSSASGDPATNADGSIDL SKVT LNIGDQIAGTEQVLQASGEL  
 DDVPYKIEWSSFTSGPPQIEALNAGQIDFAITGNT PPIIGGPTNTKVVSAYNNDALGDVI  
 LVAPDSSITSVADLAGKKVAVARGSSAHGHLIQ QLEKAGVSVDDEINLLQPSDAKAAFO  
 NGQVDAWAVWDPYSSQAELEGAQVLVRGAGLVSGHGFVGASDEALDDPAKEAALADFLDR  
 VADSYEWAEDNTDEWATIFSQESGFDPEASQLNTRSLRHQVPLDES VNTYQNALIDAFVS  
 AGLVEDFN FEDTV DTRFEG

>RXN02614 TRANSLATE of: rxn02614.seq check: 5216 from: 1 to: 729  
 MTATLSLKPAATVRGLRKS YGTKEVLQ GIDLTINC EVTALIGRSGSGKSTILRVLAGLS  
 KEHSGSVEISGNPAVAFQEPRLLPWKT VLDNVT FGLNRTDISWSEAQERASALLAEVKLP  
 DSDAAWPLTL SGGQAQRVSLARALISEPELLL LDEPFGALDALTR LTAQDLLLKT VNTRN  
 LGVLLVTHDVSEAIALADHVLL LDDGAITHSLTVDI PGDRRTHPSFASYTAQLLEWLEIT  
 TPA

>RXN02638 TRANSLATE of: rxn02638.seq check: 9546 from: 1 to: 876  
 MVKRFGFFVEDSLPKVPLHP EESRETFYGR IISAVRTVMKAQDVQISIFGAENIPTTGG  
 ALFASTTLVIMTSFWV VSPAFVRGKRLVR FMAKKEIFDTPVVG TLMRWMKHVSVD RSAGA  
 GSMEDARKRLDAGSLVGIFPEATVSR SFEIKELKTGAVRIADSANVPLLPLIIWGGQRII  
 TKDIERDFGRSHIPVFISVGE PVDASGDPDEATERLYEAMKKLLDETRTAYEQKYGPFEG  
 GELWRPKSLGGGAPTLEQAKMLEIAERERRQAKRAAKVAKKRTTFIRKIFKK

>RXN02662 TRANSLATE of: rxn02662.seq check: 3 from: 1 to: 264  
 MRRKLTTTLENKPGARLGGFRALAPT SKIALVFL LLIFLLAIFAPLIAKYDPLASGTPVQ  
 PPSGEHWFGTDAIGRDIFSRVATAPEPP

>RXN02794 TRANSLATE of: rxn02794.seq check: 5710 from: 1 to: 1074  
 MLLSARTHTSFQELGLNASRRKAINWTLALT VVLIASMFVGV LIGASGTSVFSTWTVISH  
 HLFGT ELGGSDTADAI IWYIRTPRVLLAAI VGAGLALAGAIMQVLVRNMLADPYILGVNS  
 GASCGAAAALLFGVGAGFGDYALQGS AFLGAMAASGLIFFVARAAGRISSTRLLMSGVAI  
 GYMLSAATSFLIFSSDSAEGSRSVLFWLLGSLGLAAWNGPMAIIFLIVGIALALLMVLGP  
 QLDALNSGDETALT LGVSPDRLRILL LVITCLLVGSMVMAGSIGFIGLVIPHLARRFVS  
 GKHRMLPVSALMGAILLIWADIAARTLLAPQEIPIGIITALIGAPFLLILVRRMHTY

>RXN02809 TRANSLATE of: rxn02809.seq check: 5264 from: 1 to: 375  
 NLSVPAALTNALS YLSAEWNNKAAGIVSYGSAMGVRAAEHLRGILSELQIAHVQKTGLLS  
 IFTDFEYPNFKPSEQGISSVDAMLEQLV VVWTKAMSTIRESANVYHLRTPHKS GELPDWDS  
 PLFVF

>RXN02836 TRANSLATE of: rxn02836.seq check: 9870 from: 1 to: 555  
 MTIDEGRRQFEVNVFGAMALTRLVLPHMQKQKWGTIVNITSMGGKIYTPLGGWYHGTFKA  
 LEALSDALRLEVAPFGIDVVVIEPGGIATEWGGIAADNLDAVSKDSAYKRQADAVSKSLR  
 SEANSNRNSPPSVVADAIGKAVTARHPKTRYAIGFGAKPLIASRNILTD RQFDPVITRAT  
 GVPRD

>RXN02922 TRANSLATE of: rxn02922.seq check: 7833 from: 1 to: 1080

MISPQTIIDNLAFLAEIAATAAQREQDREFSRDLAKQLSAGGFTKLRIPEVEFGGLGFSL  
PEAFEVLVAAAAADSNIAGQLRPHFLAVESLLIAPYSEHRTKWLKIAEKGVVIGNALTE  
VGNKPGELKTKIRKEGESYVLSDTKFYSTGSLYADWIQVHAKDEEDQDVFAFVDRDASGV  
VLVDYWDEFGQQLFASGTSFFEKVVVDPLDIVTRDYTAPSAFQALAQSHHLSTLTGISQA  
ITRDIVTYVQNRTRIFSHGSGDLPRFDPQVQVVEVKAKSYAVEKIFQGFQELDLVVD  
KAKAGTATEVDLAADVLSAYQAQLAVAPLVLSQATQAFEVGADALNGGHVAAQYITIGSL

>RXN02923 TRANSLATE of: rxn02923.seq check: 3360 from: 1 to: 738  
LSILLGGTSDIAGEIATLTCHGEDVLAARRPEAAQGLAEDLRQRGATSVHVLSTFDAQV  
LDTHRELVKKTQELAGEISLAVVAFGILGDQERAETDETHAVEIATVDYTAQVSMPLTVLA  
DELRAQTTPAAIVAFSSIAGWRARRPNYVYGSTKAGLDAFCQGLADSLHGTHVRLIARF  
GFVIGSMTTGMKPAPMSVYPRDVAAAVVSAYTSKKRSTTLWIPGRLRVLAWIMRMVPRPV  
WRKMPR

>RXN02929 TRANSLATE of: rxn02929.seq check: 8015 from: 1 to: 1038  
VLKRIFLNPWVATALSIVILGFVVLFSFGSGVIDLSPTAVIRHLSGQDTLTPRDQAIFFD  
IRLPRIIAGVIVGATLAISGASYQAVFRNPLADPYLLGVSAGSGLGVTAVIVGGTVLGFS  
APSIGVIGAAFGVGAVALATLMVSRGVGQGSSTTVILAGVAVAAFASSIQTYYQRHI  
DTVARVYVWMLGNLNVNWMISIFIVAVVAGLCAAVIMSCARLLDVMAGVDVEARTLGVD  
GLVRIGIVIVATLGTAAVVSISGLIGFVGIIIVPHALRLIVGPGHRILLPLSFVWGAIFLV  
LADTAGRTLMAPELPGVVTAALGAPFFLFILRRTSRQRPVKRSA

>RXN02933 TRANSLATE of: rxn02933.seq check: 4913 from: 1 to: 810  
MPLSGKIGGFIVAVFVLAALSFIWTFDFVQAFQERLEGSSLRHLLGTDYGRDVLQ  
IMVGSRTLLVGIIAIAAALIGTPLGIAAGMRGMVETFVMRGADMLAFAALLAIIS  
GAVFGASTWSAMVAIGIAGIPSFARVARAGTLQVTSQDFIAAARLSKVSSARIALRHILP  
NITSMLIVQASVAFALAILAEALSFLGLGTTTPDPSWGRMLQTAQASIGVTPMLAVWPG  
AAIALTVLGFNLFGDGLRDAIDPKREVGRA

>RXN02947 TRANSLATE of: rxn02947.seq check: 6735 from: 1 to: 1314  
MTAAQTKPDLTITAGKLSRLAEAAQAPMGEATVEKVHAAGRKARERIEYLLDEGSF  
VEIDALARHRSKNFGLDAKRPVTDGVVTGYGTIDGRKVCVFSQDGAFFGGALGEVYGEKI  
VKVMDLAIKTGVPPLIGINEGAGARIQEGVVSGLYSQIFYRNTQASGVIPQISLIMGACA  
GGHVYSPALTDFFIVMVDQTSKMFITGPDVIKTVTGEDVTQEELGGAHMHMATSGTSHYSA  
SDDSDALDWRELTSYLPNNRAETPRQEAIDIMIGSIQENINDVDLELDTIIPDSPNQPY  
DMKEVISRIVDDAEFFEIQEDYAENILCGFARVEVRSVGIVANQPTQFAGCLDIKASEKA  
ARFIRTCDAFNIPILEFVDVPGFLPGTNQEFDGIIRRGAKLLYAYAEATVGKITVITRKS  
YGGAYCVMGSKDMGAGLV

>RXN02955 TRANSLATE of: rxn02955.seq check: 3206 from: 1 to: 522  
MMNFKSIVCVTAQVFSRQVLHSPSTWSEELSKLLFVWLSFAGSAFLFGERGHIAVDFA  
RKLVPVSAQRVLQVIVQLLIVVFAILGMIWGGYLAASIAWNQQLTALPLTLGWVYVVIPIA  
GVFIALFAIIDLIEVATGKEEYPLVDESEEPDLDELEAQSAIDSASSAEGRN

>RXN02966 TRANSLATE of: rxn02966.seq check: 4215 from: 1 to: 1407  
MLFERIYEEGLAQASYFIGCQREGKAIIVDARRDIQTYLDLAAKNMVISAVTETHIHAD  
YLSGTRELAAATGAEIFLSGEGGADWQYGFYGTGTTLMHNSTIKLGNITITAKHTPGHTPEH  
LSFLITDGAVSKDPGFMLSGDFVFGVDVGRPDLLDEAAGGVDTRFAGAQQLFHSLKEQFL  
ALPDHIQVYPGHGAGSPCGKALGAIPTTVGYEKANAWWAPYLRSDDEAGFVEELLDGQP  
DAHAYFARMKKQKQGPVAVLSTLSPLVKLEAEVVEKLGSEAVFVDTREQNQVHLGTVVG  
ALNIPRGAKASNFAAWVIDPQKDAQDLIVLAPDANTAADFRDALLRVGIDTVRYFTNSID  
GLPTFVPELISPAELAETNYDALIDIRAKSEFAAGSIPGAQQLSGGSAMWRLNELPAGGT  
LVTFCQSGARNTVVANALRRAGFTVIELEGSYAWEKSAANPKNLQTAV

>RXN02979 TRANSLATE of: rxn02979.seq check: 3131 from: 1 to: 234  
MTAPNTLKQTTLRSEFSCVSKIENKLNGLDGVDAEVKFSSGRILVDHDPKSVSIK  
DLVAAVAEVGYTAKPSAI

>RXN02987 TRANSLATE of: rxn02987.seq check: 9782 from: 1 to: 234  
MTAPATLKNTTLRSDEFTCPSCVAKIENKLNGLDGVNAEVKFSSGRILITHDPQKVSVR  
DLVTAAVAEVGYTAKPSAI

>RXN02991 TRANSLATE of: rxn02991.seq check: 416 from: 1 to: 615  
MANTVRATVLYDAPGPKGRRFNLIITILTVVLGLALLFWIGSMLSGNGQLDANKWTPFIN  
SQTWTTYILPGLWGTLKSAVFSVILALVMGTALGLGRISEIRILRWFCVIIETFRAPV  
LILMIFAYQMFAQYNIVPSSQLAFAAVVFGLTMYNGSVIAEILRSGIASLPKGQKEAAIA  
LGMSSRQTTWSILLPQAVAAMLPAI

>RXN02992 TRANSLATE of: rxn02992.seq check: 8686 from: 1 to: 222  
IVPLGNTLIALTKNTTIASVIGVGEASLLMKATIENHANMLFVVFAIFAVGFMITLTPMG  
LGLGKLSERLAVKK

>RXN02993 TRANSLATE of: rxn02993.seq check: 5702 from: 1 to: 672  
VAEYVNSIADDDKGDHPTIEWRESPSAQRETLIQNGEVDMAATYSINAGRSESVNFGG  
PYLLTHQALLVRQDDRIETLEDLDNGLILCSVSGSTPAQKVVDVLPVQVQLQEYDITYSSC  
VEALSQGNVDALTTDATILFGYSQQYEGDFRVVEMEKDGEPFTDEYYIGLKKDDQEGTD  
AINAALERMYADGTFQRLLTENLGEDSVVVEEGTPGDLSFLDAS

>RXN02996 TRANSLATE of: rxn02996.seq check: 4074 from: 1 to: 669  
MNNNVSDQKLSGKELAALEKQAAKTLELGDKKWIYLIAGVVLFAIALVLPHIRGVMGWQVL  
TSLNVAEDAGITLGEYGFYWLGTIGVFLLSLGTVVFKRTWMAWISWIFSCVTLVFAVFAI  
WMRQTTTSTQVNFVNIGMMLAVIAAILAVWGLSSVILARSDRQMEIAEMRAENPDLDGVA  
ATQRALLEQQQSNPEDNPLLVDORRARIARRREREQDAQGEQA

>RXN03060 TRANSLATE of: rxn03060.seq check: 6265 from: 1 to: 852  
MSNPAASTPANNSDDVAKENWDSSFTPKTDIDSSQPVNNSTGEAAARAVNLYKAYGQGD  
TVTALDHVNVEFEKNKFTAIMGPSGSGKSTLMHCMAGLDAATGGSAFIGDSDLRLKDK  
MTSLRRDRLGFIQSFNLVPTLTASENITLPTDIAGRKIDQSWFDEITSRLGLTERLKH  
PAELSGGQQQVRVACARALVSRPEIIFGDEPTGNLDSNSSREVLDILRTAVDQDDQTVVIV  
THDAKAASYADRVIFLADGRIVNQLFDPTIEEILATMNGIEDIA

>RXN03065 TRANSLATE of: rxn03065.seq check: 80 from: 1 to: 393  
MISIGTDLVHISAFAEQLAQPGSSFMVFSAGERRKANERQASRYAEHLAGRWAAKESFI  
KAWSQAIYGQPPVIAEEAVVWRDIEVRADAWGRVAIELAPELAADVRESIGEFSSSLIS  
HDGDYAVERAC

>RXN03079 TRANSLATE of: rxn03079.seq check: 7356 from: 1 to: 1017  
LSRTGVSKPKLTAPVVIIGTLVLLIIAFTASMLGPTVPLNELATNPVVTDIRAPRII  
IAALVGAALAVSGAIMQTVFHNPLADPGIVGVSSGAAVAALVLAIVTGASFFGQWTVFPA  
FVGALVTVAVVYLIASSRAMDGRGADPATLVLVGMAITAFGLAVISSATANAPQDSELS  
VTFWNLGDLVSRTWEHVGVAIPIIIVGLILAIGGSRDNLNLLLGDSSTAQTSGLNVNRARI  
ILLALAAALLTATAVAVSGTITFVGLVPHLVRIVLGADHRALLPAAAILGATFVIVSDTV  
ARMIFSPIVLQTVGVVAFIGSPIFLYLLLSMRKRRGLGL

>RXN03080 TRANSLATE of: rxn03080.seq check: 3725 from: 1 to: 780  
MPQLVEIRDNLNVEFSPSRHAVKNVSFSAPAGKVTALIGPNGAGKSTALSAIAGLVESTGEV  
MVGSGVASKSAKARARLLSLVPQNTLRIIGFSARDVVAMGRYPHRGRFAVETDADRAT  
DDALRAINALDIAEQPVNELSGGQQQLIHIGRALAQDTAVVLLDEPVSALDLRHQVEVLQ  
LLRARANSGETTVIVVLHDLNHVARWCDHAVLMADGEVVSQGDIREVLEPATLSTVYGLPI  
AVRDDPETSSLRVIPHPNPF

>RXN03081 TRANSLATE of: rxn03081.seq check: 3848 from: 1 to: 459  
MKKSLIAIVASALVLSGCTSDSSDSSGTSGETTSITTSVAAADGAFPRVTLDSSIT  
LESKPERIAVLTPEAASLVLPITGADRVVMTAEMDTADEETAALASQVEYQVKNNGRLDP  
EQVVAGDPDLVIVSARFDTEQGTIDILEGLNVP

>RXN03082 TRANSLATE of: rxn03082.seq check: 9827 from: 1 to: 321  
MVMPEASMLTGLIREAGGTPVVDLSLGAAGTITADPEQVVAMAPEIIIIQDFQKGRENFA  
NFLSNPALANVPAIENDKIFYADTVTTGVTAGTDITGLQQAEMLS

>RXN03084 TRANSLATE of: rxn03084.seq check: 3960 from: 1 to: 918  
MSSRRKLSSALIVLLAAALPLTACSSSSSEEEASTSSATREFTDAHGTTEVPENPQRVVVL

EPLELDTAIALGITPVGA AVANNVTGIPAYLGVDGIEPVGTVSEPNIEAIAALEPDLILG  
TDSRHA EIYDRLESIAPTVFMTHVDPWKDNVVFIGDALGKKQESEDLIQGFNDKCEEIK  
SEHDVEGKTVNMIRPRDEQTMSTLYGPTSFAGSSLEACGLTIPDQEWKDDLQADIAPENFM  
LATADYVFVTTATDVTDENELFEVIRENREQFPSTLVDTSYWVSGVGPLGGSKVLEDIDA  
FLDAQQ

>RXN03095 TRANSLATE of: rxn03095.seq check: 5530 from: 1 to: 369  
MNADKKMCGMNPDSQYVELAVEVFGLLADATRVRIILALRNSGELSVNHLADIVDKSPAA  
VSQHLARLRMARIVSTRQEGQRVIFYKLTNEHASQLVSDAIFQAEHTIADGQTPPHHRER  
EQS

>RXN03097 TRANSLATE of: rxn03097.seq check: 8524 from: 1 to: 555  
ISASAGAIGWLILEYIFKKTSSLGLLLGALAGLVITPAAGYVTYLSATIMALIGGICC  
YIVINYIKVKLKYHDALDAFGIHGVGGIIGAVLTAVFQSKKANPDIENGFIYTGDIHIIL  
VQILCVTAVVIFSIVMTFIIAKVIKLITPLSVTEQETNIGLDKIVHGEHAYFEGELNRFN  
KHIRY

>RXN03103 TRANSLATE of: rxn03103.seq check: 5397 from: 1 to: 243  
MSAKRTFTRIGAILGATALAGVTLTACGDSSGGDGFLLAIENGSVNVGTTYDQPGGLGRN  
PDNSMSGLDVEDVAEYVIQLHR

>RXN03109 TRANSLATE of: rxn03109.seq check: 7721 from: 1 to: 654  
MUVKEVDVEKQKAGRVPGAIAKRRTVRIVLFVALGAIVIAASLWSILVGQYTIPIRDLPA  
ILASGPTGAQTMAEQVWQIRMPRIVLGLLVGAALGVAGALLQAVFSNPLAEPSTIIGVTS  
GAGVGAAVIVFNLTFLGTSTVAVGAFITAVITTILVYQLARSGRVQVINLILTGIIN  
AVSGALTSVLDLHRADELPRRNIFCRWVPHGSHGARQR

>RXN03110 TRANSLATE of: rxn03110.seq check: 3354 from: 1 to: 1362  
VLIERIYDEDLAQASYFIGCQAHNTAVVVDPRRDIAVYLDMAKKNMEIVGVTETHIAD  
YLSGTRELAATNATMYVSGEGGADWQYEFDAERICDGEIRLGNLVLTAHVTPGHTPEH  
LSFLLKDGAFADPEGFMLTGDFVFAGDLGRPDLLEAAGGVDTRFEGARQMFKSLKEKFL  
TLPDHIQIFPGHSGSACGKALGSVPSTTLGYERQFAWWGKYLEADDEQGFIDELLEGQP  
DAPAYFGRMKRQNRQGAIPMAGARELLPQLEASDLHDVIVVDTRSADEVHQGTAVAGVNIP  
AGNSMAKFGSWTVDPKDSRALVLLAASQIGAMEMWDMVRVGDVNAVGFITNFDGVDLV  
APQTVSPDQLDELEYDLLLLDVRNRSEVEEGYIPGALHINGASVLWNLEKLPRDGKIVSYC  
KSGTRSSIAASTLRNAGFDVVELQGSYDNWVRHN

>RXN03111 TRANSLATE of: rxn03111.seq check: 3457 from: 1 to: 6036  
LKTLLRAAVAAGAGTNVSDIVERANALLALVADDLIGTLFPFGFDPVAVANNSEDPAFDTAQ  
SAVSVPGIFVSQIATLDSLEAQRLDVDQAVSSIGHSGVGLGVHLLNDATRADELVAIAQL  
IGAAITRTARMTGLIAQGDNMPLMSIAGISREQLQQAIDAACAEPVPAEIRPVIGLRNSRD  
SYVLVGRPDNDARVVKVIEAMAAKDKKAIEDKLRGGSFAFSPRITPLKVQAAFFHPAMNMA  
VEQTVAWATTAGLDVELTREIAADVLVNPVDWVARVNEAYEAGARWFLDVGPDGGIVKLT  
ANILEGRGADSFYVGDAAGQAKIFDAGMAPELPVDYQEFAPRVEHVDGTPRLVTKFTELT  
GRTPMMLAGMTPPTTVDPPIVAAAANGGHWAEAGGGQVTPELLETHIAQLTDMLEPGINA  
QFNSMFLDPYLWKMQIGGKRLVPKARANGASIDGIVITAGIPEKDEAVLVKELMRDGF  
WIAFKPGAQVNSVLAIKEVPELPIIIQIEGGVAGGHHSWEDLDELLIATYGVKVRALD  
NVVLCVGGGIGSPERAADYVTGSWSTSYGLPAMPVDGILVGTAAMATKEATTSQAVKELL  
VSTQGSDEWVPAGGAKNGMASGRSQLGADIHEIDNSFAKAGRLLDEVAGDETAVQARRDE  
IIEAIGKTAKVYFGDIGSMTYEQWLNRYLELSGPVDGQWIDASWAARFAQMLERAERLI  
EQDHGQFEPSTVEDGVDKLVAAYPHAATDLLTPADVAVFLGLCRTPGKPVNFVPVIDKD  
VRRWWRSDSLWQSHDDRYTADQVAII PGVVAVAGITKANEPVADLLDRFVDATIERIDEH  
DSRSRDIMGKVLSSPGTFWAGRNIPSVIHSGLHADKWSRSEFEAFHSPTGANLVYEDAEH  
AMLTVPPLAGSTAFGTTELKIRFTSPIDALPSAVPLVTQEDAEAAANGELTRIAAGGTLAT  
VNNGTATWETSVDAGVIADYNNVTAGYLPASVVPAPHTAPDVLVGRAPVAFVAVKSAVIP  
GTDSASVVEGMLSLVHLEHHIVLKS DVPTDGALKVSATADEVVDLTLGRLVIVRAEIA  
EGNLIATLAERFAIRGRKGNVARTNTSALPTTVDTPRSARAVATVVAPESMRPFAVISG  
DRNPIHVS DVAASLAGLPVIVHGMWTSAGELIAGAAFNDEQIQTPAAKVVEYTATMLA  
PVLPGEEIEFSVERS AVDNRP GMGEVRTVTATVNGNLVLTATAVVAAPSTFYAFPGQGIQ  
SQGMGEARRNSQAARAIWDRADAHTRNKLGF SIVEIVENNPREVTVAGEKFFHPDGVLY  
LTQFTQVGMATLGVAQIAEMREAHALNQRAYFAGHSVGEYNALAAAYAGVLSLESVLEIVY

RRGLTMHRLVDRDENGSLSNYALAALRPNMGLTADNVFDYVASVSEASGEFLEIVNYNLA  
GLQYAVAGTQAGLAALRADVENRAPGQRAFILIPGIDVPFHSSKLRDGVGAFREHLDSLI  
PAELDLVDLVGRYIPNLVARPFELTEEFVASMAEVVESTYVNEILADFKAAASADKQKLAR  
TLIELLAWQFASPVRWIETQDLLIKGLQAERFVEVGVGSAPTLANMMGQTLRLPQYADA  
TIEVLNIERDRPVVFATDEVVREVAVEETPAAPAETTETPATPATPAPVAAAAPATGGPR  
PDDISFTPSDATEMLIAIWTKVRPDQMGATDSIETLVEGVSSRRNQLLLDLGVEFGLGAI  
DGAADAELGDLKVTVSKMAKGYKAFGPVLSDAAADALRRLTGPTGKRPGYIAERVTGTWE  
LGQGWADHVVAEUVIGAREGASLRGGDLASLSPASPASASDLDSLIDAAVQAVASRRGVA  
VSLPSAGGAAGGVVDSAAALGEFAEQVTGHDGVLAQAARTILTQLGLDKPATVSVEDTAE  
DLYELVSKELGSDWPRQVAPSFDEEKVVLDDRWDASAREDL SALLANSQQLISMSQAQA  
KLLQHKLNSLDLMISQLGSRTKLLGLRRQCCG

>RXN03126 TRANSLATE of: rxn03126.seq check: 1681 from: 1 to: 894  
VQEESKQKDLQADIARITAVKSDTVPNSSQSMTFGAAWNNDIVRGFKQHELWLQLGWQDIKQ  
RYRRSVLGPLWITIATGVMALALGLLYSVLFKIPAEFLPHVTVGLIINWFISGCIKEGS  
DIFIDNEGLIKQLPSALSVHVYRLVWKQALFLAHLNLVIWVILMMIFPRPLGWDVLLIIPA  
MFLLVINGVWVVMFFGIIATRYRDVSPLEAGTQLLFYVTPIVWMTSTLQSQSAEIGNRA  
RLAELNPLYHYLEIVRAPMVGADLPAYHWWIVLAFTFVGLGLALLAMKQWRFRVSYWV

>RXN03132 TRANSLATE of: rxn03132.seq check: 1885 from: 1 to: 420  
MNVNQQLGARTAMNHPETATVLRISDMVSTETNPRRKSRLQLIYATASAWPHYPIAHA  
AQAAVQLARPMRVFELQSFEGVKHALHHIDLPALEWDIMGFPEPDTLPILLSDLRDPF  
YATTAVPPQSTPRSAHRSTH

>RXN03157 TRANSLATE of: rxn03157.seq check: 7995 from: 1 to: 438  
GHLDIVTRAAAQFSEVTILVTANPNKNSGLFTVAERMDLIRESTAHLDNVKVDTWASLLV  
DYTTEHGIGALVKGLRSSLDYEYELPMAQMNRRRLTGVDTFLLTDEKYGYSSTLCKEVA  
RFGGDVSGLLPEVVAKAVTEKYSNQH

>RXN03160 TRANSLATE of: rxn03160.seq check: 3585 from: 1 to: 468  
VNRIAEIARSFGVLGFSAGGPTAHLGYFRTEFVERRRWLDDRQYSEIVALSQLLPGPS  
SQVGMMLGYHRAGFSGMAIAWLMFTWPSLALMAAFALLFDATSASWTLGLLAAVAVVFK  
RSHRAWRGSMASPTGRRPPSGVGLGASRVLGPPQRG

>RXN03164 TRANSLATE of: rxn03164.seq check: 9986 from: 1 to: 870  
MIYRRVGNISGLKLPALISLGLWHNFGDDKPLSTQRSIIHRAFDRGVTHFDLANNYGPPAGS  
AETNFGRIREDLKSHRDELISSKAGWDMWPGPYGFGGSRKYLVSLLDQSLTRLGLDYV  
DIFYHHRPDPDTPLEETMYALRDIVASGKALYVGISSYGPETAEAAEFMAEEGCPLLIH  
QPSYSIINRWVEEPGDDGENLLQSAANGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG  
KSLSEGMLNVNNIDMVRKLNIDIAQERQSLAQMALAWVLREQREYAGLP

>RXN03183 TRANSLATE of: rxn03183.seq check: 124 from: 1 to: 417  
EAEATAGKFEVQPLVGKDGVGSTLGGYNNGINVNSENKATARDFIEFIINEENQTFAD  
NSFPPVLASIYDDESLEQYPYLPALKESLENAAPRPVSPFYPAISKAIQDNAYAALNGN  
VDVDQATTDMKAAIENASS

>RXC00354 translate of: RXC00354.seq check: 80 from: 1 to: 813  
MGKLLFVDIGGTLDDYSNEVPRSAVDAIRKARAKGHRVYLSSGRSSAEVTSQWLDIGVDGLIG  
ANGGYVESAQESVFHRRLSGEETRHIVEWLYNRGLEFYLESNNGLYASRGFREASKPVLSRLS  
EKTDVTVDSMYPDMFWGASLDRDDVNKISYIFNSQEDLDAAREAFPNEHTTWGGQTGALF  
GTIGVSVNKKIGVDRLLKYL NADRANTIAFGDSDEDL SFEASAYGVAMGEATESLKAAADL  
VTDVAGQDGLRNAFLKLELIDA

>RXC01748 translate of: RXC01748.seq check: 8341 from: 1 to: 780  
MADAKKQADKAAKKQVRAAKKAQRKETRSQMWQVFNMQRKQDKALIPLLLLAILGIPLVFLIGLIWGG  
QWWMLPIGIAAGVVAAMFIFTRRVERDVYKRAEQQGAAGWAVENLRSGVGMTWRTKTAVAVTTQMDAV  
HRVIGLCGVVLVGEPSPHRLKPMLAQQKKRLNRVAPGPVVEIITGNNEGQTPIAKLQRELVKLPRNYK  
KNDVAALAARIEAMDNVGNAPGGSPLPKGPLPKGASMSGMNRARRRQAERKGEA

>RXC01749 translate of: RXC01749 .seq check: 7382 from: 1 to: 1617



VSFLVENQLLALVVIMTVGLLLGRIKIFGFRLGVAAVLFVGLALSTIEPDISVPSLIYVVGLSLFVYTI  
GLEAGPGFFTSMTKTGLRNNALTLGAI IATTALAWALITVLNIDAASGAGMLTGALTNTPMAAVVDAL  
PSLIDDTGQLHLIAELPVVAYSLAYPLGLVILVLSIAIFSSVFKVDHNKEAEEAGVAVQELKGRRI RVT  
VADLPALENIPELLNLHVIVSRVERDGEQFIPLYGEHARIGDVLTVVGADDELNRAEKAIGELIDGDPY  
SNVELDYRRIFVSNTAVVGTPLSKLQPLFKDMLITRIRRGDTDLVASSDMTLQLGDRVRVVPAPAEKLRE  
ATQLLGDSYKKLSDFNLLPLAAGLMIGVLVGMVEFPLPGSSSLKLG NAGGPLVVALLLGMINRTGKFVW  
QIPYGANLALRQLGITLFLAAIGTSAGAGFRSAISDPQSLTIIGFGALLTLFISITVLFVGHKLMKIPF  
GETAGILAGTQTHPAVLSYVSDASRNELPAMGYTSVYPLAMIAKILAAQTLLFLLI

>RXC01971 translate of: RXC01971.seq check: 8803 from: 1 to: 831  
MSKKKPRPIPVPAQFIPGLIDAHTHLASCGLDLAGLVERAKEAGVEKLCTVGDGLAEAEALAEAAQQFG  
NVFAACAIHPTKADQLDGAARALTQMAADPNCVAIGETGLDSYWKHDPEDTAALDVQEEALRWHIDL  
AISADKPLMIHNREADADLMRVLADAPPPKDTILHCFSSPLDVAKEALDRGYVLSFAGNVTFKRNEELR  
EAARIAPISQILIEDAPYMTPEPFRGSRNEPSLIGHTALCIAEVRGMAVEDVAAALNENFDRVYGVTN  
L

>RXC02697 translate of: RXC02697.seq check: 1664 from: 1 to: 1527  
MTLFQRLTNPVVLGGLAGVLLLLGSFGGAIRYRGGVLDALGLNFLAFGHAQGISNTVLWVGQLLLLIGA  
WVHLGRRLFKKKVADDTADAADLGLVKRTLYAMVVPLIFAAPMMSRDVSYLMQGAMLRDGFDPYTEGA  
AVNPGPMLLEVSHDWRNTTTPYGPLHLWIGDMITTVGDNVTLG VVAYKILSIIGLAVTGWSIVRIAQH  
FGANPAIALWIGVANPVMIIHMIGGMHNEESLMVGLVSVGLLLALKKR FVAGVALIAVAVSLKATAAIAL  
PFVWVWIGMHFAGFLATKKGKDSPTLKQQVPAFFATGAAGVAVTG VVVSAITWASGASGWWISEISGNS  
KVINPLAFPSLVASVITMVAEVFVDDFDYNAVNVVRSISMLIMLGLLVCCWVLFQRNERRAVTGTA  
YAVAFVNSVTLTPWYASLISLLGTFKPPMWLIRFAAGASVFIALMFTGSGNHQLYNIVTVIIAAIIAW  
LATVVIFDDTDPATTATEKPSPTVS

>RXS00148 translate of: RXS00148.seq check: 5482 from: 1 to: 2211  
MTSIPNFSDIPLTAETRASESHNVDAKGVWNTPEGIDVKRVFTQADRDEAQAAGHPVDSLPGQKPFMRG  
PYPTMYTNQPWITIRQYAGFSTAESAFAFYRRNLAAQKGLSVAFDLATHRGYDSDNERVVGDVGMAGVA  
IDSILDMRQLFDGIDLSSSVSMTMNGAVLPILAFYI VAAEEQGVGPEQLAGTIQNDILKEFMVRNTYI  
YPPKPSMRIISNIFEYTSKMPRFNSISISGYHIQEAGATADLEAYTLADGIEYIRAGKEVGLDVKF  
APRLSFFWGISMYTFMEIAKLRAGRLLWSELVAKFDPKNAKSQSLRTHSQTSGWSLTAQDVYNNVART  
IEAMAATQGHQTSLHTNALDEALALPTDFSARIARNTQLLLQQESGTVRPVDPWAGSYVVEWLTNELAN  
RARKHIDEVEEAGGMAQATAQGI PKLRIEESAARTQARIDSGRQALIGVNRYVAEEDEEIEVLKVDNTK  
VRAEQLAKLAQLKAERNDAEVKAALDALTAAARNEHKEPGDLDQNLKLAVDAARAKATIGEISDALEV  
VFGHEAEIRTLSGVYKDEVGKEGTVSNERAIALADAFEAEGRPRIFIAKMGQDGHDRGQKVVASA  
YADLGMDVDVGPLFQTPAEAAARAADVDVHVGMSSLAAGHLTLLPELKKELAAALGRDDILVTVGGVIP  
PGDFQDLYDMGAAAIYPSGTVIAESAIDLITRLAAHLGFDLDVDVNE

>RXS00149 translate of: RXS00149.seq check: 63 from: 1 to: 1848  
LTDLTKTAVPEELSENLETWYKAVAGVFARTQKKDIGDIAVDVWKKLIVTTPDGVDINPLYTRADESQR  
KFTEVPGEFFPTRGTTVDGERVWGVTETFGHDS PKNINA AVLNALNSGTTTTLGFEEFSEEFTAADLKVA  
LEGVYLNMAPLLIHAGGSTSEVAAALYTLAEAGTFFAALTGLSRPLTAQVDGSHSDTIEEAVQLAVNA  
SKRANVRAILVDGSSFSNQGASDAQEIGLSIAAGVDYVRRLLVDAGLSTEAAALKQVAFRAVTFDEQFAQI  
SKLRVARRLWARVCEVLGFPELAVAPQHAVTARAMFSQRDPWVNMLRSTVAFAAGVGGATDVEVRTFD  
DAIPDGVPVGSRNFAHRIARNTNLLLEESHLGHVVDPAAGGSYFVESFTDDLAEKAWAVFSGIEAEGGY  
SAACASGTVTAMLDQTWEQTRADVSRKKKLTGINEFPNLAESPLPADRRVEPAGVRRWAADFEALRNR  
SDAFLEKNGARPQITMIPLGPLSKHNIRTGFTSNLLASGGIEAINPGQLVPGTDAFAEAAQAAGIVVVC  
GTDQEYAETGEGAVEKLREAGVERILLAGAPKSFEGSAHAPDGYLNMTIDAAATLADLLDALGA

>RXS00948 translate of: RXS00948.seq check: 5347 from: 1 to: 1119  
MANVVLVDRMEPLVSKLFTPIQIRDITIPNRVWMSMCTYS AATGSGLPDTHQAHYAARAAGGVGLVM  
VEATGVNVPVAPISPVDLGLWSDQIEPFSRVTAAIRAGGAVPAVQLAHAGRKASTDAPWNGGGYVGPET  
NGWETVGPSPPLAFPLPAPRELTVSEIQEVVQQFAGAAVRADQAGFDVVEIHAAGHYLLHNLSPISNK  
RTDSYGGSLENRARIIVLEVIDAIRAVWPEEKPVFMRISTTDWVEENPQDDRESWTLSQSRQLALWASEH  
GVDLIDASSGGLDIVPIPHDRDYQTAKAADLHASTGVTVAAGRIDDAQTAHNLVDSGDVNAVFLGRPL  
LKDPSSWANQAALALGAEPYVHQYDYVL

>RXS01166 translate of: RXS01166.seq check: 5407 from: 1 to: 1305  
MGYTNLNDTRVL RAGSCDAWRTMSPLVQQGSEAVFRRIMGLSRRPDRKPGFDDVPFHGAAVRVPGLKH  
GTLVNAAPLKVLGARGEPNPASSYRFEYITGDSAGRAITATGAVLFSTRPWTGTGPRPAIAMAPSTQGVA

QHCDPSHTCAIGLNAFYDKPFDAAIAYELPVILWFLAHGLDVVFIDYPRDPATGVQYYCDSIAAAKSL  
DAVLASRQLGLSPEAPLGLWGFSQGGGATGWAAQLQDYAPDVRPKAAVVGAPPVDLFRVLDTVDGGLLT  
GVIAYAIAGLAVNSSEMFEIIMSVLNERGVSDVLKNITSCAGGSLLASGYSSSRGWTHQGTPLADILDD  
LPLVVAEFGKQKLGRVAPEIPVLLWGSKNDDVIPIDPIRELRDSWADKGTPLTWHEsqAPRVPGRTGLN  
HFGPYFRNLEKYSGLWIDHLV

>RXS01746 translate of: RXS01746.seq check: 830 from: 1 to: 753  
MTAPRDPFFPADLSIRASAEPiEQRLGLIDYQEAWDYQAELATRRANDEIPDQLLILEHPSVYTAGKR  
TQPEDLPTNGLPVINADRGGRTIWHGPGQLVIYPIIKLADPIDVVDYVRRLEEALIQVVGDMGVAGAGR  
IDGRSGVWVPAHDGWVDSKVAAIGIRITRGVAMHGVAINCNDTDFYEHIIPCGIADAGLSTLSRELKR  
DVSVEELVEPSIRALDDALAGRLVVS DHSFGSAPDPTKNLPKRG

>RXS01747 translate of: RXS01747.seq check: 6480 from: 1 to: 1044  
VTIAPEGRRLLRVEARNSETPIETKPRWIRNQVKNQPEYQDMKERVAGASLHTVCQEAGCPNIHECWES  
REATFLIGGANCSRRCDFCMINSARPEPLDRGEPLRVAESVREMQLNYSTITGVTRDDLDDEGAWLYSE  
VVRKIHENPHTGVENLVPDFSGKKDLLQEVFESRPEVFAHNVETVPRIFKRIRPAFRYERSLDVIRQA  
RDFGLVTKSNLILGMGETKEEITEALQDLHDAGCDIITITQYLRPGPLFHPPIERWVKPEEFLEHADA  
EMGFAAVMSGPLVRSSYRAGRLYAQAMEFRGEEIPAHLAHLKDTSGGSTAQEASTLLERYGASEDTPV  
SFN

>RXS01879 translate of: RXS01879.seq check: 6847 from: 1 to: 933  
VKITAKAWAKTNLHLGVGPAHDDGFHELMTVFQTIDLFDTVTTLTDEELVEEGSVVKQLSVTGARGVP  
EDASNLAWRAVDALVKRRAEKTPLSAVSLHISKIPVAGGMAGGSADAAATLRAVDWIGPFGEDTLL  
VAAELGSDVPFCLLGGTMRGTGRGEQLVDMLTRGKLHWVVAAMAHGLSTPEVFKKHDELNPESHMDISD  
LSAALLTGNTAEVGQWLHNDLTSAAALSLRPELRSVLQEGIRSGAHAGIVSGSGPTTVFLCESEHKAQDV  
KEALIDAGQVYAAYTATGPAASTADQGAHILTVS

>RXS02023 translate of: RXS02023.seq check: 8728 from: 1 to: 768  
MAPKQTPSPEKNRNLVGPVLQRRQTEGTFDQRLLEMRADHNWKHADPWRVLRIQSEFVAGFDALHEMPK  
AVTVFGSARIKEDHPYKAGVELGEKLVAADYAVVTGGGPGMEAPNKGASEANGLSVGLGIELPHEQH  
LNPYVDLGLNFRYFFARKTMFLKYSQAFVCLPGGFGTLDELFEVLCMVQTKVNPFPVILIGTEFWAGL  
VDWIRHRLVEEGMIDEKDVDRLMLVTDLDLQAVKFIVDAHAGLDVARLHN

>RXS02106 translate of: RXS02106.seq check: 9598 from: 1 to: 1056  
MNNHFELKVPGGKLVVDVTTDLDSIADVKSIGDFFLEPDEAFFALGRALQGASVGDNTRDLQAKLDAA  
LAEYDDVELHGFSTADIALAVRRVAVTGAQDFTDYEWELHHPGVLPPTPLNVALDELLEDQVAGQRGPTM  
RIWDWDDRATVIGSFQSYVNEINQEGVNEHGVTVVRMSGGGAMFMEGGNCITYSLYAPESLVAGLSYE  
QSYEYLDWRVIAALKTHDWDVAYVPINDITSTGGKIGGAAQKRRSGAVLHHVTMSYDIDADMMTQVLR  
GKVKISDKGLRSKRRVDPLRRQTGASREQIIDTLKSTFSARYGAQEVELSDEDAAGHDLVKTKYATE  
EWTKRVQ

>RXS02228 translate of: RXS02228.seq check: 9755 from: 1 to: 903  
VVTPIAVVGPTASGKSALGIALAHKLDGEVNVNDSMQLYKGM DIGTAKLTVEEREGIAHHQLDVWDVTE  
TASVARFQSDAVADVEDIMSRGKTPILVGGSMLYVQSLVDDWQFPPTDSAVRARFEARLADIGVEALHA  
ELTQLDPEAAAVIESNDPRRTVRALEVIELTGQPFQASQPPKDAPPRWGTRIIGLKTTPPEWLNPRIEQR  
TARMFEQGFVAEVEHLVQQGLIADSTAGRAIGYSQVLAAMAGEMTWEDAFERTVTGTRRYVRRQRSWFN  
RDHRVSWVDASGDPTAQALEILGLQ

>RXS03212 translate of: RXS03212.seq check: 3878 from: 1 to: 1452  
ASLNWSVIVPALVIVLATVVGIGFKDSFTNFASSALSAVVDNLGWAFILFGTVFVFFIVVIAASKFGT  
IRLGRIDEAPEFRTVSWISMFAAGMGIGLMFYGTTEPLTFYRNGVPGHDEHNVGVAMSTTMFHWTLHP  
WAIYAIIVGLAIAYSTFRVGRKQLLSSAFVPLIGEKGAEGWLGLKIDILAIATVFGTACSLGLGALQIG  
AGLSAANIIEDPSDWTIVGIVSVLTLAFIFSAISGVGKGIQYLSNANMVLAAALLAIFVFFVVGPTVSILN  
LLPGSIGNYLSNFFQMAGRTAMSADGTAGEWLGSWTIFYWAWWISWSPFVGMFLARISGRSIREFILG  
VLLVPAGVSTVWFSIFGGTAIVFEQNGESIWDGAAEEQLFGLLHALPGGQIMGIIAMILLGTFFITS  
DSASTVMGTMSQHGGQLEANKWVTAAGVATAAIGLTLTLLSGGDNALSNLQNVITIVAATPFLFVIGLMF

>RXS03220 translate of: RXS03220.seq check: 3878 from: 1 to: 960  
MGLREILSSKWLVRILLVGIGLGVAQQLTGINSIMYYGQVVLIEAGFSENAALIANVAPGVIAVVGAFI  
ALWMMDGINRRRTTLITGYSLTTISHVLIGIASVAFVPGDPLRPVILTLVVVFGSMQTFLNVATWVML

SELFPLAMRGFAIGISVFFLWIANAFGLFFPTIMEAVGLTGTFMFAGIGVVALIFIYTQVPETRGR  
LEEIDEDVTSGVIFNKDIRKGKVH